

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 13:19:17 ; Search time 362.925 Seconds
(without alignments)
822.038 Million cell updates/sec

Title: US-10-646-873-42

Perfect score: 3583
Sequence: 1 MDRVTRYPILGIPQAHKGTG.....HKNNMAERWESRIVASEDD 679

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21:*

- 1: geneeqp1980s:*
- 2: geneeqp1908s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003s:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*
- 9: geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3583	100.0	679	2	AAW79676 Human CS1
2	3583	100.0	679	4	AAE07319 Human CS
3	3583	100.0	679	6	ADA26379 Predicted
4	3583	100.0	679	8	ADN17172 CS198 pro
5	3583	100.0	692	8	AdX97562 Pancreat
6	3579	99.9	679	4	AAW78590 Human pro
7	3559	99.3	679	7	ADG14341 Human NC2
8	3503.5	97.8	672	4	AAW79574 Human pro
9	1132	31.6	215	2	AAW79681 Human CS1
10	1132	31.6	215	4	AAE07324 Human CS
11	1132	31.6	215	6	ADA26384 Synthetic
12	1132	31.6	215	8	ADN17177 CS198 pro
13	839	23.4	172	4	AAW73987 Human col
14	236	6.6	43	8	ABO60042 Human gen
15	205	5.7	910	7	ABM85635 Human pro
16	205	5.7	913	7	ADJ70212 Human hea
17	205	5.7	1103	7	ADD45973 Human pro
18	205	5.7	1103	8	ADJ75439 Marker ge
19	205	5.7	1103	8	ADJ75352 Marker ge
20	205	5.7	1103	8	ADP54378 Human pro
21	205	5.7	1103	8	ADP55745 Human pro
22	205	5.7	1103	8	ADP23410 PRO poly
23	205	5.7	1103	8	ADP23408 PRO poly
24	205	5.7	1103	9	ADY14898 PRO poly

25	205	5.7	1103	9	ADY18598	ADY18598 PRO poly
26	199.5	5.6	948	6	ADA55374	ADA55374 Human pro
27	195.5	5.5	917	6	ABP75463	ABP75463 Human sec
28	195.5	5.5	1090	9	ADY14900	ADY14900 PRO poly
29	190	5.3	57	4	AAW75071	AAW75071 Human col
30	189	5.3	36	2	AAW79677	AAW79677 Synthetic
31	189	5.3	36	4	AAE07320	AAE07320 Human CS
32	189	5.3	36	6	ADA26380	ADA26380 Synthetic
33	189	5.3	36	8	ADN17173	ADN17173 CS198 pep
34	180	5.0	3149	7	ADJ70520	ADJ70520 Human hea
35	177	4.9	3262	7	ADB79961	ADB79961 Mouse ser
36	177	4.9	3262	9	ADV97841	ADV97841 Murine pr
37	176.5	4.9	1321	9	ADV97797	ADV97797 Murine pr
38	175	4.9	35	2	AAW7679	AAW7679 Synthetic
39	175	4.9	35	2	AAE07322	AAE07322 Human CS
40	175	4.9	35	6	ADA26382	ADA26382 Synthetic
41	175	4.9	35	8	ADN17175	ADN17175 CS198 pep
42	175	4.9	1008	7	ABO80673	ABO80673 Pseudomon
43	173	4.8	2468	6	ABR64281	ABR64281 Angiogene
44	173	4.8	2468	7	ADE62723	ADE62723 Human pro
45	173	4.8	2468	7	ADE62719	ADE62719 Human pro

ALIGNMENTS

RESULT 1
AAW79676 standard; protein; 679 AA.
ID AAW79676

AC AAW79676;
DT 11-JAN-1999 (first entry)
DE Human CS198 protein.

XX Gastric/intestinal tract; GI tract; cancer; disease; detection; CS198;
XX human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
XX gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
XX pancreatitis.

OS Homo sapiens.
XX W09844159-A1.
XX 08-OCT-1998.

XX 30-MAR-1998; 98MO-US006251.
XX PF 30-MAR-1997; 97US-00828855.
XX PR 31-MAR-1997; 97US-00828855.

XX (ABBO) ABBOTT LAB.
XX Billing-Medel PA, Cohen M, Colpites TL, Friedman PV, Gordon J;
XX Granada EX, Hayden M, Hodges SC, Klags MR, Kratochvil JD;
XX Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 1998-542714/46.

PT New gastrointestinal polynucleotides, CS198, and their detection - used
PT for developing products for the diagnosis and treatment of
PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
PS Claim 26; Page 100-102; 127pp; English.

CC This sequence represents the human CS198 protein which is used in a
CC method to detect the presence of a target CS198 polynucleotide in a test
CC sample. The CS198 gene is useful as a marker for gastrointestinal (GI)
CC tract disorders. The methods and products can be used in detecting,
CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
CC or determining the predisposition to diseases and conditions of the GI
CC tract, such as GI tract cancer, Barrett's oesophagus, gastric ulcer,
CC gastritis, leiomyoma, polyp, Crohn's disease, ulcerative colitis, and

CC pancreatictis
XX Sequence 679 AA;

Query Match 100.0%; Score 3583; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 9,9e-290;
Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRVTRYPILIGIPQAHKGTGLVLDGDTSYTHLVCMGPEASGCODEPQTMPTDHRQAQG 60
DB 1 MDRVTRYPILIGIPQAHKGTGLVLDGDTSYTHLVCMGPEASGCODEPQTMPTDHRQAQG 60
QY 61 VORQGVSYVHAATGQPSRGLSHENREDEGMQVYRIGARDAHQGRPTMALRPDEGDKE 120
DB 61 VORQGVSYVHAATGQPSRGLSHENREDEGMQVYRIGARDAHQGRPTMALRPDEGDKE 120
QY 121 MKTVRLDAGDADPRRLCDLEREMAVIQGQAVRKSSTVATLQGTIPDHGDPPTPGPRSTP 180
DB 121 MKTVRLDAGDADPRRLCDLEREMAVIQGQAVRKSSTVATLQGTIPDHGDPPTPGPRSTP 180
QY 181 LEEVNVNREQIDFLAARQFLSLQANKGAPHSPPARTPGTTPGASQAPKAKNKHILA 240
DB 181 LEEVNVNREQIDFLAARQFLSLQANKGAPHSPPARTPGTTPGASQAPKAKNKHILA 240
QY 241 NGHVVPIKPYQKGVREENKRAVPTMASVQVNDPGSLASVESPGTPKETPIREIRILA 300
DB 241 NGHVVPIKPYQKGVREENKRAVPTMASVQVNDPGSLASVESPGTPKETPIREIRILA 300
QY 301 QERADLREQRLQATDHQELVEIPTRPLITKLSLITAPRRERGRPSLYVQORDIVQETQ 360
DB 301 QERADLREQRLQATDHQELVEIPTRPLITKLSLITAPRRERGRPSLYVQORDIVQETQ 360
QY 361 REEDHRRRGHLVGRASPDMWSEGOPLRRLSSDLSLSPAPARADPAPEVRKNRI 420
DB 361 REEDHRRRGHLVGRASPDMWSEGOPLRRLSSDLSLSPAPARADPAPEVRKNRI 420
QY 421 PPDAVQPLSPGTQLEFSAFGAFGKPSLSLTAEKATSPKATWSPPHLSSESGKPLST 480
DB 421 PPDAVQPLSPGTQLEFSAFGAFGKPSLSLTAEKATSPKATWSPPHLSSESGKPLST 480
QY 481 KOEASKEPRGCPQANRGVWMEYFLRLRLFRADPEQQAQVPHYWGEVAGADALRLQK 540
DB 481 KOEASKEPRGCPQANRGVWMEYFLRLRLFRADPEQQAQVPHYWGEVAGADALRLQK 540
QY 541 SOSDGLERERESVLRQEVAEERRNLPFEVSPPTDENSDONSRSQASGITGSYS 600
DB 541 SOSDGLERERESVLRQEVAEERRNLPFEVSPPTDENSDONSRSQASGITGSYS 600
QY 601 VSESPFSPILHSHVAVTVEPVDASAPPGQRKEQWYAGINPSDGINSEVLRAIRVTRH 660
DB 601 VSESPFSPILHSHVAVTVEPVDASAPPGQRKEQWYAGINPSDGINSEVLRAIRVTRH 660
QY 661 KNMAERWESRIYASEDD 679
DB 661 KNMAERWESRIYASEDD 679

RESULT 2
AAE07319 ID AAE07319 standard; protein; 679 AA.
XX
XX AAE07319;
XX 06-NOV-2001 (first entry)
XX
XX Human CS 198 protein.
XX
XX CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
XX gastritis; Crohn's disease; ulcerative colitis; pancreaticitis;
XX Barrett's oesophagus; gene therapy; drug screening; human.
XX
XX Homo sapiens.
XX

FH Key Location/Qualifiers
FT Misc-difference 353 /note="Encoded by CGGN"
XX
XX US2001010904-A1.
XX
XX 02-AUG-2001.
XX
XX 30-MAR-1998; 98US-00050516.
XX
XX 31-MAR-1997; 97US-00828855.
XX
XX (BILL/) BILLINGEL P A.
XX (COHE/) COHEN M.
XX (COLP/) COLPITTS T L.
XX (FRIE/) FRIEDMAN P N.
XX (GORD/) GORDON J.
XX (GRAN/) GRANADOS E N.
XX (HAYD/) HAYDEN M.
XX (HODG/) HODGES S C.
XX (KLAS/) KLAS M R.
XX (KRAT/) KRATOCHVIL J D.
XX (ROBE/) ROBERTS-RAPP L.
XX (RUSS/) RUSSELL J C.
XX (STRO/) STROUPE S D.
XX
XX Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX Granados EN, Hayden M, Hodges SC, Kلاس MR, Kratochvil JD;
XX Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 2001-496163/54.
XX N-PSDB; AAD13637.
XX
XX Detecting the presence of target CS 198 polynucleotide, useful for
XX detecting or diagnosing diseases of the gastrointestinal tract, comprises
XX contacting test sample with at least one CS 198-specific polynucleotide.
XX
XX Claim 17; Page 49-51; 68pp; English.
XX
XX The invention relates to a method of detecting the presence of a target
XX CS 198 polynucleotide comprising contacting the test sample with at least
XX one CS 198-specific polynucleotide. The method is useful for detecting
XX diseases of the gastrointestinal (GI) tract organs, particularly cancer.
XX The CS 198 polynucleotides, polypeptides and antibodies are useful for
XX detecting, diagnosing, staging, monitoring, prognosticating, preventing,
XX treating or determining predisposition to diseases and conditions of the
XX GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
XX ulcerative colitis, pancreaticitis and Barrett's oesophagus. The CS 198
XX polypeptides are useful as standards or reagents in diagnostic
XX immunosays, as components or as target sites for various therapies.
XX Antibodies directed against at least one epitope contained within these
XX polypeptides are useful as delivery agents for therapeutic agents, in
XX diagnostic tests and for screening for conditions or diseases associated
XX with CS 198, particularly cancer. Monoclonal antibodies may also be used
XX for the generation of chimeric antibodies for therapeutic use. The CS 198
XX polynucleotide is also useful in gene therapy and drug screening. The
XX method of the invention provides an alternative, non-surgical diagnostic
XX method capable of detecting early stage GI tract disease such as cancer.
XX The present sequence is human CS 198 polypeptide
XX
XX Sequence 679 AA;
XX

Query Match 100.0%; Score 3583; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 9,9e-290;
Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRVTRYPILIGIPQAHKGTGLVLDGDTSYTHLVCMGPEASGCODEPQTMPTDHRQAQG 60
DB 1 MDRVTRYPILIGIPQAHKGTGLVLDGDTSYTHLVCMGPEASGCODEPQTMPTDHRQAQG 60
QY 61 VORQGVSYVHAATGQPSRGLSHENREDEGMQVYRIGARDAHQGRPTMALRPDEGDKE 120
DB 61 VORQGVSYVHAATGQPSRGLSHENREDEGMQVYRIGARDAHQGRPTMALRPDEGDKE 120

QY 481 KOEASKPRGCPQANRGVWMEYFRLRLFRAPDEPOQAQVPHVWMEVAGAPALRLQK 540
DB 481 KOEASKPRGCPQANRGVWMEYFRLRLFRAPDEPOQAQVPHVWMEVAGAPALRLQK 540
QY 541 SQSSDLLERERESVLRREQVAAERERNALEPEVSPPTDENSDONSRSQASGITGSYS 600
DB 541 SQSSDLLERERESVLRREQVAAERERNALEPEVSPPTDENSDONSRSQASGITGSYS 600
QY 601 VSESPFSPPIHLHSNVATWEDPVDSAPPGQRKKEQWYAGINPSDGINSEVLEAIRVTRH 660
DB 601 VSESPFSPPIHLHSNVATWEDPVDSAPPGQRKKEQWYAGINPSDGINSEVLEAIRVTRH 660
QY 661 KNMAAERESRIYASEED 679
DB 661 KNMAAERESRIYASEED 679

RESULT 4
ADN17172
ID ADN17172 standard; protein; 679 AA.
AC ADN17172;
DT 17-JUN-2004 (first entry)
DE CS198 protein #1.
KM Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.
XX Unidentified.
OS US2004043406-A1.
PN 04-MAR-2004.
PD 22-AUG-2003; 2003US-00646873.
PF 31-MAR-1997; 97US-00828855.
PR 30-MAR-1998; 98US-00050516.
XX (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M A.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUSJ/) RUSSELL J C.
PA (STRO/) STROUPE S D.
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados BN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;
PI Robert-Rapp L, Russell JC, Stroupe SD;
XX WPI; 2004-313754/29.
DR GENBANK; D87440.
XX
PT Diagnosing diseases such as cancer of the gastrointestinal tract, by
PT detecting aberrant expression or activity of the CS198 polypeptide, and
PT associated treatment methods.
PS Claim 17; SEQ ID NO 42; 679P; English.
XX
CC The invention relates to reagents and methods for detecting diseases of
CC the gastrointestinal (GI) tract. The method involves detecting the
CC presence of target CS198 polynucleotide in the test sample. The methods
CC and compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the CS198 polypeptide, such as cancer

CC of the gastrointestinal tract. These are also useful in gene therapy. The
CC present sequence is a CS198 protein used to illustrate the method of the
CC invention.
XX
SQ Sequence 679 AA;
Query Match 100.0%; Score 3583; DB 8; Length 679;
Best Local Similarity 100.0%; Pred. No. 9,9e-290;
Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDRVTRYPILGIPQAHRTGLVIDGTSYTHLVCMGPEASGQDEPQTPTDHRQOG 60
DB 1 MDRVTRYPILGIPQAHRTGLVIDGTSYTHLVCMGPEASGQDEPQTPTDHRQOG 60
QY 61 VORQGVSYVHAATGQSPRGHSENREDGKQVYRLGAADALQGRFTWALRPEDGDK 120
DB 61 VORQGVSYVHAATGQSPRGHSENREDGKQVYRLGAADALQGRFTWALRPEDGDK 120
QY 121 MKTYRLDAGDADPRRLCDLEREMAVIQGQAVKSSVTATLQGTPDHDPRTPPRSTP 180
DB 121 MKTYRLDAGDADPRRLCDLEREMAVIQGQAVKSSVTATLQGTPDHDPRTPPRSTP 180
QY 181 LEENVVDREQIDPLAARQFLSLBQANKGAPHSSPARGTPTGASQAPKAFNKCHLA 240
DB 181 LEENVVDREQIDPLAARQFLSLBQANKGAPHSSPARGTPTGASQAPKAFNKCHLA 240
QY 241 NGHVVPYIKPVQKGVRENNVRAVPTWASVOVDDPGSLASVSPGPKETPIRETRLA 300
DB 241 NGHVVPYIKPVQKGVRENNVRAVPTWASVOVDDPGSLASVSPGPKETPIRETRLA 300
QY 301 QERADLREORGLROATDQELVEIPTRPLTLTKSLITABRRERGRPSLYVQDIOVETQ 360
DB 301 QERADLREORGLROATDQELVEIPTRPLTLTKSLITABRRERGRPSLYVQDIOVETQ 360
QY 361 REEDHRRREGLVHVGASTPDMVSEGPQGLRALSSDSITSPADPARAADPAPEYRKVRI 420
DB 361 REEDHRRREGLVHVGASTPDMVSEGPQGLRALSSDSITSPADPARAADPAPEYRKVRI 420
QY 421 PPDAYOPLYSPGTPOLEFSFAGAFGKPSLSLTAEAKAATPKATMTSPRHLSESGKPLST 480
DB 421 PPDAYOPLYSPGTPOLEFSFAGAFGKPSLSLTAEAKAATPKATMTSPRHLSESGKPLST 480
QY 481 KOEASKPRGCPQANRGVWMEYFRLRLFRAPDEPOQAQVPHVWMEVAGAPALRLQK 540
DB 481 KOEASKPRGCPQANRGVWMEYFRLRLFRAPDEPOQAQVPHVWMEVAGAPALRLQK 540
QY 541 SQSSDLLERERESVLRREQVAAERERNALEPEVSPPTDENSDONSRSQASGITGSYS 600
DB 541 SQSSDLLERERESVLRREQVAAERERNALEPEVSPPTDENSDONSRSQASGITGSYS 600
QY 601 VSESPFSPPIHLHSNVATWEDPVDSAPPGQRKKEQWYAGINPSDGINSEVLEAIRVTRH 660
DB 601 VSESPFSPPIHLHSNVATWEDPVDSAPPGQRKKEQWYAGINPSDGINSEVLEAIRVTRH 660
QY 661 KNMAAERESRIYASEED 679
DB 661 KNMAAERESRIYASEED 679

RESULT 5
ADX97562
ID ADX97562 standard; protein; 692 AA.
AC ADX97562;
DT 21-APR-2005 (first entry)
XX
XX Pancreatic cancer associated human protein, SEQ ID 110.
XX pancreas tumor; cytostatic.
KM Homo sapiens.
OS
XX

PN BP1471075-A2.
 XX
 PD 27-OCT-2004.
 XX
 PF 31-MAR-2004, 2004EP-00090124.
 XX
 PR 31-MAR-2003, 2003DE-01015834.
 XX
 PA (HINZ/) HINZMANN B.
 PA (ROSE/) ROSENTHAL A.
 PA (PILAI/) PILARSKY C.
 PA (DAHL/) DAHL E.
 PA (SPEC/) SPECHT T.
 PA (LICH/) LICHTNER R.
 XX
 PI Rosenthal A, Pilarsky C, Dahl E, Specht T, Bruemendorf T,
 PI Lichtner R, Staud E, Roepcke S, Li X,
 DR WPI, 2004-768082/76.
 DR N-PSDB, ADX97491.
 XX
 PT New nucleic acid differentially expressed in pancreatic tumor tissue, for
 PT use as diagnostic agents and in screening for therapeutic agents.
 XX
 PS Claim 2, SEQ ID NO 110, 28bp, German.
 XX
 CC The invention relates to a novel human nucleic acid sequence of the
 CC pancreas and its encoded protein. The invention further comprises:
 CC proteins and peptides, preferably isolated, that contain a sequence
 CC encoded by the novel nucleic acid, and methods for diagnosis and
 CC treatment of pancreatic cancer, using a substance that inhibits or binds
 CC to the protein or its DNA, including: an antisense oligonucleotide, short
 CC interfering RNA or ribozyme directed against the pancreatic protein, an
 CC organic molecule, particularly having a molecular weight below 5000,
 CC especially 300, that binds to the pancreatic DNA, an aptamer or
 CC (monoclonal) antibody, preferably human or humanized, that binds to the
 CC pancreatic DNA, or an anti-idiotypic antibody raised against the
 CC monoclonal antibody, any of which may be derivatized with a reporter
 CC group, cytotoxic compound, immunostimulant and/or radioisotope. The novel
 CC human pancreatic protein and their encoding DNA have cytostatic
 CC activity. The novel sequences are useful for inhibiting transcription
 CC and/or expression of genes and proteins associated with pancreatic
 CC cancer. This sequence represents one of the novel human pancreatic
 CC proteins of the invention. Note: This sequence is not shown in the
 CC specification, it has been electronically downloaded from a DVD-ROM
 CC provided with this specification by the European Patent Office.
 XX
 SQ Sequence 692 AA;
 Query Match 100.0%; Score 3583; DB 8; Length 692;
 Best Local Similarity 100.0%; Pred. No. 1e-289;
 Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 QERADLRBGRGLRQATDHOELVEIPTRPLTKSLITAPRRGRPSLYVQORDI VQETO 360
 DB 314 QERADLRBGRGLRQATDHOELVEIPTRPLTKSLITAPRRGRPSLYVQORDI VQETO 373
 QY 361 REEDHRRRGGLVGRASTPDWVSEGPQPLRLDSSDITLSPAPARADPAPEYKVNRI 420
 DB 374 REEDHRRRGGLVGRASTPDWVSEGPQPLRLDSSDITLSPAPARADPAPEYKVNRI 433
 QY 421 PPDAYOPLTSPGTQLEFSARFAGCKPSLSSTAARAKATSPKATMSPPHLSSESGKPLST 480
 DB 434 PPDAYOPLTSPGTQLEFSARFAGCKPSLSSTAARAKATSPKATMSPPHLSSESGKPLST 493
 QY 481 KOEASKPRGCGPOANRGVVRMEYFRLRLRRAPDEPOQAQVPHVGMVEVAGAPALRLQK 540
 DB 494 KOEASKPRGCGPOANRGVVRMEYFRLRLRRAPDEPOQAQVPHVGMVEVAGAPALRLQK 553
 QY 541 SOSDLERERESVLRQEVAAEERNNALFEEVSPPTDENSDONSRSQASGITGSYS 600
 DB 554 SOSDLERERESVLRQEVAAEERNNALFEEVSPPTDENSDONSRSQASGITGSYS 613
 QY 601 VSESPFEPPIHLHSVAVTVEDPVDSAPPGQKQWYAGINPSGINSVLEALRTVRH 660
 DB 614 VSESPFEPPIHLHSVAVTVEDPVDSAPPGQKQWYAGINPSGINSVLEALRTVRH 673
 QY 661 KNAMERWESRITYASEED 679
 DB 674 KNAMERWESRITYASEED 692
 RESULT 6
 AAM78590
 ID AAM78590 standard; protein; 679 AA.
 XX
 AC AAM78590;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 1252.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US004098.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 PA (HYSE-) HYSQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
 PI Ma Y, Zhao Qa, Wang D, Zhang J, Ren F, Chen R, Wang ZW,
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 DR WPI, 2001-476283/51.
 DR N-PSDB; AAK51723.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX

PS Claim 20; Page 3512-3514; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoietic regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukemia, nervous system disorders, arthritis and
CC inflammation. Note: Record for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication

XX Sequence 679 AA;

Query Match 99.9%; Score 3579; DB 4; Length 679;

Best Local Similarity 99.9%; Pred. No. 2,1e-289; Mismatches 1; Indels 0; Gaps 0;

Matches 678; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDRVTRYPILGIPQAHNGTGLVLDGDTSYTHLVCMGPEASGWDGPOTWPTDHRQQG 60
DB 1 MDRVTRYPILGIPQAHNGTGLVLDGDTSYTHLVCMGPEASGWDGPOTWPTDHRQQG 60
QY 61 VORQGVSYVHAATGQSPRGLSHENREDEGMQVYRLGARDAGQRTWALRPEDGDKX 120
DB 61 VORQGVSYVHAATGQSPRGLSHENREDEGMQVYRLGARDAGQRTWALRPEDGDKX 120
QY 121 MKTYRLDAGDADPRRLCDLERERNAVIOGQAVKSSVTATLQGTDPHGDPRTPPSTP 180
DB 121 MKTYRLDAGDADPRRLCDLERERNAVIOGQAVKSSVTATLQGTDPHGDPRTPPSTP 180
QY 181 LEENVVDREQIDFLAARQFLSLFOANKGAPHSPPAGTTPGASQAPKFNKPHLA 240
DB 181 LEENVVDREQIDFLAARQFLSLFOANKGAPHSPPAGTTPGASQAPKFNKPHLA 240
QY 241 NGHVVPKIPQVKGAVREENKRAVPTWASVQVDDPGSLASVSPGPKETPIERETRLA 300
DB 241 NGHVVPKIPQVKGAVREENKRAVPTWASVQVDDPGSLASVSPGPKETPIERETRLA 300
QY 301 QERADLREORGLROATDHOELVEIPTRLTLTLTAPRRRGPSLYVQDIOVETQ 360
DB 301 QERADLREORGLROATDHOELVEIPTRLTLTLTAPRRRGPSLYVQDIOVETQ 360
QY 361 REEDHREGLHVGRASPTDWTSEGGPQGLRALSSDLSLSPAPARADPAEVRKNRI 420
DB 361 REEDHREGLHVGRASPTDWTSEGGPQGLRALSSDLSLSPAPARADPAEVRKNRI 420
QY 421 PPDAVQPLSPGTQLEFSAGFAGKPSLSLTAEKATSPKATWSPRHLSSESGKPLST 480
DB 421 PPDAVQPLSPGTQLEFSAGFAGKPSLSLTAEKATSPKATWSPRHLSSESGKPLST 480
QY 481 KOEASKPRGCGPOANRGVWRWEYFRLRLRRADEPOQAQVPHWGEVAGALRLQK 540
DB 481 KOEASKPRGCGPOANRGVWRWEYFRLRLRRADEPOQAQVPHWGEVAGALRLQK 540
QY 541 SOSDDLREERESVLRBOEVAEERRNALPPEVSPPTDENSQNSRSSQASGITGSYS 600
DB 541 SOSDDLREERESVLRBOEVAEERRNALPPEVSPPTDENSQNSRSSQASGITGSYS 600
QY 601 VSEBPPSPHILHNSVANTVEDPVDSAPRGQRKEQWAGINPDSGINSETLRIYTRH 660
DB 601 VSEBPPSPHILHNSVANTVEDPVDSAPRGQRKEQWAGINPDSGINSETLRIYTRH 660
QY 661 KNAAMERESRIYASEDD 679
DB 661 KNAAMERESRIYASEDD 679

RESULT 7
ADG14341

ID ADG14341 standard; protein; 679 AA.

XX ADG14341;

AC ADG14341;

DT 26-FEB-2004 (first entry)

XX Human NC2.

XX Human NC2.

XX Human NC1; NC2; NC3; PHH1; pancreas beta-cell; insulin; antidiabetic;
KW neuroprotective.

XX Homo sapiens.

XX WO2003078631-A1.

XX 25-SEP-2003.

XX 06-MAR-2003; 2003WO-JP002620.

XX 15-MAR-2002; 2002JP-00071592.

XX (KANF) KANEKA CORP.

XX Niwa H, Yamashita K;

XX WPI; 2003-767524/72.

XX N-PSDB; ADG14344.

XX Familial persistent hyperinsulinemic hypoglycemia of infancy (PHH1)
PT patient-expressed genes for detecting and screening e.g. proliferative
PT insulin-producing cells in treatment of PHH1.

XX Claim 1; SEQ ID NO 2; 34pp; Japanese.

CC The present invention relates to human NC1, NC2 and NC3 proteins and
CC coding sequences (ADG14340-ADG14345). The coding sequences are useful for
CC detecting and screening proliferative insulin-producing cells as well as
CC differentiation and proliferation of such cells and their precursors as
CC analogous cells in treatment of e.g. PHH1 and diseases due to
CC differentiation/proliferation abnormality, diseases of the nervous system
CC and pancreas. The coding sequences are also useful as spontaneous NC1, NC2 and
CC NC3 were isolated from the pancreas of PHH1 patients, which were used in
CC testing for the detection of proliferative insulin-producing cells or
CC pancreas beta-cells by Northern analysis.

XX Sequence 679 AA;

Query Match 99.3%; Score 3559; DB 7; Length 679;

Best Local Similarity 99.1%; Pred. No. 1e-287; Mismatches 2; Indels 0; Gaps 0;

Matches 673; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDRVTRYPILGIPQAHNGTGLVLDGDTSYTHLVCMGPEASGWDGPOTWPTDHRQQG 60
DB 1 MDRVTRYPILGIPQAHNGTGLVLDGDTSYTHLVCMGPEASGWDGPOTWPTDHRQQG 60
QY 61 VORQGVSYVHAATGQSPRGLSHENREDEGMQVYRLGARDAGQRTWALRPEDGDKX 120
DB 61 VORQGVSYVHAATGQSPRGLSHENREDEGMQVYRLGARDAGQRTWALRPEDGDKX 120
QY 121 MKTYRLDAGDADPRRLCDLERERNAVIOGQAVKSSVTATLQGTDPHGDPRTPPSTP 180
DB 121 MKTYRLDAGDADPRRLCDLERERNAVIOGQAVKSSVTATLQGTDPHGDPRTPPSTP 180
QY 181 LEENVVDREQIDFLAARQFLSLFOANKGAPHSPPAGTTPGASQAPKFNKPHLA 240
DB 181 LEENVVDREQIDFLAARQFLSLFOANKGAPHSPPAGTTPGASQAPKFNKPHLA 240
QY 241 NGHVVPKIPQVKGAVREENKRAVPTWASVQVDDPGSLASVSPGPKETPIERETRLA 300
DB 241 NGHVVPKIPQVKGAVREENKRAVPTWASVQVDDPGSLASVSPGPKETPIERETRLA 300
QY 301 QERADLREORGLROATDHOELVEIPTRLTLTLTAPRRRGPSLYVQDIOVETQ 360
DB 301 QERADLREORGLROATDHOELVEIPTRLTLTLTAPRRRGPSLYVQDIOVETQ 360

```

Db 301 QEREDLDQKRLKATHQELVEIPTRPLTKSLITAPRRERKRPKTYQORDIYQETQ 360
Qy 361 REEDRRREGLVHGRASTPDWVSEGPQGLRRALSSDSILSPAADAADPAPEVKYVRI 420
Db 361 REEDRRREGLVHGRASTPDWVSEGPQGLRRALSSDSILSPAADAADPAPEVKYVRI 420
Qy 421 PPDAVQPYLSPECTPOLFEFSAFGAFGKPSGLSTAEAKAATSPKATMSPPHLSSESKPLST 480
Db 421 PPDAVQPYLSPECTPOLFEFSAFGAFGKPSGLSTAEAKAATSPKATMSPPHLSSESKPLST 480
Qy 481 KOEASKPRGCGQANRGVVRWEYFRLRLRFRAPDEPOAOVPHVGMGEVAGAPALRLQK 540
Db 481 KOEASKPRGCGQANRGVVRWEYFRLRLRFRAPDEPOAOVPHVGMGEVAGAPALRLQK 540
Qy 541 SOSDLERERESVLRROEVAEERRNALFPEVFSPTDENSDQNSRSSQASGITGSYS 600
Db 541 SOSDLERERESVLRROEVAEERRNALFPEVFSPTDENSDQNSRSSQASGITGSYS 600
Qy 601 VSESPFSPHLSNVAMTWEDPVDAPPGQKKEQWYAGINPSDGINSEVLEAIRVTRH 660
Db 601 VSESPFSPHLSNVAMTWEDPVDAPPGQKKEQWYAGINPSDGINSEVLEAIRVTRH 660
Qy 661 KNAMABERWESRIYASEEDD 679
Db 661 KNAMABERWESRIYASEEDD 679

```

RESULT 8
AAW79574 standard; protein; 672 AA.

AAW79574;

06-NOV-2001 (first entry)

Human protein SEQ ID NO 3220.

Human: cytokine; cell proliferation; cell differentiation; gene therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation.

Homo sapiens.

WO200157190-A2.

09-AUG-2001.

05-FEB-2001; 2001WO-US004098.

03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00620325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00663561.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT, Aundri V, Zhou F, Xu C, Cao Y;
Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Xue AJ, Yang Y, Wejntman T, Goodrich R;
WPI; 2001-476283/51.
DR N-PSDB; AAK52707.

Nucleic acids encoding polypeptides with cytokine-like activities, useful
in diagnosis and gene therapy.

Claim 20; Page 288; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW78333-AAW80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication

XX Sequence 672 AA;

Query Match 97.8%; Score 3503.5; DB 4; Length 672;
Best Local Similarity 99.3%; Pred. No. 4.2e-283;
Matches 666; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

```

Qy 10 LGIPQAH-RGTGLVIDGTSYTHLVCMGPASGCGDEPQTWPTDHAQCGVQROGSY 68
Db 2 LGIPGANTRGTLVDGDTSYTHLVCMGPASGCGDEPQTWPTDHAQCGVQROGSY 61
Qy 69 SVHAYTGQSPRGHSENREDEGQVYRLGARDAHQRPYALRPEDEDEKEMKTYRLDA 128
Db 62 SVHAYTGQSPRGHSENREDEGQVYRLGARDAHQRPYALRPEDEDEKEMKTYRLDA 121
Qy 129 GDADPRRLCDLEREREMAVIQQGAVKSSSTVALTQSTPDHGDERTGPPRSTPLEENVDR 188
Db 122 GDADPRRLCDLEREREMAVIQQGAVKSSSTVALTQSTPDHGDERTGPPRSTPLEENVDR 181
Qy 189 EQIDFLAARQOFLSLQANKGAPHSPPARGTPTGASQAPKAFKPHLANGVPLK 248
Db 182 EQIDFLAARQOFLSLQANKGAPHSPPARGTPTGASQAPKAFKPHLANGVPLK 241
Qy 249 POKGVVRENNKVRVPTWASVQVDDPGSLASVSPGPKETPIEREIRLQAREADLR 308
Db 242 POKGVVRENNKVRVPTWASVQVDDPGSLASVSPGPKETPIEREIRLQAREADLR 301
Qy 309 EORGRLQATDHOELVEIPTRPLTKSLITAPRRERKRPKTYQORDIYQETQREEDHRE 368
Db 302 EORGRLQATDHOELVEIPTRPLTKSLITAPRRERKRPKTYQORDIYQETQREEDHRE 361
Qy 369 GLHVGRASTPDWVSEGPQGLRRALSSDSILSPAADAADPAPEVKYVRIIPDAYQPY 428
Db 362 GLHVGRASTPDWVSEGPQGLRRALSSDSILSPAADAADPAPEVKYVRIIPDAYQPY 421
Qy 429 LSPGTPOLEFSAFGAFGKPSGLSTAEAKAATSPKATMSPPHLSSESKPLSTKOEASKRP 488
Db 422 LSPGTPOLEFSAFGAFGKPSGLSTAEAKAATSPKATMSPPHLSSESKPLSTKOEASKRP 481
Qy 489 RCGPOANRGVVRWEYFRLRLRFRAPDEPOAOVPHVGMGEVAGAPALRLQKSSQSSDLLE 548
Db 482 RCGPOANRGVVRWEYFRLRLRFRAPDEPOAOVPHVGMGEVAGAPALRLQKSSQSSDLLE 541
Qy 549 RERESVLRROEVAEERRNALFPEVFSPTDENSDQNSRSSQASGITGSYSVSESPFS 608
Db 542 RERESVLRROEVAEERRNALFPEVFSPTDENSDQNSRSSQASGITGSYSVSESPFS 601
Qy 609 PIHLHSNVAMTWEDPVDAPPGQKKEQWYAGINPSDGINSEVLEAIRVTRHNNAAEERH 668
Db 602 PIHLHSNVAMTWEDPVDAPPGQKKEQWYAGINPSDGINSEVLEAIRVTRHNNAAEERH 661
Qy 669 ESRIVASEEDD 679
Db 662 ESRIVASEEDD 672

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RESULT 9
AAW79681
ID AAW79681 standard; protein; 215 AA.

```

XX AC AAW79681;
XX DT 11-JAN-1999 (first entry)
XX DE Human CS198 protein C-terminal.
XX KW Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
XX KW human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
XX KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
XX KW pancreatitis.
XX OS Homo sapiens.
XX PN M09844159-A1.
XX PD 08-OCT-1998.
XX PF 30-MAR-1998; 98WO-US006251.
XX PR 31-MAR-1997; 97US-00828855.
XX PA (ABBO) ABBOTT LAB.
XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
XX PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX DR WPI; 1998-542714/46.
XX PS New gastrointestinal polynucleotides, CS198, and their detection - used
XX PT for developing products for the diagnosis and treatment of
XX PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
XX PS Claim 26; Page 103; 127pp; English.
XX CC This sequence represents the C-terminal of the human CS198 protein which
XX CC is used in a method to detect the presence of a target CS198
XX CC polynucleotide in a test sample. The CS198 gene is useful as a marker for
XX CC gastrointestinal (GI) tract disorders. The methods and products can be
XX CC used in detecting, diagnosing, staging, monitoring, prognosticating,
XX CC preventing or treating, or determining the predisposition to diseases and
XX CC conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
XX CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative
XX CC colitis, and pancreatitis.
XX SQ Sequence 215 AA;
XX
XX Query Match 31.6%; Score 1132; DB 2; Length 215;
XX Best Local Similarity 100.0%; Pred. No. 7,8e-86;
XX Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 465 MSPRLSSSGKPLSTKQKASKPPRGCGQANRGVVMVYFPLRPLRFPADPEPQOAVPH 524
XX DB 1 MSPRLSSSGKPLSTKQKASKPPRGCGQANRGVVMVYFPLRPLRFPADPEPQOAVPH 60
XX QY 525 VMGHEVAAAPLRLQKSSDLERERESVLRBOEVVEERNNLFPVFSPPTDENSDQ 584
XX DB 61 VMGHEVAAAPLRLQKSSDLERERESVLRBOEVVEERNNLFPVFSPPTDENSDQ 120
XX QY 585 NSRSSSQASGCTGYSVSESPFPIHSHNVAMTVEDPVDAPPGQKKEQWYAGINPS 644
XX DB 121 NSRSSSQASGCTGYSVSESPFPIHSHNVAMTVEDPVDAPPGQKKEQWYAGINPS 180
XX QY 645 DGINSEVLEAIRVTRHKNAAMERWESRIYASEDD 679
XX DB 181 DGINSEVLEAIRVTRHKNAAMERWESRIYASEDD 215
XX
XX RESULT 10
XX AAE07324
XX ID AAE07324 standard; protein; 215 AA.
XX

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AC AAE07324;
XX DT 06-NOV-2001 (first entry)
XX DE Human CS 198 protein C-terminal portion.
XX KW CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
XX KW gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
XX KW Barrett's oesophagus; gene therapy; drug screening; human.
XX OS Homo sapiens.
XX PN US2001010904-A1.
XX PD 02-AUG-2001.
XX PF 30-MAR-1998; 98US-00050516.
XX PR 31-MAR-1997; 97US-00828855.
XX PA (BTL/) BILLINGEL P A.
XX PA (COHE/) COHEN M.
XX PA (COLE/) COLPITTS T L.
XX PA (FRIE/) FRIEDMAN P N.
XX PA (GORD/) GORDON J.
XX PA (GRAN/) GRANADOS E N.
XX PA (HAYD/) HAYDEN M.
XX PA (HODG/) HODGES S C.
XX PA (KIAS/) KIAS M R.
XX PA (KRAT/) KRATOCHVIL J D.
XX PA (ROBE/) ROBERTS-RAPP L.
XX PA (RUS/) RUSSELL J C.
XX PA (STRO/) STROUPE S D.
XX PI Billingel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
XX PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX DR WPI; 2001-496163/54.
XX PS Claim 17; Page 52-53; 68pp; English.
XX CC The invention relates to a method of detecting the presence of a target
XX CC CS 198 polynucleotide comprising contacting the test sample with at least
XX CC one CS 198-specific polynucleotide. The method is useful for detecting
XX CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
XX CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
XX CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
XX CC treating or determining predisposition to diseases and conditions of the
XX CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
XX CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
XX CC polypeptides are useful as standards or reagents in diagnostic
XX CC immunoassays, as components or as target sites for various therapies.
XX CC Antibodies directed against at least one epitope contained within these
XX CC polypeptides are useful as delivery agents for therapeutic agents, in
XX CC diagnostic tests and for screening for conditions or diseases associated
XX CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
XX CC for the generation of chimeric antibodies for therapeutic use. The CS 198
XX CC polynucleotide is also useful in gene therapy and drug screening. The
XX CC method of the invention provides an alternative, non-surgical diagnostic
XX CC method capable of detecting early stage GI tract disease such as cancer.
XX CC The present sequence is C-terminal portion of human CS 198 polypeptide
XX SQ Sequence 215 AA;
XX
XX Query Match 31.6%; Score 1132; DB 4; Length 215;
XX Best Local Similarity 100.0%; Pred. No. 7,8e-86;
XX Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

```

QY 465 MSPRLSSSGKPLSTKQKASKEPRGCPQANRGVVRWEYFLRLPFRAPDEPQQAQVPH 524
DB 1 MSPRLSSSGKPLSTKQKASKEPRGCPQANRGVVRWEYFLRLPFRAPDEPQQAQVPH 60
QY 525 VWGWEVAGAPALRLQKSSDILLERERESVLRREQVAEERRNALPPEVFSPTPDNSDQ 584
DB 61 VWGWEVAGAPALRLQKSSDILLERERESVLRREQVAEERRNALPPEVFSPTPDNSDQ 120
QY 585 NSRSSSQASGITGSYSVSESPFSPILHNSVAVTVEPVDAPPGQRKKEQWYAGINPS 644
DB 121 NSRSSSQASGITGSYSVSESPFSPILHNSVAVTVEPVDAPPGQRKKEQWYAGINPS 180
QY 645 DGINSEVLEAIRVTTHKNAEMERWESRIYASEDD 679
DB 181 DGINSEVLEAIRVTTHKNAEMERWESRIYASEDD 215

RESULT 11
ADA26384 standard; protein, 215 AA.
ADA26384;
20-NOV-2003 (first entry)

Synthetic peptide based on CS198 protein #5.
CS198; cancer diagnosis; cancer staging; cancer monitoring;
cancer prognosticating; cancer prevention; cancer;
gastrointestinal tract disorder; gene therapy.
Synthetic.
US2003082619-A1.
01-MAY-2003.
23-OCT-2002; 2002US-00278547.
31-MAR-1997; 97US-00828855.
30-MAR-1998; 98US-00050516.

(BILL/) BILLINGEL P A.
(COHE/) COHEN M.
(COLP/) COLPITTS T L.
(FRIE/) FRIEDMAN P N.
(GORD/) GORDON J. E N.
(GRAN/) GRANADOS E N.
(HAYD/) HAYDEN M A.
(HODG/) HODGES S C.
(KLAS/) KLAS M R.
(KRAT/) KRATOCHVIL J D.
(ROBE/) ROBERTS-RAP L.
(RUSS/) RUSSELL J C.
(STRO/) STROUPE S D.

Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
Grandos EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;
Roberts-Rapp L, Russell JC, Stroupe SD;
WPI; 2003-596961/56.

Detecting the presence of a target CS198 polynucleotide in a test sample
comprises contacting the sample with a CS198 specific polynucleotide and
detecting the presence of the target CS198 polynucleotide in the test
sample.
Claim 52; Page 52; 67pp; English.

The invention describes a method of detecting the presence of a target
CS198 polynucleotide in a test sample. The method comprises contacting
the test sample with at least one CS198 specific polynucleotide or its
complement, and detecting the presence of the target CS198 polynucleotide

CC in the test sample, where the CS198-specific polynucleotide has at least
CC 50% identity to a polynucleotide having any of the 27 fully defined
CC sequences of 34-2894 bp (51-27) given in the specification, or their
CC fragments or complements. The composition and methods are useful in
CC diagnosis, staging, monitoring, prognosticating, preventing or treating,
CC or determining the predisposition of an individual to, diseases and
CC conditions of the gastrointestinal tract, e.g. cancer and in gene
CC therapy. This is the amino acid sequence of a synthetic peptide based on
CC the predicted human CS198 protein sequence derived from the CS198
CC consensus sequence shown in seq id 27.
SQ Sequence 215 AA;

Query Match 31.6%; Score 1132; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 7.8e-86;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 465 MSPRLSSSGKPLSTKQKASKEPRGCPQANRGVVRWEYFLRLPFRAPDEPQQAQVPH 524
DB 1 MSPRLSSSGKPLSTKQKASKEPRGCPQANRGVVRWEYFLRLPFRAPDEPQQAQVPH 60
QY 525 VWGWEVAGAPALRLQKSSDILLERERESVLRREQVAEERRNALPPEVFSPTPDNSDQ 584
DB 61 VWGWEVAGAPALRLQKSSDILLERERESVLRREQVAEERRNALPPEVFSPTPDNSDQ 120
QY 585 NSRSSSQASGITGSYSVSESPFSPILHNSVAVTVEPVDAPPGQRKKEQWYAGINPS 644
DB 121 NSRSSSQASGITGSYSVSESPFSPILHNSVAVTVEPVDAPPGQRKKEQWYAGINPS 180
QY 645 DGINSEVLEAIRVTTHKNAEMERWESRIYASEDD 679
DB 181 DGINSEVLEAIRVTTHKNAEMERWESRIYASEDD 215

RESULT 12
ADN17177 standard; protein, 215 AA.
ADN17177;
17-JUN-2004 (first entry)

CS198 protein #2.
Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.
Unidentified.
US2004043406-A1.
04-MAR-2004.
22-AUG-2003; 2003US-00646873.
31-MAR-1997; 97US-00828855.
30-MAR-1998; 98US-00050516.

(BILL/) BILLINGEL P A.
(COHE/) COHEN M.
(COLP/) COLPITTS T L.
(FRIE/) FRIEDMAN P N.
(GORD/) GORDON J.
(GRAN/) GRANADOS E N.
(HAYD/) HAYDEN M A.
(HODG/) HODGES S C.
(KLAS/) KLAS M R.
(KRAT/) KRATOCHVIL J D.
(ROBE/) ROBERTS-RAP L.
(RUSS/) RUSSELL J C.
(STRO/) STROUPE S D.

Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
Grandos EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;

PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 2004-313754/29.
XX
PT Diagnosing diseases such as cancer of the gastrointestinal tract, by
XX detecting aberrant expression or activity of the CS198 polypeptide, and
PT associated treatment methods.
XX
PS Claim 17; SEQ ID NO 47; 67bp; English.
XX
CC The invention relates to reagents and methods for detecting diseases of
CC the gastrointestinal (GI) tract. The method involves detecting the
CC presence of target CS198 polynucleotide in the test sample. The methods
CC and compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the CS198 polypeptide, such as cancer
CC of the gastrointestinal tract. These are also useful in gene therapy. The
CC present sequence is a CS198 protein used to illustrate the method of the
CC invention.
XX
SQ Sequence 215 AA;
Query Match 31.6%; Score 1132; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 7.8e-86;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 465 MSPRLSSSGKPLSTQKASKPPGCPQANRGVWMEYFLRLRPADEPQAOVPH 524
DB 1 MSPRLSSSGKPLSTQKASKPPGCPQANRGVWMEYFLRLRPADEPQAOVPH 60
QY 525 VMGMEVAGAPALRLQKSSDLERERESVLRREQVEAEERRNALPPEVFSPTDENSDQ 584
DB 61 VMGMEVAGAPALRLQKSSDLERERESVLRREQVEAEERRNALPPEVFSPTDENSDQ 120
QY 585 NSRSSSQASGITGSYSVESPPFSPIHLHSNVAMTVEDPVDAPPGQKKEQWYAGINPS 644
DB 121 NSRSSSQASGITGSYSVESPPFSPIHLHSNVAMTVEDPVDAPPGQKKEQWYAGINPS 180
QY 645 DGINSEVLEAIRVTRHKNMAERMESRIYASEED 679
DB 181 DGINSEVLEAIRVTRHKNMAERMESRIYASEED 215
RESULT 13
AA673987
ID AA673987 standard; protein; 172 AA.
XX
AC AA673987;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:4751.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma.
XX
OS Homo sapiens.
XX
FN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PE 28-SEP-2000; 2000WO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
PR 03-NOV-1999; 99US-0163280P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX WPI; 2001-235357/24.
XX
DR N-PSDB; AAH33418.
DR

XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 11; Page 6550-6551; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AA673514 to AA677788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patient's own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAH7789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 172 AA;
Query Match 23.4%; Score 839; DB 4; Length 172;
Best Local Similarity 87.0%; Pred. No. 1.6e-61;
Matches 167; Conservative 0; Mismatches 5; Indels 20; Gaps 1;
QY 488 PRGCPQANRGVWMEYFLRLRPADEPQAOVPHVMGMEVAGAPALRLQKSSDDL 547
DB 1 PRGCPQANRGVWMEYFLRLRPADEPQAOVPHVMGMEVAGAPALRLQKSSDDL 40
QY 548 ERESEVTLREQVEAEERRNALPPEVFSPTDENSDQNSRSSQASGITGSYSVESPPF 607
DB 41 ERESEVTLREQVEAEERRNALPPEVFSPTDENSDQNSRSSQASGITGSYSVESPPF 100
QY 608 SPIHLHSNVAMTVEDPVDAPPGQKKEQWYAGINPSDGINSEVLEAIRVTRHKNMAER 667
DB 101 SPIHLHSNVAMTVEDPVDAPPGQKKEQWYAGINPSDGINSEVLEAIRVTRHKNMAER 160
QY 668 MESRIYASEED 679
DB 161 MESRIYASEED 172
RESULT 14
AB060042
ID AB060042 standard; protein; 43 AA.
XX
AC AB060042;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon protein #6276.
XX
KW Human; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
FN US2003194704-A1.
XX
PD 16-OCT-2003.
XX
PE 03-APR-2002; 2002US-00029386.
XX
PR 03-APR-2002; 2002US-00029386.
XX
PA (PENN/) PENN S G.
XX (RANK/) RANK D R.
PA


```

Qy 472 ESSGKPLSTKOEAS-----KPPR-GCP-QANRGVNRWEYRRLRP-----LRF 511
Db 637 EOCQ-PEATVEAEAAAGSEKPSQMFPPQVSSPVQEKDVLPR---KILPAEDRALRE 691
Qy 512 RAPDEP-----OOAOVPHVWGWEVA 531
Db 692 RGPPOPLPAVQPSGPIINMETRPGSYFSKYSEAAELRSTASLATQESDV-----MV 744
Qy 532 GAPALRLQKSSDILLERERESVLRREQEVAER-----RNALFPEV-----573
Db 745 GPFKLRSRKORTLSMIEEIRAAOEREELRKORQVLOSTQSPRTKNA--PSLPSRTCYK 802
Qy 574 -----FSPTPDENSDONRSSSQAGITGSYSVESPPFFSPHLSNVAMTVE 621
Db 803 TAPGKIEKVPSPSPTTGGPSLQPDLPAPBAAG-----TORP-----KNLMQTIM 847
Qy 622 DPVDSAPPQQRK--EOWYAGINPSDGINSEVLEAIRVTRHKNAABERMSRIYASEED 679
Db 848 EDYETHKSKRBRMDSSYTSKLSCKVTSVLEATRVNRRKSAALALWEAGIYANOEBE 907

```

Search completed: March 3, 2006, 13:35:18
 Job time : 366.925 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 13:26:31 / Search time 42.8912 Seconds
(without alignments)
1523.185 Million cell updates/sec

Title: US-10-646-873-42

Perfect score: 3583

Sequence: 1 MDRVTRYPILGIPQAHRTG.....HKMAERWESRIYASEED 679

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3583	100.0	679	T00636	hypothetical prote
2	189	5.3	3942	T42730	Bassoon protein -
3	179.5	5.0	3938	T42761	hypothetical diver
4	168.5	4.7	1794	T38459	elastin - hu
5	167	4.7	7962	T38346	neurofilament prot
6	166	4.6	1200	A46194	adenomatous polypo
7	166	4.6	2843	1 RBHUP	hypothetical prote
8	164.5	4.6	1280	T00365	A kinase anchor pr
9	162	4.5	885	T09225	ALR protein - huma
10	159	4.4	4957	T03455	translation initia
11	159	4.4	5262	T03454	hypothetical prote
12	158	4.4	1039	A12284	gene APPL protein
13	156.5	4.4	1791	T02345	microtubule-associ
14	156	4.4	1616	T37183	immediate-early pr
15	156	4.4	2774	A43359	hypothetical prote
16	155.5	4.3	1446	A45344	SPAZ protein - yea
17	154.5	4.3	1262	T22523	hypothetical prote
18	154.5	4.3	1466	A36426	exo-alpha-glucosid
19	154.5	4.3	3507	T34513	tight junction pro
20	154	4.3	913	S20590	hypothetical prote
21	153.5	4.3	1736	A47747	hypothetical prote
22	153	4.3	1655	T32633	SNFbeta protein -
23	152	4.2	780	T00366	microtubule-associ
24	151.5	4.2	1647	A45252	microtubule-associ
25	151	4.2	733	A45301	hypothetical prote
26	151	4.2	5337	T41564	glucan 1,4-alpha-g
27	150.5	4.2	2022	T48818	adenomatous polypo
28	150	4.2	2922	T48818	
29	150	4.2	2845	T49505	

30	147.5	4.1	541	2	T19304	hypothetical prote
31	147	4.1	531	2	T08760	hypothetical prote
32	146	4.1	1321	2	T00037	hypothetical prote
33	145.5	4.1	1027	2	T46481	hypothetical prote
34	145.5	4.1	2142	2	B35098	MHC class II hist
35	145	4.0	1390	2	T14004	trif protein - sil
36	145	4.0	1744	2	A54970	tensin, cardiac mu
37	145	4.0	4162	2	T42633	connectin/titin -
38	144.5	4.0	880	2	D89756	protein T23E7.2b
39	144.5	4.0	891	2	T22560	hypothetical prote
40	144.5	4.0	1743	2	T15893	hypothetical prote
41	144	4.0	2339	2	A42566	omega-conotoxin-se
42	143.5	4.0	1634	2	T26517	hypothetical prote
43	143.5	4.0	6642	2	T29757	protein UNC-89 - C
44	143	4.0	660	1	Q08E3	BHLFI protein - hu
45	143	4.0	666	2	B70803	hypothetical prote

ALIGNMENTS

RESULT 1

T00636

hypothetical protein F21856.2 - human

C/Species: Homo sapiens (man)

C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C/Accession: T00636

R/Name: J.E.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhart-Schultz, K.; C

regescu, A.; Avila, J.; Liu, S.; Bruce, R.; Quan, G.; Montgomery, M.; Ow, D.; Nolan, M.;

submitted to the EMBL Data Library, January 1998

A/Description: Sequence analysis of a 3.5 Mb contig in 19p13.3 between CDC34 and D19S342

A/Reference number: Z14195

A/Accession: T00636

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Cross-references: UNIPROT:O81VT2; UNIPARC:UP100000745CD; EMBL:AC004030; NID:G2804590;

C/Genetics:

A/Map position: 19p13.3

A/Introns: 594/1; 637/3; 650/3

A/Note: F21856_2

Query Match	Score	Match	Length	DB ID	Description
1	3583	100.0%	679	T00636	hypothetical prote
2	189	5.3	3942	T42730	Bassoon protein -
3	179.5	5.0	3938	T42761	hypothetical diver
4	168.5	4.7	1794	T38459	elastin - hu
5	167	4.7	7962	T38346	neurofilament prot
6	166	4.6	1200	A46194	adenomatous polypo
7	166	4.6	2843	1 RBHUP	hypothetical prote
8	164.5	4.6	1280	T00365	A kinase anchor pr
9	162	4.5	885	T09225	ALR protein - huma
10	159	4.4	4957	T03455	translation initia
11	159	4.4	5262	T03454	hypothetical prote
12	158	4.4	1039	A12284	gene APPL protein
13	156.5	4.4	1791	T02345	microtubule-associ
14	156	4.4	1616	T37183	immediate-early pr
15	156	4.4	2774	A43359	hypothetical prote
16	155.5	4.3	1446	A45344	SPAZ protein - yea
17	154.5	4.3	1262	T22523	hypothetical prote
18	154.5	4.3	1466	A36426	exo-alpha-glucosid
19	154.5	4.3	3507	T34513	tight junction pro
20	154	4.3	913	S20590	hypothetical prote
21	153.5	4.3	1736	A47747	hypothetical prote
22	153	4.3	1655	T32633	SNFbeta protein -
23	152	4.2	780	T00366	microtubule-associ
24	151.5	4.2	1647	A45252	microtubule-associ
25	151	4.2	733	A45301	hypothetical prote
26	151	4.2	5337	T41564	glucan 1,4-alpha-g
27	150.5	4.2	2022	T48818	adenomatous polypo
28	150	4.2	2922	T48818	
29	150	4.2	2845	T49505	

QY 421 PPADYQVYLSTGRTQQLERSARGARCKPSLSTAAKAAATSPKATMSPPRHLSSESGKPLST 480
DB 421 PPADYQVPLSLSTGRTQQLERSARGARCKPSLSTAAKAAATSPKATMSPPRHLSSESGKPLST 480
QY 481 KQASKEPPRGCPQANRGVMEYFRLRLPRAPADEPQQAQVPHVWGMEVAGALRLQK 540
DB 481 KQASKEPPRGCPQANRGVMEYFRLRLPRAPADEPQQAQVPHVWGMEVAGALRLQK 540
QY 541 SQSSDLLERERESVLRREQVAEERRNALPPEVFSPTPDENSQNSRSSQASGITGSYS 600
DB 541 SQSSDLLERERESVLRREQVAEERRNALPPEVFSPTPDENSQNSRSSQASGITGSYS 600
QY 601 VSESPFSPRIHLHNVAMTVDDPVDASAPGQKKEQWAGINPSDGINSEULALRYTRH 660
DB 601 VSESPFSPRIHLHNVAMTVDDPVDASAPGQKKEQWAGINPSDGINSEULALRYTRH 660
QY 661 KNAEAERESRIYASEED 679
DB 661 KNAEAERESRIYASEED 679

RESULT 2

Basoon protein - mouse
T42730
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42730
J:Dieck, S.; Sammarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, R.; Cell Biol. 142, 499-509, 1998
A:Title: Basoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized
A:Reference number: 222249; MUID:98345363; PMID:9679147
A:Accession: T42730
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3942 <DIE>
A:Cross-references: UNIPROT:O88737; UNIPARC:UPI0000029858; EMBL:Y17034; NID:G3413809; P1
A:Experimental source: strain 129 SVJ
C:Genetics:
A:Map position: 9P1
A:Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
A>Note: basoon
C:Function:
A:Description: may be involved in cytomatrix organization at the site of neurotransmitter
A>Note: component of the presynaptic cytoskeleton
C:Keywords: coiled coil; zinc finger

Query Match 5.3%; Score 189; DB 2; Length 3942;
Best Local Similarity 20.1%; Pred. No. 0.016;
Matches 165; Conservative 102; Mismatches 252; Indels 302; Gaps 39;

QY 38 PEASGWGQDE---PQTWPTD-HRAQO---GVORQGVSVVHAYTG----- 75
DB 666 PEAPKGEAEHPVFKYQSLSDTGSYSDGVSSQSEITGVVQOEVLQDSAG 725
QY 76 -----QSPRGLHSNREDEGWYRLGAR-----DAHQGPT--WALRPEDG---EDK 119
DB 726 VTGPRPSPSEIH-----KVGSILRPSELGAQVAPSAEWSKPPSSSSAAVEDQ 773
QY 120 EMKTYRL-----DAGDAPRLCDLEREMAVIYQGAVKSSTVATLQSTPDHG----- 168
DB 774 KRRPHSLSIMPEAFPSD--BELGDIIEBDSILAMG---RQREQDTAESSDDFGSGLRHDY 829
QY 169 -----DPTGPPTSTPLEENVVDREQIDFLAARQQLSLSEQ---ANKG-APHSSP 215
DB 830 VEDSESGSLPLPQP PARADWTDEFPKRQLLEMSAEEDNLEEDTAVSGRLAKHS-- 887
QY 216 ARGTPAGTTPGASQAPKAFNKPILAN-----GHVIVIKP-----QYKGVIRE----- 257
DB 888 AQKASARPPSSSQEPKR-RLPHNATGYEELSEAGAEPTDSSGALQGGILRRKTEL 946
QY 258 -----ENIVR-----AVPTMASVQVV 273

DB 947 NSTGSGHELDLQGGPPDNLDRPRELEMEISITGSPEDRSKGHSSTLPASTPYTS---G 1003
QY 274 DDGSLASV-----SPGPKETPIREITRLAER-----RADLREQGLR 314
DB 1004 TSPSTLSLEEDSDSPSRRLQLEAKQOKARHSHGILLPTTEDSSEEBELREBEL 1063
QY 315 QATDHOELVEIPRPLTLTKSLITAPRERGRPSLYQORDIVQETOREBDRREGLVGR 374
DB 1064 R--EQEMREVEQQRHS-----TAKTRIDKELARQ-----RE-----R 1099
QY 375 ASTPDVWSEGPQGLRRLAUSDLSLSPAPRAAD---PAPEYKVRNRPIDAYQPLSP 431
DB 1100 SKTP-----PNLSPIDBASPTBELRQAALMBELRRSSCSSEYSP---- 1138
QY 432 GTQLERSARGARCKPSLSTAAK-----AATSPKATMSPPRHLSSESGKPLSTKQA 484
DB 1139 -SPSLSEAEETLDGGPRLYKSSSEYNLPAPFMYLSTETPSSGSTTSPSGRLPKASBEA 1197
QY 485 -----SKPPRGCPQANRGVMEYFRLRLPRAPADEPQQAQVPH 524
DB 1198 YEDMKRAEMLQROQGVAGARGPHGSPQTPG-----RQGSFEYQDTQ-DH 1245
QY 525 VWGMEVAGAPALRLQKSQSSDLLERERESVLRREQVAEERRNALPPEVFSPTPDENSQ 584
DB 1246 DYG---GRASQPEVAESTPAGLGAAYEEILQTSQSIARWR----- 1282
QY 585 NSRSSQASGIT-----GSYSSESPFSPRIHLHNVAMTVDDPVDASAPGQKKEQWY 638
DB 1283 --QASSDILGFTDCKKEKQPLNAESAAYDPMQNGGRLTPGTSPTQLAAPVS-----F 1334
QY 639 AGINSPDGINSEVLEAIRVTRHKNAEAERESRIYASEED 679
DB 1335 STSTSSDSSGGRVLPVRYVQH-----FAKEPD 1363

RESULT 3

Basoon protein - rat
T42761
N:Alternate names: brain-specific synapse-associated protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42761
J:Dieck, S.; Sammarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, R.; Cell Biol. 142, 499-509, 1998
A:Title: Basoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized
A:Reference number: 222249; MUID:98345363; PMID:9679147
A:Accession: T42761
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3938 <DIE>
A:Cross-references: UNIPROT:O88778; UNIPARC:UPI000007E7DE; EMBL:Y16563; NID:G3413503; P11
A:Experimental source: strain Sprague Dawley; Brain
C:Function:
A:Description: may be involved in cytomatrix organization at the site of neurotransmitter
A>Note: component of the presynaptic cytoskeleton
C:Keywords: coiled coil; zinc finger

Query Match 5.0%; Score 179.5; DB 2; Length 3938;
Best Local Similarity 20.0%; Pred. No. 0.056;
Matches 161; Conservative 102; Mismatches 249; Indels 291; Gaps 39;

QY 38 PEASGWGQDE---PQTWPTD-HRAQO---GVORQGVSVVHAYTG----- 75
DB 650 PEAPKGEAEHPVFKYQSLSDTGSYSDGVSSQSEITGVVQOEVLQDSAG 709
QY 76 -----QSPRGLHSNREDEGWYRLGAR-----DAHQGPT--WALRPEDG---EDKE 120
DB 710 VTGPRPSPSEIH-----KVGSIMRPSILBAQVAPSAEWS-KPPSGSAVEDQK 756
QY 121 MKYTRL-----DAGDAPRLCDLEREMAVIYQGAVKSSTVATLQSTPDHG----- 168
DB 757 RRPHSLSIMPEAFPSD--BELGDIIEBDSILAMG---RQREQDTAESSDDFGSGLRHDY 812

QY 169 -----DPTGPRSTPLEENVVDEQIDFLAARQOFLSLEQ---ANKG-APHSPA 216
 DB 813 EDSSEGLSLPPLPPQPADADMTDEEFMRROILEMSABEDNLEEDTAVSGGLAKG--A 870
 QY 217 RGTPTGTTGASQAQKANK---PHLA-----NGHVPIKPOVGVVRE----- 257
 DB 871 QASARPPRESSQSSVALPKRLPHNAATTGEBLLSEGPAPFTGALOGGLRRKTTGL 930
 QY 258 -----ENKVR-----AVPTWASVOV 272
 DB 931 NSTGLMNSTSIDLOGGSDPNLDREPELEMESLTSPEPDRSGEHSSTLPASTPSYTS--- 987
 QY 273 VDDPGSLASVE---SPTGPKETPIERIRLAQR-----EADLAHQGL 313
 DB 988 GTSPTSLSLBEDSDSSPSRRQRLBEAKQQRKARHSHGPLLPTIEDSSEEBELBEEL 1047
 QY 314 RQATHQGLVLEPTPLTKLSLITAPRRERGRPSLYVQORDVQSTQREEDHRRGLHVG 373
 DB 1048 LR--EQKKRREVEQQRIRS---TAKTRKDEKELRAQR-----KRE----- 1083
 QY 374 RASTPDWVSEGPQGLRRRLSSDSILSPAPDARAAD---PAPEVRKVNRIPPDAYOPYLS 430
 DB 1084 RSKT-----PSNLSTPREDASPTBELRQAAMEELHRSSGSEVSP--- 1123
 QY 431 PGTPOLEPSAFGAFKPSLSLTAENK-----AATSPKATMSPHNLSESSGKPLSTKOE 483
 DB 1124 --SPILDSBAETLDDGPTRLYKSGSEVNLPAFMSLCSPTETPSGSGSTTPSSGRPLKSAE 1181
 QY 484 ASKPRGCGQARGVVWMEYFRLPLRFRAPDEPQOAVPHVWGMEVAGAPALRL--QKSO 542
 DB 1182 ARE-----DMKRKAELOKQCGAAGARCPH-----CGSPQPTGPRKQ 1219
 QY 543 SS-----DLERE-----RESVLRBOEVAERENALFPEVFSPT 577
 DB 1220 GSFPEVOTLIDHYGSAQPADGTPAGLGAITYEELLTOSIARMQASSRLDAF--T 1277
 QY 578 PDENSQNSRSSQASGITGSYSVSESPFSPILHNSVAMTVEDPVDASAPGQKKEQM 637
 DB 1278 EDKKEK-----QFLNABSAYMDPMKQKQGLPTGTSPTQLAAVPS----- 1318
 QY 638 YAGINPSDGINSEVLEAIRTRH 660
 DB 1319 PFTSTSSDSSGGRVLPDVRTOH 1341

RESULT 4
 T38459
 hypothetical divergent repeat-containing protein - fission yeast (Schizosaccharomyces po

C/Species: Schizosaccharomyces pombe
 C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
 C/Accession: T38459, T38380
 R/Harris, D., McDonald, S., Barrett, B.G., Rajandream, M.A., Walsh, S.V.,
 submitted to the EMBL Data Library, February 1996
 A/Reference number: Z21794
 A/Accession: T38459
 A/Molecule type: DNA
 A/Residues: 1-1148 <HAR>
 A/Cross-references: UNIPROT:Q10172; UNIPARC:UPI0000169027; EMBL:Z69368; PIDN:CAA93290.1;
 R/McLean, J., Harris, D., Barrett, B.G., Rajandream, M.A., Walsh, S.V., Wood, V.
 submitted to the EMBL Data Library, September 1997
 A/Reference number: Z21790
 A/Accession: T38380
 A/Molecule type: DNA
 A/Residues: 1457-1794 <MCL>
 A/Cross-references: UNIPARC:UPI000016208D; EMBL:Z70691; PIDN:CAA94638.1; GSPDB:GN00066;
 A/Experimental source: clone G25G10
 C/Genetics:
 A/Map position: 1
 A/Map position: 1
 SPDB:SPAC25G10.09c

Query Match 4.7%; Score 168.5; DB 2; Length 1794;
 Best Local Similarity 20.9%; Pred. No. 0.09; Indels 185; Gaps 27;
 Matches 123; Conservative 68; Mismatches 213; Indels 185; Gaps 27;

QY 150 QAVKSSVTATLQSTPDHGDRTP-----GPPRSTPLEENV-----VDREQIDFLAA 196
 DB 1188 QTLNPPSVSTVQSKPLBSNTHTEPVKATSSPSASSLLEBARARITAEARMMERLAA 1247
 QY 197 RQOFLSLEQANKGAPHSP---ARGTPAGT-----TPGASQAQKAFKPHLANGHVPI 247
 DB 1248 ---LGIKPRQKGTTPSPAPVNSATSTPVAATAQOIQGKQASAVSSVPAVASISITP- 1302
 QY 248 KPQYGVVREENKVRAPVTASVOVDDPGSLA-SVESPTGPKETPIERIRLAQRAD 306
 DB 1303 -PAVPTQVQHPQKQIFTLA---VKDPTSTSTSFNAPTPQQAPLENQF-----SK 1350
 QY 307 LREQGLQADTHQELVLEPTPLTKLSLITAPRRERGRPSLYVQORDVQSTQREEDHRRGLHVG 354
 DB 1351 MSLEPVRPAVPTSPKQIPDSSNVHAPPPVQPMNAMPSHNAVAKPSABERKDSFGSV 1410
 QY 355 -----IVQETQREEDHRRGLHVGAS--TPDWVSEGP-----QGLRRALSSDS 397
 DB 1411 SSGSNVSSIEBETSTMPKASQPTNPGAPSNHAPQVVPAPMHAVALPQKAPGVNTN-- 1468
 QY 398 ILSPAPDARAADPAPEVRKVNRIPPDAYOPYLSPTPOLEPSAFGAFKPSLSLTAENKA 457
 DB 1469 --APAPSSAPAPAP--VQQLPAPV-----PVPVPSMIPSYVAQOPSSVADATAPS 1516
 QY 458 ATSPKATMS-----PRHLSSESS-----GKPLSTKQEASKP----- 487
 DB 1517 STLPSQSSFAHVSPAPAPAPQHPSAALSSAPADNSPHRSSPAPQEPVQKQALNNI 1576
 QY 488 -----PRGCPQANKGVVWMEYFRLPLRFRAPDEPQOAVPHVWGMEVAGAP 534
 DB 1577 APATNLGTSQSSPSPMGMVNNNG-----SPLANNAAGQPSLA--VP-----AVPSAP 1621
 QY 535 A-----LRLQKQSSDLLERRERSVLRBOEVAERENALFPEVFSPTDENSQNSGS 588
 DB 1622 SNHFNPPAKMQPPAPSPLOPSGHSD--NWSQGHDEE-----EEDSEBDIRS 1666
 QY 588 SSOAS-----GITGSYSVSESPFSPILHNSVAMTVEDPVDASAP 629
 DB 1667 SDOAALAAKLPFGMAPAHPVSTPV-----RQGSAPP 1700

RESULT 5

I38346
 elastic titin - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 C/Accession: I38346
 R/Labeit, S., Kolmerer, B.
 Science 270, 293-296, 1995
 A/Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
 A/Reference number: A57430; MUID:96026330; PMID:7569578
 A/Accession: I38346
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-7962 <RES>
 A/Cross-references: UNIPROT:Q10465; UNIPARC:UPI000011010C; EMBL:X90565; NID:91017426; P
 C/Genetics:
 A/Map position: 2q31-2q31
 OMIM:188840

Query Match 4.7%; Score 167; DB 2; Length 7962;
 Best Local Similarity 19.2%; Pred. No. 0.69; Indels 228; Gaps 30;
 Matches 121; Conservative 81; Mismatches 199; Indels 228; Gaps 30;

QY 70 VHAATGQSPRGHSHNRDEGQVYRLDA-BDAHCGRTPLALRPDGHGKEXKRYRLDA 128
 DB 5747 VEDYT-EPEQPYEE--PDDEYEIKVAKKEVH---EMEDFEQGYIEREGYDE 5800
 QY 129 GDADPRRLCDLERERNAVIOGAVRKSTVATLQSTPDHGDRTPGPPRSTPLEENVVDR 188
 DB 5801 GR-----EEM-----EAYQER 5812

QY 189 EQIDFLAQQPLSLAQANKGAPHS--SPARGTPA-----GTPGASQAP 248
DB 5613 EVIVV-----QKEVVEEHERKVPKVPKAP-----PPPVYIKKPYEK-----IE 5855
QY 249 POUKGVVREENKRAVPTWASVOVVDPGSLASVESGTPKETPIEREI-----RLAQE 302
DB 5856 KTSRMEEEKVQVTKVPE--YSKKIV-----PQKSPRTVQEEVIEVKVPVHTK 5903
QY 303 READLRQKRLQATDHOELVEITRPLTKLSLITAPRERKGRPSLYQORDIYOETORE 362
DB 5904 KMTVSEKMPFASHTHEEVSATVE-----VQKEIYTE----- 5936
QY 363 EDHRRREGVHG---RASPDMVSEGPQGLRRALSISLSPADARADAPAEVRKYNR 419
DB 5937 -----EKIVAVSKGVPPKVPPELPE-----KPAEEVA--PVPKPKVPE 5975
QY 420 IPPDAYOPLSPGTPOLEFSAFGAFGRSSLSTAENKAATSPKATMSPRH--LSSESGKP 477
DB 5976 -PP-----APKVPVPPKPKVPPEKKP--VPVPEKPEAPAPKVPVPPKPKVPPEKLPVP 6025
QY 478 LSTQESKSPRPGCPQANRGVVMWEYFRRLPLFRAPDEPOQAOVPHVWGVNAGAPALR 537
DB 6026 VAKKEKA--PPAKVPEVQKGVVTEKITTIVQREESP--PPAVPRIP----- 6068
QY 538 LQKSSQDILERESEVLRREOEVAERBNALPEVFSPTPDENSDQNSRSSQASGITG 597
DB 6069 -----KKVYPEEKVPVPRKEEVPPPPKVPALPK--KVPPEEKV----- 6105
QY 598 SYSVESPPFSPPIHASNVAWTVEDPV--DSAPPGQK-----KEQWYAGINSPDINS 649
DB 6106 -----AVEVPYAKKAPPPRAVSKKTVVEEKRFVA--EKLTSF 6141
QY 650 EYLEAIRVTRHAKNMAERWESRIYASED 678
DB 6142 AVPQREVTREHVSABEEMW---YSEEBE 6167

RESULT 6

A46194
neurofilament protein NF-220, high-molecular-weight splice form - longfin squid
C/Species: Loligo pealeii (longfin squid)
C/Date: 22-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: A46194
R/May, J.; Hellmich, M.R.; Jaffe, H.; Szaro, B.; Pant, H.C.; Garner, H.; Batey, J.
Proc. Natl. Acad. Sci. U.S.A. 69, 6963-6967, 1992
A/Title: A high-molecular-weight squid neurofilament protein contains a lamin-like rod c
A/Reference number: A46194; MUID:92357751; PMID:1379729
A/Accession: A46194
A/Status: nucleic acid sequence not shown, not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1200 <MAX>
A/Cross-references: UNIPROT:Q25388; UNIPARC:UPI00000808FB; GB:M94389; NID:g161291; PID:9
A/Experimental source: stellate ganglion
A/Note: sequence extracted from NCBI backbone (NCBI:P:113499)
C/Superfamily: neurofilament triplet H protein
C/Keywords: alternative splicing

Query Match 4.6%; Score 166; DB 2; Length 1200;
Best Local Similarity 20.0%; Pred. No. 0.077;
Matches 137; Conservative 91; Mismatches 312; Indels 144; Gaps 29;
QY 23 LDGISTYTHLVCGPPEASGGOEPQWPPDHAQOCVQGVSYVHATGQPSRGL 82
DB 502 LTTSTSY-----CGDEADDEGKSDSDTHTEAEER-----TRADSDADTGTGL 546
QY 83 HSEKREDEGQVYRAGADAHQGRPTWALREDEGDEKEMKTYRLDAGDAPRRCLDRE 142
DB 547 DEVEER-----SVLKSEKDKSVKDD---DEEBEENDQTSVEVDEADALEKQKSESD 599
QY 143 RMAVIOGQAVKRSVATLQSTPDHGD-----PRTGPPSPSTP 180
DB 600 KTESDKAESERAEVSKAT---TPESDKAESVKSERSISITSETAFIDKSPKSGSKDTL 656

QY 181 LEENVVDREQIDFLAQQPLSLAQANKGAPHS-----SPARGTPA-----GTPGASQAP 231
DB 657 FQSDKTSPTLV-----LERMSLQCAPTEKPLSDTTSKPVVSEPALSPVSVNSGATSP 711
QY 232 KAKNPHLANGHVPIKPOVKGVVREENKRAVPTWASVOVVDPGSLASVESGTPKE- 290
DB 712 AERMTSPISGS-----EKSAKSPVRS-----ATKSPVSEKSGSKSP--VPSER 757
QY 291 --PIEREI-----RLAQERADLRQKRLQATDHOELVEITRPLTKLSLITAPRE 343
DB 758 ALSPVLSKSVHSTAMSHTSRSPTASEKSVKSP--HSERTASPT---ASPTIMEPAKS 812
QY 344 RGRPSLYQORDIYOETORE--EDHRRREGVHGASTPDMVSEGPQGLRRALSISLSPA 402
DB 813 ---PK-----DESEKELSPRESVWGSQKQITSSSAKSVPS--EKADSEKSAISPT 860
QY 403 PDARADPA-----PEVRKNRIP--PDAYOPLSPGTPOLEFSAFGAFGRSSL 450
DB 861 PSEKVDSEASAPTHSDRSESGKARSAPWTSDHKSPIDFEKAESKSLSYKSDHDK 920
QY 451 STEAKAATSPKATMSPRHLSSESGKPLSTQESKSPRPGCPQANRGVVMWEYFRRLPLR 510
DB 921 SPVPESEKSEKARSFPV--SEKASEKARSFPVSEPAKSPVSEKASEKARSFPV 979
QY 511 FRAPDEPOQAOV---HWGWEVAGAPAL---RLQKSSQDILERESEVLRREOEVA 562
DB 980 SEKASEKARSFPVSEKASEKARSFPVSEKDESEKAKSPVSDQARFPV---PEKA 1036
QY 563 EERRNALFP---EYSPPTPDENSDQNSRSSQA-----SGITGSYSVESPPFSPHIL 612
DB 1037 ESEKARSAPVTSSEHVSFPVSEKSEKARSAPVTSSEHVSFPVSEKASEKAKSPV-- 1094
QY 613 HSNVAWTVEDPVDSAPPGQKKEQ 636
DB 1095 -----ASEPAKSPVSEKASE 1111

RESULT 7

RBRHAP
adenomatous polyposis coli protein - human
N/Alternate names: polyposis coli locus protein DP2.5; tumor suppressor APC
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: A37261; B39658; A44928; A49319; I54271
R/Kinzler, K.W.; Nilbert, M.C.; Su, L.K.; Vogelstein, B.; Bryan, T.M.; Levy, D.B.; Smith,
chui, S.F.; Horii, A.; Ando, H.; Miyoshi, Y.; Miki, Y.; Nishihio, I.; Nakamura, Y.
Science 253, 661-665, 1991
A/Title: Identification of FAP locus genes from chromosome 5q21.
A/Reference number: A37261; MUID:91335210; PMID:1651562
A/Accession: A37261
A/Molecule type: mRNA
A/Residues: 1-2843 <KIN>
A/Cross-references: UNIPROT:P25054; UNIPARC:UPI0000502E5; GB:M74088; NID:g182396; PID:9
R/Joshi, G.; Carlson, M.; Thilveris, A.; Albertsen, H.; Gelber, L.; Samowitz, W.; Grode
Arlington, J.; McPherson, J.; Wasmuth, J.; Le Paslier, D.; Abderrahim, H.; Cohen, D.; Ley
Cell 66, 601-613, 1991
A/Title: Identification of deletion mutations and three new genes at the familial polypoe
A/Reference number: A39658; MUID:91330307; PMID:1678319
A/Accession: B39658
A/Molecule type: DNA
A/Residues: 1-183; 'L', 185-969; 'N', 971-1308; 'G', 1310-1324; 'SS', 1326; 'HSTLE', 1332-1354; 'P',
A/Cross-references: UNIPARC:UPI00001CAEBO; GB:M73548; NID:g190163; PID:AAA60354.1; PID:5
R/Miki, Y.; Nishihio, I.; Horii, A.; Miyoshi, Y.; Utsunomiya, Y.; Kinzler, K.W.; Vogelstein
Cancer Res. 52, 643-645, 1992
A/Title: Disruption of the APC gene by a retrotransposon insertion of LI sequence in a cc
A/Reference number: A44928; MUID:92119623; PMID:1310068
A/Accession: A44928
A/Molecule type: DNA
A/Residues: 1506-1525 <NIK>
A/Cross-references: UNIPARC:UPI00000354E5; GB:S78214; NID:g243541; PID:ABB21145.1; PID:6
A/Note: sequence extracted from NCBI backbone (NCBI:N:78214; NCBI:P:78218)
R/Spirito, L.; Olechwang, S.; Groden, J.; Robertson, M.; Samowitz, W.; Joshi, G.; Gelber


```

Db      1404 FTTT---TTGEGDGLSYNQRSLQRWEKDELGLSTISPYL--YANINFPNLKQDYPD 1457
Qy      348 -----SLYVQR-----DIYQET 359
Db      1458 WSSRCQIMKLMRKVPADKAPYLQKADKNRAHRINKVQKQASQINKQTKGVGIART 1517
Qy      360 QREEDHR-----EGLHVGASTPDWSEGFQGLRRALSSTLS----400
Db      1518 DRPALHLRIPQPGALGSPPAAPLTFIGSPTTLAGLS-----TSADGLKXPA 1567
Qy      401 ---PAPD-----ARAAP---APEVRKNRIP--PDAYQPYLS-----430
Db      1568 GSVPGPDSRGELFLKLPPQVPAQPSQDPFGALAPVPLEPRFPPTAPPTYPYPPSPPTGAPA 1627
Qy      431 -----PAPD-----PCTPOLFSAFGAFGKP-----SLSSTAEKAKATSPK 462
Db      1628 QPMLGASSRPGAGQGEHTTTPGTTPRQPSPTPDPFLKPCPSLDNLAVPESPGVGCK 1687
Qy      463 AT---MSPRHLSESGKPLSTKOE---ASKPPRGCPQANRGVVRWEYFRLRLRFRAPDE 516
Db      1688 ASEPLSPPPGESR-KALEVKKBELGASSPSYGP--NLGFV-----DS 1729
Qy      517 PQOAVPVYWGVEVAGAPALRLQKSSDLERERESVLRREQEVAERRNA---LPEE 572
Db      1730 PSSG--THLGLLELTPDVFKAPLTPRASQVEPQSGLRLQEPQALAPSPSHPD 1787
Qy      573 VFSPTPDNSDQNSRSSQASGITGSYSVSESPFSP 609
Db      1788 IFRP-----GSYT---DPYAQP 1801

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RESULT 11

ALR protein - human
 C1:Species: Homo sapiens (man)
 C1:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C1:Accession: T03454
 R1:Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano, Oncogene 15, 549-560, 1997
 A1>Title: Structure and expression pattern of human ALR, a novel gene with strong homolog
 A1:Reference number: 214954; MID:97388474; PMID:9247308
 A1:Accession: T03454
 A1:Status: preliminary; translated from GB/EMBL/DBJ
 A1:Molecule type: mRNA
 A1:Residues: 1-5262 <PRA>
 A1:Cross-references: UNIPROT:O14666; UNIPARC:UP10000110107; EMBL:AF010403; NID:g2358284;
 A1:Gene: ALR
 A1:Map position: 12
 C1:Superfamily: acute lymphoblastic leukemia protein, ALR type
 C1:Keywords: alternative splicing

Query Match 4.4%; Score 159; DB 2; Length 5262;
 Best Local Similarity 21.4%; Pred. No. 1.2;
 Matches 162; Conservative 82; Mismatches 241; Indels 272; Gaps 43;

```

Qy      37 GPRA-----SGWQ-DE--PQWPTDHRAGGV-----OROG-----VSYS 69
Db      1438 GPAQAQAVLISGDQDPBEVTPADLPAGAVQSLAEDEKKKQKRGKSKLEGMPAYL 1497
Qy      70 VHAVTGQSPBRGLHSEKREDEGWVYRLGARDAHQGPWTAL-RPR---DG--EDKEMKT 123
Db      1498 QBAFGP-----KELLDLSRK---ALPAGV-----GRPSGLGTPKAKGKGSGSERLELPT 1544
Qy      124 YRLDAGDAPRRLCDLERERMAVITQGAVKKSTVATLQSTPRHGDPRTPGPRSTPLEE 183
Db      1545 SQ---KGDGP-----DIDEESRGLEGKADTPGPEDEGVKASPVSPDEKGTGEBGLTS 1598
Qy      184 NVVDREIDIDFLAARQQLSLQANKGAPHSAPAGTPAGTTPGASQAPKAFNPHLANGH 243
Db      1599 D-LDRISTEEL-PMESKDLQQLFKDVLVSEREGHLCGG-TPLGEGSRTPLOQRFQGG- 1654

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Qy      244 VPIKPOVKGVREENKRAVPWTASVQVVD-----DPGSLAS--VESPTPKET 291
Db      1655 -LPL-----GNLPSSSPMDSITPGLCQSPFLDSRRGCFSPSEBPSPMTWGSQGTPTST 1708
Qy      292 PIEREIRLAQERAD--LREQGLRQATDQELVEIPT-RPLTKLSLITAPRERGRP- 347
Db      1709 FTTT---TTGEGDGLSYNQRSLQRWEKDELGLSTISPYL--YANINFPNLKQDYPD 1762
Qy      348 -----SLYVQR-----DIYQET 359
Db      1763 WSSRCQIMKLMRKVPADKAPYLQKADKNRAHRINKVQKQASQINKQTKGVGIART 1822
Qy      360 QREEDHR-----EGLHVGASTPDWSEGFQGLRRALSSTLS----400
Db      1823 DRPALHLRIPQPGALGSPPAAPLTFIGSPTTLAGLS-----TSADGLKXPA 1872
Qy      401 ---PAPD-----ARAAP---APEVRKNRIP--PDAYQPYLS-----430
Db      1873 GSVPGPDSRGELFLKLPPQVPAQPSQDPFGALAPVPLEPRFPPTAPPTYPYPPSPPTGAPA 1932
Qy      431 -----PAPD-----PCTPOLFSAFGAFGKP-----SLSSTAEKAKATSPK 462
Db      1933 QPMLGASSRPGAGQGEHTTTPGTTPRQPSPTPDPFLKPCPSLDNLAVPESPGVGCK 1992
Qy      463 AT---MSPRHLSESGKPLSTKOE---ASKPPRGCPQANRGVVRWEYFRLRLRFRAPDE 516
Db      1993 ASEPLSPPPGESR-KALEVKKBELGASSPSYGP--NLGFV-----DS 2034
Qy      517 PQOAVPVYWGVEVAGAPALRLQKSSDLERERESVLRREQEVAERRNA---LPEE 572
Db      2035 PSSG--THLGLLELTPDVFKAPLTPRASQVEPQSGLRLQEPQALAPSPSHPD 2092
Qy      573 VFSPTPDNSDQNSRSSQASGITGSYSVSESPFSP 609
Db      2093 IFRP-----GSYT---DPYAQP 2106

```

RESULT 12

A12284
 translocation initiation factor IF-2 [imported] - Nostoc sp. (strain PCC 7120)
 C1:Species: Nostoc sp. PCC 7120
 A1:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C1:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C1:Accession: A12284
 R1:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Res. 8, 205-213, 2001
 A1>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A1:Reference number: AB1807; MID:21595285; PMID:11759840
 A1:Accession: A12284
 A1:Status: preliminary
 A1:Molecule type: DNA
 A1:Residues: 1-1039 <KUR>
 A1:Cross-references: UNIPROT:Q8YQ11; UNIPARC:UP100000CE912; GB:BA000019; PIDN:BA075531.1,
 A1:Experimental source: strain PCC 7120
 A1:Gene: infB
 C1:Superfamily: translocation initiation factor IF-2; translocation elongation factor Tu homc

Query Match 4.4%; Score 158; DB 2; Length 1039;
 Best Local Similarity 20.3%; Pred. No. 0.18;
 Matches 107; Conservative 59; Mismatches 180; Indels 180; Gaps 25;

```

Qy      142 ERMVAVTQGAVKKSTVATLQSTPRHGDPRTPGPRSTPLEBNVVDREQIDFLAARQQL 201
Db      53 EKLAATNGSKKELNATSHKPSAPAGSRNRPAPQK-----QQQIL 94
Qy      202 S-----LEQANKGAPHSAPAGTPAGTTPGASQAPKAFNPHLANGHVPPIKPOVKGV 255
Db      95 EIRKPKILNNTSNMPEASVANNQIASSEANSAPAPRPATP-----VSPKPTAPS-- 146
Qy      256 REENKRAVPWTASVQVVDPSGLASVESPTPKET---IREREIRLAQER-EADLREQR 311

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Db 147 -----RPVPLNLS-----ETPOKPAPEAPEAQAQAKIAVEKPEKSAQRP 190
Qy 312 GLRQATDHQELVELPTPLTKLSL-ITTA-----PRERGRPLVYORDVQTOQEED 364
Db 191 GKPRQPKPQLVAPSRPTAEKLDLSEITGAPGEKPLIKRDP-----PRD 237
Qy 365 HRRBGLHVGRATDPMWSEGPQGLRRALSISLSPADARADPA-----PEVRKVR 419
Db 238 ERDQA-----KPRVAKAQAQET--SSAPVQKQAPRAGLVKPE-QKVR 278
Qy 420 IPPDAYQPYLSPGTPQLEFSAFGAFKPSLSLTAAKAATS PKATMSPRHLSSESGKPLS 479
Db 279 -----PGAPSGD-----GIRPORVPR-----SADAAFWA 303
Qy 480 TKQASKPRPGCQANRQVAVMEYFRLRP-LRFRAPDEPOQAVPHWGW-----529
Db 304 T-----PPRGVPGGGRGEA-GDTAALAPDLLLRPPRLLAGKKKQEEIITDIKE 356
Qy 530 ---VAGAPALRLQ-----KSQSDLLERRESVLRQ-----EVAERRNALF 570
Db 357 KAGKAGVGVKGVKPLVEDPDEDELDLDEGLIEPATVQVSLIARPPKKAARSAAATA 416
Qy 571 PEVFSPT-----PDENSQNSRSSQAS-----GITGSYSVE 603
Db 417 APISPTTRGKRSSHNRDQNRROETEVKREPEREKVAVTGAMTVOE 462

RESULT 13

hypothetical protein KIAA0324 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C:Accession: T02345
R:Ricke, D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, D.;
re, J.; White, S.; Ueng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L.
submitted to the EMBL Data Library, March 1998
A:Description: Sequencing of human chromosome 16p13.3.
A:Reference number: Z14664
A:Accession: T02345
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1791 <R1C>
A:Cross-references: UNIPROT:O60382; UNIPARC:UPI00000730AE; EMBL:AC004493; NID:G2936648;
C:Genetics:
A:Map position: 16
A:Introns: 1610/2; 1706/2
A>Note: KIAA0324

Query Match 4.4%; Score 156.5; DB 2; Length 1791;
Best Local Similarity 21.7%; Pred. No. 0.44;
Matches 118; Conservative 66; Mismatches 186; Indels 173; Gaps 22;
Qy 170 PRTGPPRSTPLEENVNDREQIDFLAARQPLSLQANKGAPHS--PAKSTPAQTTPG- 226
Db 443 PRTGPRERS--SASSPEMKDGLPRTPSRRSRSGSPGLRDSGTPSRHSLSGSSPGM 498
Qy 227 -----ASQAPKAF-----NKPHLANGHVPIRPQVKGAVREBK 260
Db 499 KQIPRTPSRGRSECDSSPEPKALPQTTPRSRSPSPPLNKKCLTP-----QREKS- 549
Qy 261 VRAVPTMASVQVDDPGSLASVSPGTPKETPIREIRLAQREADLR-----EORG--- 312
Db 550 -----GSSSVQDK-TYAKTPLGSRSGSSGQELDVPRSPSPQERSSD 592
Qy 313 -----LRQATDHQELVELPTPLTKLSLITAPRRGRPRLVYQORDVQTOQE 360
Db 593 SSPDSKAKTPTPLRQSRSGSSPEVDSKRL-----SPRRSRSGSSPEV-KDKPRAP 644
Qy 361 REEDHRRBGLHVGRATDPMWSEGPQ--GLRRALSSSIISPADA-----405
Db 645 RAQS-----GSDSPPEKAPAPRALPRSRSGSSSKGRGPPSEGGSSSTESSPEHPPK 696
Qy 406 -----RAADPAPEVVKVIRIPDAYQPYLSPTQLEFSAFGAFKPSLSLTAAKAATS 460

Db 697 SRTARSGSRSPPEPKTSRTP--RRRSRSPBELTRKARLSRRSRSSASSPETRSTRP 753
Qy 461 PKATMS-----RHLSSESGKPLSTQBAKP--PGCQANRQVAVME 502
Db 754 PRRRSRSPVSPPEPAEKSRSSRRRSASPRTTTSRRGSPFPKPRGL-QRSRSRRE 812
Qy 503 YFRLRPFAPRDEPOQAVPHWGWVAGAPALRLQKQSDLLER-----ESV 554
Db 813 KTTTRRRDSSGSSQSTR-----RQGRSRSRVYRRRRGSGSYHSRP 857
Qy 555 LRREQVAEERRNALPEVESPTPDNSQN-----SRSSQASGITGSYSVESE 605
Db 858 ARQESSRSTRRR--RGRSTRPTSRKRSRSTRSPAPKRSRSPATHRSTRTP 913
Qy 606 PFS 608
Db 914 LIS 916

RESULT 14

gene APXL protein - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I37183
R:Schiaffino, M.V.; Baezi, M.T.; Rugerli, E.I.; Reniet, A.; Galli, L.; Ballabio, A.
Hum. Mol. Genet. 4, 373-382, 1995
A:Title: Cloning of a human homologue of the Xenopus laevis APX gene from the ocular albu
A:Reference number: I37183; MIMD:95315933; PMID:7795590
A:Accession: I37183
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1616 <RES>
A:Cross-references: UNIPROT:Q13796; UNIPARC:UPI0000125D05; EMBL:X83543; NID:G790999; PID:
F32-104/Domain: GLGF domain homology <GLG>

Query Match 4.4%; Score 156; DB 2; Length 1616;
Best Local Similarity 20.8%; Pred. No. 0.41;
Matches 156; Conservative 68; Mismatches 248; Indels 278; Gaps 39;
Qy 37 GPBASGWDDEPQTWRDHAQGVQGVSYSS-----VNAATGQSPSR 80
Db 541 GABGCSAGQEP--PRASRAEKASORLASITWADGESSRICROETPLILSLTQBGKR 597
Qy 81 GLHSENRDEGWQVYRLGARDAHQGRPT-----NALRPE-----DGEDKEMKTYRLD- 127
Db 598 --PSSSPED--SATRRPRPDVAHGKTRSDSRPATTLRNKIEIGMNRKAKLOKSRTVALTA 652
Qy 128 AGADAPRRLCDLREERNAVITQGAVKRSSTVATLQSTRD-----167
Db 653 AGEALD-----GTGRVRAIGGGTQEGPLAGTYK--DLKKAQAVLRATSPKRDLD 703
Qy 168 -----GDPRT-----PGPR-----177
Db 704 PNPGLYPESLHRMGDPDTPVPHWEAGLAQPPSSSGGPHPRPIGRRRFTAEQKLKSY 763
Qy 178 STPLEENVV-----DREQIDFLAARQPL-----SLQANKGAPH 212
Db 764 SEPEKMEVGLTGYSHQNPRISEDTVGTFADBNKFEETSKVPQRRAKQALNIFR 823
Qy 213 SSPAGTTPAGTT-----PGASQAP-----KAF 234
Db 824 DKPERPTARTQVGTGTEPWRSTSLGDSLNAHSALEKAGTSDLRRLRGTAFAVQASWEQ 883
Qy 235 NKP-----HLANGV-VPIKQ-----YKGVAREENKVAVPTMASVQVDDPGSL 279
Db 884 RKPLEARSGRCHSADILDVSLDPOERPQHVHGRSRSSPSTDTYKQEAIVELRQAG-- 941

QY 280 ASVESKCTPKE---PIREIRLADGREADLREQGLRQATDHOELVEIPTRPLTKLSL 336
 Db 942 ----DPGEERELPSVRAEESQSTPRQADQCRRESFGQHPSPQKAPNPPTSELSH 997
 QY 337 ITA---PRERGRPELVYORDIVQETQREEDHREGLHVGRASTP-DVNSEGPQGL-R 390
 Db 998 CIGAPRLPEEGGRACLT-----PRDYR-----YSEESTPADIGPRAQSGSL 1041
 QY 391 RALSIDS-----ILS--PAPDAPADPAPEVRK---VNRIPDA-----YOPYLSPTGP 434
 Db 1042 HARQDSWPFVSALISKRAPO-RPPPKRPPRYATGADAPADAPVGLGRPPPTSPSA 1100
 QY 435 QLE--PSARGARGKSSLSLTAEKATSPKATMSPR---HLSSESGKPLSTQEAASKPR 489
 Db 1101 SLDYVYARLSLSHSPSVFSSAQPO--DTEKATVCERQSHVSGDASRPL--PEALLP- 1154
 QY 490 GCPQANRGVMEVFPRLRPFRAPEPQOAVPHVMEVAGAPALRLQKSSDPLER 549
 Db 1155 -----KQHLRLQTRMTETSRSPSPQAPQO---KLTDKPLLLQ-DEDSRIR 1199
 QY 550 ERES-----VLRQEVAEERRNL 569
 Db 1200 VMDNTTVGMVPIKIVHSESQPEKESQSL 1229

RESULT 15

A43359

microtubule-associated protein MAP1A - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: A43359; S22108

R.Jiangkop, A.; Hammarback, J.A.; Muller, R.; Vallee, R.B.; Garner, C.C.

J. Biol. Chem. 267, 16561-16566, 1992

A/Title: Microtubule-associated proteins 1A and 1C2. Two proteins encoded in one messeng

A/Reference number: A43359; NCBI:92355629; PMID:1379599

A/Accession: A43359

A/Molecule type: mRNA

A/Residue: 1-2774 <LAN>

A/Cross-references: UNIPROT:P34926; UNIPARC:UPI000012EBQ2; GB:M83196; NID:G205537; PIDN:

A/Note: sequence extracted from NCBI backbone (NCBIN:111039, NCBI:P.111040)

R.Crawchik, A.

Submitted to the EMBL Data Library, June 1992

A/Reference number: S22108

A/Accession: S22108

A/Status: preliminary

A/Molecule type: mRNA

A/Residue: 73-364 'NRURS', 370, 'OKN', 374, 'PSPKGL', 381-751, 'RSMWSQNNAAOR', 764, 'D', 766, 'LR

A/Cross-references: UNIPARC:UPI00001752D; EMBL:X66840

A/Experimental source: strain Sprague Dawley

C/Superfamily: microtubule-associated protein MAP1B

C/Keywords: microtubule binding; phosphoprotein

Query Match 4.4%; Score 156; DB 2; Length 2774;

Best Local Similarity 20.7%; Pred. No. 0.8; Mismatches 256; Indels 246; Gaps 33;

Matches 151; Conservative 75; Mismatches 256; Indels 246; Gaps 33;

QY 38 PEASGNGOE-----POTWPTD-HRAQGVORQGVSYVHAVTGQSPGLHSEN 86
 Db 1376 PEQKGRDLDEKDTAELIDKGPPEKDLIDREDQ-QR-----AGPPAEKDKASEQ 1424
 QY 87 REDEGQVYRLGARDAHQGR-----PTW 109
 Db 1425 RQTDLQQTQATEPRDRARQBRDSBKOKSLERDRPEKORILVQEDRAPESHSTPEPTQ 1484
 QY 110 ALRPPD---GEDEVKMTYRLDAGDADPRRLCDLEREMAV-IOGQAVKSSVTA-----T 160
 Db 1485 TDRAPRKGTDTDKQKKE-----EASEKEQVLEQKDMALGKEGETLIDQEARTAEQDET 1538
 QY 161 LGGTPPHGDPRTGQPPRSTPLEENVVDR---EOIDFLAARQGLSLEQANKGAPHSPPAR 217
 Db 1539 LKEDKTQGGKSSFVEDKTTTSKETVLDDQKAEKADSV-EOQDGAALKEKTRALGLESPAE 1597

QY 218 GTPACTTGASQAPKAFKPHLANG--HVPDIKQVKGVEENKVRAPPTMASVQVVD 275
 Db 1598 GSKA-----REDEKMYGEQDVQGMKRTSTPRGPGQKE-----FVPAMBG----- 1641
 QY 276 PGSILASVESPGTPKETPIEREIRLAQE-----READLREQ 310
 Db 1642 -----XSPEGEVYVMDRDTTLQDQVMBELSCDKVMFPHELDQGANPRYCEBERES 1694
 QY 311 RGLRQATHQELVEI---PTRPLTKLSLITAPRERGRPSLYVORDVQV-----TQRE 362
 Db 1695 TPLDGPPEQOETPLQHTPRSPWTSDFDQFQEPLOKQ--LEVERMTAESVGLPPEBE 1751
 QY 363 EDHREGLHV--GRASTPDWVSEGPQGLRLRALSDSLSPAPDARADP----- 410
 Db 1752 DGLTSPPEIISPPASPPBMTCQ-----RVSPAPQGESFVDTSESTAPMNEPTTISW 1804
 QY 411 ---APEYKVNRIIPDAYOPYLSPTQLE-----FSAFGAFKPSLSLTAEKKATS 460
 Db 1805 LAEIPFWVKORPLPPAPLSPAPAPPTPAPEHTVPFS-WGLAEDSVAAVQGA-- 1861
 QY 461 PKATSPHLSSESGKPLSTQEAASKPRGCPQANRGVVMYFRLRPLRFPADPEPQA 520
 Db 1862 -----ELGEPYSPLOKDYRKAEGEREGG----- 1887
 QY 521 QVPHVMEVAGAPALRLQKSSDPLERERESVLRQEVAEERRNLPEVFPSP--P 578
 Db 1888 -----AGAP-----DSSFSKVPBAGSLATRDQYB-----PQREPTYP 1926
 QY 579 DENSDQNSRSSQ--ASGITGSYSVESPPFPIHLSNVANTVEDPVDSADPGQRKKEQ 636
 Db 1927 DERSFYADIVQMLDGLGPRCPTREPP-----LGAAGDM-----PPHLSTKEB 1971
 QY 637 WTGINPS 644
 Db 1972 -AAGCNTS 1978

Search completed: March 3, 2006, 13:36:29
 Job time : 47.8912 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 13:19:17 ; Search time 259.327 Seconds

(without alignment)
1847.299 Million cell updates/sec

Title: US-10-646-873-42

Sequence: 1 MDRTVRRYPIGLIPQAHRTG.....KKNMAKRWESRIVASEDD 679

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3583	100.0	679	1 CS021_HUMAN	081VY2 homo sapien
2	3260	91.0	685	1 CS021_PONPY	05IBD3 pongo pygma
3	2061.5	57.5	648	1 CS021_MOUSE	09d279 mus musculu
4	246	6.9	848	2 05XG05_XENLA	05XG09 xenopus lae
5	210.5	5.9	880	2 08C5M1_MOUSE	08C5M1 mus musculu
6	209.5	5.8	711	2 04S389_TETNG	04S389 tetraodon n
7	207.5	5.8	870	2 05U301_RAT	05U301 rattus norv
8	205	5.7	1103	1 AKAP2_HUMAN	09Y2d5 homo sapien
9	205	5.7	1103	2 05T721_HUMAN	05T721 homo sapien
10	203	5.7	1095	2 07S696_NEUCR	07S696 neurospora
11	197.5	5.5	1978	2 05KDX5_CRYNE	05KDX5 cryptococcu
12	195.5	5.5	949	2 05J744_HUMAN	05J744 homo sapien
13	194	5.4	1978	2 05S7P1_CRYNE	05S7P1 cryptococcu
14	193.5	5.4	319	2 09K6F7_HUMAN	09K6F7 homo sapien
15	192	5.4	1558	2 05KXK6_CRYNE	05KXK6 cryptococcu
16	189	5.3	1404	2 080VW7_MOUSE	080VW7 mus musculu
17	189	5.3	3941	2 BSN_MOUSE	088737 mus musculu
18	188	5.2	1266	2 080T06_MOUSE	080T06 mus musculu
19	187	5.2	1358	2 05SV03_CRYNE	05SV03 cryptococcu
20	185.5	5.2	1379	2 07S3B3_NEUCR	07S3B3 neurospora
21	185	5.2	1338	1 ACINU_MOUSE	09J1X8 mus musculu
22	184.5	5.1	6586	2 05ZFL1_MAGGR	05ZFL1 magnaporthe
23	183	5.1	1337	2 052KGI_MOUSE	052KGI mus musculu
24	183	5.1	1707	1 MDCL_MOUSE	05P8V9 mus musculu
25	182.5	5.1	1389	2 08T2C7_NEUCR	08T2C7 neurospora
26	182	5.1	1264	1 04UW12_XANCP	04UW12 xanthomonas
27	181.5	5.1	1283	1 RFIPI_HUMAN	06Wk24 homo sapien
28	180	5.0	1100	2 06ZP93_MOUSE	06ZP93 mus musculu
29	180	5.0	3925	1 BSN_HUMAN	09UPa5 homo sapien
30	179.5	5.0	3937	1 BSN_RAT	088778 rattus norv
31	177	4.9	3262	2 09E0U5_MOUSE	09E0U5 mus musculu

RESULT 1	CS021_HUMAN	STANDARD;	PRT;	679 AA.
AC	081VY2;			
DT	13-SEP-2005 (Rel. 48, Created)			
DT	13-SEP-2005 (Rel. 48, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Protein C19orf21.			
GN	Name=C19orf21;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OC	Homo			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	TISSUE=Brain, and Colon;			
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,			
RA	Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Dickenson L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McKernan P.J., McKernan K.J., Gay L.J., Huijck S.W.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Lu X., Gibbs R.A.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,			
RT	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	EMBL: BC042125; AAH42125.1; -; mRNA.			
CC	EMBL: BC052236; AAH52236.1; -; mRNA.			
DR	PIR; T00636; T00636.			
DR	Ensembl; ENSG0000009812; Homo sapiens.			
DR	HGNC; HGNC:27000; C19orf21.			
KW	coiled coil.			
FT	COILED 545 569 Potential.			
SQ	SEQUENCE 679 AA; 75357 MW; D2881CF5087E61F8 CRC64;			

32	176.5	4.9	1369	2	04RY08_TETNG	04RY08 tetraodon n
33	176	4.9	2173	1	MDCL_MOUSE	05Em68 macaca mulia
34	175	4.9	1271	2	07S817_NEUCR	07S817 neurospora
35	174.5	4.9	1115	2	0591W5_MOUSE	0591W5 mus musculu
36	174	4.9	4322	2	07XKX1_ORYSA	07XKX1 oryza sativ
37	173.5	4.8	1151	1	BTBDC_HUMAN	081Y92 homo sapien
38	173	4.8	2468	1	MAP18_HUMAN	046821 homo sapien
39	172.5	4.8	1147	2	07S757_NEUCR	07S757 neurospora
40	172.5	4.8	1160	2	06MW56_NEUCR	06MW56 neurospora
41	172.5	4.8	3277	2	07NN14_GLOVI	07NN14 gloeobacter
42	172	4.8	4221	2	04HY74_GIBZE	04HY74 gibberella
43	171.5	4.8	1099	2	0591W7_MOUSE	0591W7 mus musculu
44	171.5	4.8	1524	2	05AZ02_EMENTI	05AZ02 aspergillus
45	171	4.8	454	2	04S7V9_TETNG	04S7V9 tetraodon n

Query Match	100.0%;	Score 3583;	DB 1;	Length 679;
Best Local Similarity	100.0%;	Pred. No. 9.1e-172;		
Matches 679;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy 1	MDRVTYRYIIIGAIPOAHRGSTGLVLQDDSTYYTHALVCMGFEASGMQDEPQTPTPHRAQOG	60		
Db 1	MDRVTTRPIILAIPOAHRGSTGLVLQDDSTYYTHALVCMGFEASGMQDEPQTPTPHRAQOG	60		
Qy 61	VORQGVSYVAHYTQGPSRGLSHSENREDEGMQYVRLGARDAAOGRPTMALRPEDGEDKE	120		
Db 61	VORQGVSYVAHYTQGPSRGLSHSENREDEGMQYVRLGARDAAOGRPTMALRPEDGEDKE	120		
Qy 121	MKTYRLDAGDDPRLCLLEBRNAVYVIOGAVKRSTYATITQGTPTDHEDPTTGGPRSTP	180		
Db 121	MKTYRLDAGDDPRLCLLEBRNAVYVIOGAVKRSTYATITQGTPTDHEDPTTGGPRSTP	180		
Qy 181	LEENVVREBOIIDLFLAARQOFLSLEQANKGAHSSPARGTPTAGTTPGASQAKAFNKPHLA	240		
Db 181	LEENVVDEEQIDFLAARQOFLSLEQANKGAHSSPARGTPTAGTTPGASQAKAFNKPHLA	240		
Qy 241	NGHVVPPIKQYKGVVREENKVRAPVTMAVQVVDPGSLASVESBGTPEKPTPIREIRILA	300		
Db 241	NGHVVPPIKQYKGVVREENKVRAPVTMAVQVVDPGSLASVESBGTPEKPTPIREIRILA	300		
Qy 301	QERADLREORGLRQATDHQELVEIPTRPILTKSLITAPRRERGRPSLYQORDIVQETQ	360		
Db 301	QERADLREORGLRQATDHQELVEIPTRPILTKSLITAPRRERGRPSLYQORDIVQETQ	360		
Qy 361	REEDRRRGLVGRASTDWMVSEGGQGLRLASDSITLSPAPDRAADPAPEVRKTVRI	420		
Db 361	REEDRRRGLVGRASTDWMVSEGGQGLRLASDSITLSPAPDRAADPAPEVRKTVRI	420		
Qy 421	PPDAYQPIPLSGTPOLEFSAFGAFGKPSLSITAEAKATSPKATWSPHLSSESGKPLST	480		
Db 421	PPDAYQPIPLSGTPOLEFSAFGAFGKPSLSITAEAKATSPKATWSPHLSSESGKPLST	480		
Qy 481	KQASKPRGCGPOANRGVWMEYFRLRLRPAPADPEQAOVPHYWGEVAGAPALRIQK	540		
Db 481	KQASKPRGCGPOANRGVWMEYFRLRLRPAPADPEQAOVPHYWGEVAGAPALRIQK	540		
Qy 541	SQSSLLRERRESVLRREQVAAEERNMLFPBVFSPTDENSQNSRSSQAQSGITGYS	600		
Db 541	SQSSLLRERRESVLRREQVAAEERNMLFPBVFSPTDENSQNSRSSQAQSGITGYS	600		
Qy 601	VSESPFSPILHSHVAMTVDEPVDSPAPGORKKQYAGINPSDGINSEVLEAIRVTRH	660		
Db 601	VSESPFSPILHSHVAMTVDEPVDSPAPGORKKQYAGINPSDGINSEVLEAIRVTRH	660		
Qy 661	KNAMAEWESRIYASEDD 679			
Db 661	KNAMAEWESRIYASEDD 679			
RESULT 2				
ID CS021_PONPY	STANDARD;	PRT;	685 AA.	
AC OSRBH3;				
DT 13-SEP-2005 (Rel. 48, Last sequence update)				
DT 13-SEP-2005 (Rel. 48, Last annotation update)				
DS Protein C19orf21 homolog.				
OS Pongo pygmaeus (Orangutan).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;				
OC Pongo.				
NCBI TaxID=9600;				
NCBI (1)				
NCBI NCUBOTRIDE SEQUENCE (LARGE SCALE MRNA).				
RC Tissue=Kidney.				
RG The German cDNA consortium;				
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.				
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[illegible]

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OC NCBI TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX MEDLINE=22354683; PubMed=1246651; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikiido I., Otsu N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
 RA Balderelli R., Hall D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schramm L.M., Karpman A., Matsuda H., Baralov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frizer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guentrich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongsang A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltsev L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Raveil T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelain A., Schneider C., Sempé C.A., Seton M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomlita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilmberg L.G., Wymshaw-Borle A., Yamagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,
 RA Hirozane-Koshikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shitaki T., Waki K., Kawai J., Ishii Y., Itoh M., Kagawa I.,
 RA Hara A., Heshizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingara S.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX STRAIN=FVB/N; TISSUE=Colon;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnaa.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klauer R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tohyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McLean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalek U., Smolins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:1689-16903(2002).
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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 CC removed.
 CC
 DR EMBL/ AK020266; BAB32049.1; -; mRNA.
 DR EMBL/ BC013508; AA113508.1; -; mRNA.
 DR EMBL/ ENSMUSG0000035852; Mus musculus.
 DR MGI/ MGI:1926156; 9130017M09rik.
 KM Coiled coil.
 FT 511 534 Potential.
 SQ SEQUENCE 648 AA; 72281 MW; 1E395B70763B3D1F CRC64;

Query Match 57.5%; Score 2061.5; DB 1; Length 648;
 Best Local Similarity 62.5%; Pred. No. 1.8e-95;
 Matches 428; Conservative 66; Mismatches 148; Indels 43; Gaps 10;
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 1 MDRTYRPPIIGI POAHRTGVLVDGTSYTHVLCMPPEASGWDPEPTPDHRAQOG 59
 61 VOROGVSYSVAVYVQGPSPPGSGSENNDESGMYRIGARDAHQGRPTWALRPDGDKE 120
 60 VKRTNVSNNRNVFVQGOQSPRLTYLED-----DEE 89
 121 MKTYRL-DAGDADRRLCDLREERNVAVIQOAVKSSVTATLQGNPHGDPRTGPPRST 179
 90 IKSHYLDSSSTLCKORRELAERNAVYVQOAVKSGTATLQASDHGDIRARQPOST 149
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 150 VTEELVDTREQIDFLAARQPLSLQANKG-APHSPPARGTPTGASQAPRAFKPH 209
 229 LANGHVVDIKQVGVVRENNKVAVPTWASVQVVDPGSLASVSPGTPETPTERRIR 298
 210 LANGYTVAVTSPKKEVTLE--KSFVSPARSINHYNDGSOQOASPTPTPTERRIR 267
 299 LAQERADLRORGLRQATDHOELVETPTRLTLKLSLI-TAPRRGRPSLYVORDYQ 357
 268 LAQERADLRORGLRQATDHOELVETPTRLTLKLSLI-TAPRRGRPSLYVORDYQ 327
 358 ETQREDRRRGLAHVGRASPDPWSEGPQGLRRLASDSILSPADRAADPAPEVAKV 417
 328 ETQREDRRRGLAHVGRASPDPWSEGPQGLRRLASDSILSPADRAADPAPEVAKV 385
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 366 NRIPDAYOPLYSPGTPOLSFSAFGAFKGPSSLSIAEAKAATSPATYMSPPHLSGSGKP 445
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 446 LSTKQDASKPPRGCGQANRGVVRWYFRLRLRFAAPDEPQOAVPHWVGWVAGAPALR 503
 538 LOKSOSDILREERSVLRBOEVAERRNALFPEVFPSTP--DENSDONSRSOASGI 595
 504 LOKSOSDILREERSVLRBOEVAERRNALFPEVFPSTP--DENSDONSRSOASGI 563
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 564 TGSYSVSESPSPPIHSHNVATYEDPVDSAPPGQR-KKEQVYAGINPSGINSERVLEA 623
 655 IYVTHKNAAMERWESRYIASDEED 679
 624 TVKSKHKNLLAERWEAHYASDEN 648
 RESULT 4
 ID 05XG09 XENLA PRELIMINARY; PRT; 848 AA.
 AC 05XG09;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE LOC495240 protein.
 GN Name=LOC495240;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OC NCBI TaxId=8355;
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 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Splice;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Straubeberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RL initiative";
 RN Dev. Dyn. 225:384-391(2002).
 (2)
 RA NUCLEOTIDE SEQUENCE.
 RC TISSUE=Splicein;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stjepicon M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 (3)
 RA NUCLEOTIDE SEQUENCE.
 RC TISSUE=Splicein;
 RL Klein S., Gerhard D.S.;
 RA Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC084662; AA04662.1; -; mRNA.
 SQ SEQUENCE 848 AA; 94304 MW; D7FC3AF563828D8B CRC64;
 Query Match 6.9%; Score 246; DB 2; Length 848;
 Best Local Similarity 20.0%; Pred. No. 0.00027;
 Matches 168; Conservative 117; Mismatches 283; Indels 270; Gaps 34;
 QY 8 PILGIPQAHRTGLVLDGDTSYTHLVCMGPBASGWDGDEPQTPDHRAGQGVORGVGS 67
 DB 113 PVLEITEASE---VMDE-----VCMGHSGQGNKDEP----- 141
 QY 68 YSVNAYITQBPSPRGHSENREDEGQVY-----RLGADADAGQRTYALRDEDEDK 119
 DB 142 --FGYITYPASPNSNSRRSSRRSGKGDILPKITIKKAEKELTFHEKKPSKLPDFNEKE 199
 QY 120 EMKTYRLDAGADAPRLCDLREBRWAVIQGAVRKSIVATLQGTDPH----- 167
 DB 200 HIRAKVAPSE---EVOLEKEKRELKISQAVKKNISITTKMNPPOEKITEQLDSQ 255
 QY 168 -----GDPRTPG-----PP--RSTPLEENVVDEQIDFLARQOF 200
 DB 256 LESHQYKERKQKLOQGGSP--PAVKANHLPPVLSEFTAVAKKEDIVTEQIDFLARQOF 313
 QY 201 LSLQANCAHSSSARAGTPAG--TTP--GASQAPKAFKPHLANGVVIKQYKQYV 255
 DB 314 LNMETWNPYKPPKRSVSNLFTVPFYSSEKSKSYCTVTN---PSVPCVOSVQ 369
 QY 256 REENKVRN-----VPTW-----ASVGVNDPGLASVES--RGTPEKT 291
 DB 370 GETPLVKAERVNCISEDPTMQRMLADAPSPSSADIDQBEKYSKRAEFVNTASFT 429
 QY 292 PI-----BREIR-----LAQERADLEBQRLGATDHOELV----- 323
 DB 430 VLKDDSDLSDFPVKSVSVSLPEBQDGLDLSTKSDTVMETLSNYFMDNISDGA 489
 QY 324 -----EITRPLTKLSLITPRERG--RPSLYVQ----- 352
 DB 490 SNETMSAQHDYSLGDSQPTPVDNTLNEYLLEESKDYQDFYSSSMLQDIDOLDYHA 549
 QY 353 -----RDIYQETQRBEHDHREGLVHVGRASTPWWVSQPGRLRRLASDSISLSPADAAA 408

DB 550 GVLGVNVIOQALAEKXGKGFDSH-----SEDSQSKSVFPDNN-- 585
 QY 409 DPAPYRKVRNIRPPADYOPPLSPGTPQLERFSAAGAKGSPSLTAE AKATSPKATMR 467
 DB 586 EPLTERSEIQ-----SCSSPVPSPGRDRE-----VPEPPVSSPVQYTKITIPK-TFEG 635
 QY 468 RHLSSESGKRLSTKQKASKPRGCPQANGVWR-EYFRLRPRFRAADBPQAOVPHW 526
 DB 636 ENPOLKQNDPLSTK-SLSPTEQNTBHKQESFYSKYSQAEIR-----STASLATQ 687
 QY 527 GWEVAGP-ALRLQKSSDILLERESVLRROEVAERENALPFEVSPPTDENSQ 585
 DB 688 ETISVGPFLRKQKQXTLSMIEEIRAQERQDLKKQERQSIOGHSR-----S 739
 QY 586 SRSSQASGITGSYSV-----ESPFSPIHL-----HGVNATVE 621
 DB 740 NKSAPVLPRTVTSYKTAAPGKIEKIRNPPSPRGSPFIQDPLLEATGSGRPKLMETLM 799
 QY 622 DPVDSAPPGQRKKQWYAGINPSDGINSEYLAIRVTRHKNAMERESRIVASEDD 679
 DB 800 DPESHKTKRQKMD-----DATVLDVVRVNRKSLALKKEAGIYANRDD 846
 RESULT 5
 ID Q8CSW1_MOUSE PRELIMINARY; PRT; 880 AA.
 AC Q8CSW1;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 DE library, clone:4932411M01 product:A kinase anchor protein 2, full
 DE insert sequence.
 GN Name=Akap2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=92729253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RA NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Atakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kodera K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Riechmann M., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Staudli F., Suzuki R., Tomita R., Wagner L., Watanabe T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guentrich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Maehima U., Mazzarelli U., Mombauts P.,
 RA Nodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RA NUCLEOTIDE SEQUENCE.

QY 228 -----SQAPKAF-----NCHLIANGHV-----IKQOV--GVWREKVRVAPVTASV 270
Db 339 TQOIFPSARKQFQJOMENSROTLAAGOSTPLFSIKYTPKLSIHSDEKPTIIRPATVG 358
QY 271 QVVDPDGSLASVSPGTPEKTPPIEREITLAEQREADLREQGLRQATDHOE--LVEIPTR 328
Db 399 GTLEDGGTAAKE-----QKAPCVSESSSAGAGAN-----AAQKQEGPYSBSKR 445
QY 329 PLTYKL-----SLITAPRRE--RGRPSLYVQBDIVYEQREEDHRREGHTVGRAS 376
Db 446 GPLSTKLMAEDGFSTBARAVLTVVQKEDHGLDQFSRSVNVSLTQEBLSDGIDELSVRSQD 505
QY 377 TPDWVSEGPQGLRRALSSDSLSPAPARAADAPPEVRKNTKTPPAQYPIYLSPGTPOI 436
Db 506 TT-----VLETLISNDFSMONIISQSGASNETPSALDENSU-----ADFSLPQTPOT 550
QY 437 E-----FSAFGAFKPSLSLTAAB-----KAISPATMSP 467
Db 551 DNESEBEGSVKSFSDHGFYSPSSITLGCSPSYVDPLEYQAGLLVQNALQALAEQVKA 610
QY 468 RHLSSESSG---XPLSTKQEA-----SKPFGC---POANGVYRWEXF-----RLRP 508
Db 611 AHTSKGSGSQOQREAVTEBASQGTGSEKQPGMFAPQVSSVPQEKDILPKLPAEDRA 670
QY 509 LRFRADEPQQAQVPH-----VWGW-----EVAQAPA 535
Db 671 LREKGPSQPTAAQSGPVMNEETPEGGYSKYSAAELRSTASLTATQESDVMVGPFK 730
QY 536 LRQKQSSDLERRESVTLREQVABER-----RNLFPPEV----- 572
Db 731 LRSRKQRTLSMIEELRAAQEREELKQKQOVROSTPSPRAKNA--PSLPERTTCYKAP 786
QY 574 -----FSPPTDENSQDNRSSQSGITGYSVSESPFSPHILHSNVANTVEDPV 624
Db 789 GKLEKTKPPSPPTPEPSLQPLAPBBAAG-----TQRP-----KNLMQTLMEDY 833
QY 625 DSAPPGQRKKEQWYAGINPSDINSEVLEAIRVTRHKNAAMERNESRTIYASEED 679
Db 834 ETHKSKRRERMD-----DSSVLEATVYNNRRKALALRWENAGIYANQEEB 877

RESULT 6
Q4S389.TETNG
ID Q4S389.TETNG PRELIMINARY; PRT; 711 AA.
AC Q4S389.
DT 13-SEP-2005 (TREMblrel. 31, Created)
DT 13-SEP-2005 (TREMblrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMblrel. 31, Last annotation update)
DE Chromosome 4 SCAF14752, whole genome shotgun sequence.
DE (Fragment)
GN ORNames=GSTENG00024750001;
OS Tetradon nigroviridis (green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetradon.
NCBI_TaxID=99883;
NN NUCLEOTIDE SEQUENCE.
RP Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Maucell E., Bouneau L., Fischer C., Ocout-Costas C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dadiela C., Salinoudat M., Levy M., Boudet N., Castellano S.,
RA Anthonard V., Ublin C., Caselli V., Katinka M., Vacherie B.,
RA Blomont C., Skalli Z., Cattolico L., Poulain J., De Bernardinis V.,
RA Crnaud C., Dupret S., Bottlier P., Coutanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosaak S.,
RA Kellis M., Wolff JN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolious H.,
RT "Genome duplication in the teleost fish Tetradon nigroviridis reveals
the early vertebrate proto-karyotype.";

RL Nature 431:946-957 (2004).
 RN [2]
 RP Nucleotide Sequence.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RC Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 RL -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL, CA001014752; CAG04693.1; -; Genomic DNA.
 FT NON TER 711 711
 SQ SEQUENCE 711 AA; 77525 MW; A44ACCB1617CE84 CRC64;
 Query Match 5.8%; Score 209.5; DB 2; Length 711;
 Best Local Similarity 20.2%; Pred. No. 0.015;
 Matches 155; Conservative 91; Mismatches 244; Indels 277; Gaps 31;
 QY 13 POAHGTGLVLDGTSYTHLVCKGPEASGNGDEPQTPTDRAQGVORQVSVVHA 72
 DB 79 PDAA--PPLVVOGQGRPTTL-----LSQEDTARRSNGHAQSEDLASSGAKFEIRA 125
 QY 73 YTGQPSRGLHSENRDEBGMVRLGARDAHQRPYALRPDEDEKEMKYRLDAGDAD 132
 DB 126 FOEERRPKLFTPDE--QGVVTRR--RPT----- 152
 QY 133 PRRLCDLEREMAVYQGVAVKSSVTAATLQCTPDHGPRTGPPRSTPLEENVDRQID 192
 DB 153 -EEVQELERERQELKEQAVGRNPEIA-----HRMNPQGVPLEEQ-IDAEQLS 200
 QY 193 FLAARQFLSLEQANKGAPHSPPARGTPAGTTPGASQAP----- 231
 DB 201 SLKKQGE---RKQOKQTPVYSGGVORQAGQPGVSGPTVVTDPDLIRKEDIVERQID 256
 QY 232 -KANKKHLANG-----HVPIKPV-----KGVAEKKVR 262
 DB 257 PSSARQFLQGGATKRDVPPIYSAKPELKSRCVGDADETGHWTSKDLAGEFTCAR 316
 QY 263 AVPTMASVQV-----VDDPGSLASV--ESPGLPKETPIEREIRLAQE 302
 DB 317 AVMTILTEEDGKGFHHSFLESDSGLDEPSRAAPNGSNGSTPEDEL-----E 368
 QY 303 READLREGRLQA---TDHQLVELIPTPL-----LTKLSTLTPARRERGRPSLY 350
 DB 369 YQAGILVQNALMIAAHNEDQWPGDAPPSFVSPSPSPSPVSVSSPLSAGAPSFH 428
 QY 351 -----YQDIVQETQRE--EDIRRESLHGRASTPMVSE-----G 384
 DB 429 SPVSSSPAGRRPREVVSPDETSESQSAPEETRPQ--APSAAPPQVSPSPQSKNG 485
 QY 385 P-----QPLRRALSDDSLSPADPARADPAPEVRKVRIPPDAYQPLSPGTQLESFA 440
 DB 486 PRITQSSYAAALAS-SAPAPAPAPAAVAVPR-----PAPYRRPSPSPSPKPEFSY 537
 QY 441 FGAGKGPSSL-STAAKAKATSPKATMSPRHLSSESGKPLSTKOBASKPRGCPQANRGV 499
 DB 538 FSKSYSEAEFLSTASAS----- 554
 QY 500 RWEFRRLRLFRAPD--EPQAAQVPHWGWGVAAGAPALRLQKSSDLEERESVLRRE 558
 DB 555 -----RAPEVTP-----ASGFRLRSKORTLSIEEIRIAAQQE 590
 QY 559 QEVAEERNALPPEVFSPTPDENSQNSRSGSAGTGSYSVESPPFSYIHLASNVAW 618
 DB 591 BELKKQKQEQ--PAY--TAPSSQSHVTRTGPRTGTPCPARMAKMSNLSIPALITLAKTAP 645
 QY 619 TVEDPVDAPPGQRKQEQWYAGINPSDGINSEV--LEAIRVTRHNAW 664
 DB 646 GKIEKVRAPD-----VSPSPSEGLASDAGSEDTGSRPKQNM 683

DT 01-FEB-2005 (T-EMBLrel. 29, Created)
 DT 01-FEB-2005 (T-EMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
 DE A kinase (PKA) anchor protein 2 (Predicted).
 GN Name-Akap2, predicted.
 OS Rattus norvegicus (Rat).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP Nucleotide Sequence.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butcherfield Y.S.N., Krzyzanski M.I., Skalka H., Smalins D.E.,
 RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP Nucleotide Sequence.
 RC TISSUE=Kidney;
 RG NIH MGC Project;
 RL Submitted (NOV-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL, BC085790; AA085790.1; -, mRNA.
 DR Ensembl; ENSRNOG0000011504; Rattus norvegicus.
 DR GO; GO:0016301; F:kinase activity; IEA.
 KW Kinase.
 SQ SEQUENCE 870 AA; 95941 MW; 516C22DA6D7A2DD2 CRC64;
 Query Match 5.8%; Score 207.5; DB 2; Length 870;
 Best Local Similarity 19.1%; Pred. No. 0.024;
 Matches 161; Conservative 107; Mismatches 273; Indels 301; Gaps 32;
 QY 37 GPBASGWDGDEPQTPTDRAQGVORQVSVVHAATGQPSRGLHSENRDEGW----- 92
 DB 128 GERANGHSTQPDQD-----LGNLQAPASSSSTSSHCSSRDEFTITTL 173
 QY 93 -QVYRLGARDHAQGRPTWALRPEDGDEKEMKYRLDAGDAP--RLCDLEREMAVYQGV 150
 DB 174 KKEAKFEIRAFHBDKKPSKLFEEDEHKEQFCIR--KYRPSBEMIIEKEREIRLSQ 229
 QY 151 AVKKSSTVATLQCTPDHGDRTGPPRSTPLEENV----- 185
 DB 230 AVKKNPGIAA-----KWNPPQKKTIEQLDEHLSHKKYKEREKKAQOBQLQ 279
 QY 186 -----VDRQIDFLAARQ 198
 DB 280 LQQQQQQQLQQLQQLQQLQQLSGLCTTAPAAHEHLSDEHTKEVAVTEQIDFSARK 339
 QY 199 QFLSLEQANKGAPHSPPARGTPAGTTPGASQAPKAFENK--HLANGHVP--IKPVQGV 255
 DB 340 QFGQWMSRQ-----TLAKQ-----STPRLFSI--KPFYKPGSINSKDPPTLTPATIGT 390
 QY 256 REENKRAVPTMASVOVVDPGSLASVSPGTP--KETPIREIRLAQERADLRQGLR 314
 DB 391 VEDSSTQAAKEORALCVSESQSGAGCTGNAATGQKEGYPSEP-----SKRG-- 436

RESULT 7
 Q5U301 RAT PRELIMINARY; PRT; 870 AA.
 ID Q5U301 RAT PRELIMINARY;
 AC Q5U301,

Db	EOQC	PEATVEEA	AAAFAGSEK	PGSMFEP	PQVSSP	VEKRVLP	---	KIIPAE	RALE	884
Qy	512	RAPDEP	-----	-----	-----	-----	-----	QQAQV	PHYWG	531
Db	885	RGPPQPL	PAVAPG	PSGPI	INNEETR	PEGSYSP	KYSEAA	ELASTA	SLATG	937
Qy	532	GAPALR	LOKSS	SSDLER	ERESV	LRREGE	VAEER	-----	RNA	573
Db	938	GPFLRS	KOKPT	LSNIEE	IEIPAA	OEREBEL	KROVLO	STOSP	PRTKA	995
Qy	574	-----	-----	-----	-----	-----	-----	-----	-----	621
Db	996	TAPGKIE	VKPP	PPPT	FTTGT	GPSIQ	PLAEE	XAAG	-----	1040
Qy	622	DPVDS	APPG	QKRC	---E	QWYAG	INP	PDGIN	SEVLEA	679
Db	1041	EDYETH	HSKR	REMR	DDSS	YTSK	LSCK	YTSV	LEATRV	1100
RESULT 9										
ID	05T721	HUMAN	PRELIMINARY;							
AC	05T721									
DT	01-FEB-2005	(TREMBLrel. 29, Created)								
DT	01-FEB-2005	(TREMBLrel. 29, Last sequence update)								
DT	13-SEP-2005	(TREMBLrel. 31, Last annotation update)								
DE	A kinase (PKRA) anchor protein 2.									
GN	Name=AKAP2; ORFName=RP11-47020.3-001;									
OS	Homo sapiens (Human).									
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;									
OC	Homo.									
OX	NCBI_TaxID=9606;									
RN	[1]									
RP	NUCLEOTIDE SEQUENCE.									
RL	Lawlor S.;									
RL	Submitted (May-2005) to the EMBL/GenBank/DBJ databases.									
RP	[2]									
RL	NUCLEOTIDE SEQUENCE.									
RP	Pardian R.;									
RL	Submitted (May-2005) to the EMBL/GenBank/DBJ databases.									
RN	[3]									
RP	NUCLEOTIDE SEQUENCE.									
RA	Kimberley A.;									
RL	Submitted (May-2005) to the EMBL/GenBank/DBJ databases.									
RN	[4]									
RP	NUCLEOTIDE SEQUENCE.									
RA	Phillimore B.;									
RL	Submitted (May-2005) to the EMBL/GenBank/DBJ databases.									
DR	EMBL; AL1535806;	CA112434.1;	-;	Genomic DNA.						
DR	EMBL; AL627225;	CA110811.1;	-;	Genomic DNA.						
DR	EMBL; AL158823;	CA119560.1;	-;	Genomic DNA.						
DR	EMBL; AL158828;	CA113896.1;	-;	Genomic DNA.						
DR	EMBL; AL153598;	CA140816.1;	-;	Genomic DNA.						
DR	EMBL; AL158823;	CA112434.1;	JOINED;	Genomic DNA.						
DR	EMBL; AL158828;	CA112434.1;	JOINED;	Genomic DNA.						
DR	EMBL; AL153598;	CA112434.1;	JOINED;	Genomic DNA.						
DR	EMBL; AL627225;	CA112434.1;	JOINED;	Genomic DNA.						
DR	EMBL; AL153558;	CA119560.1;	JOINED;	Genomic DNA.						
DR	EMBL; AL627225;	CA119560.1;	JOINED;	Genomic DNA.						
DR	EMBL; AL1535806;	CA140816.1;	JOINED;	Genomic DNA.						
DR	EMBL; AL158823;	CA140816.1;	JOINED;	Genomic DNA.						
DR	EMBL; AL158828;	CA140816.1;	JOINED;	Genomic DNA.						
DR	EMBL; AL153598;	CA113896.1;	JOINED;	Genomic DNA.						
DR	EMBL; AL627225;	CA113896.1;	JOINED;	Genomic DNA.						
DR	EMBL; AL1535806;	CA119560.1;	JOINED;	Genomic DNA.						
DR	EMBL; AL158823;	CA110811.1;	JOINED;	Genomic DNA.						

DR	EMBL	AL353598	CA110811.1	JOINED	Genomic DNA
DR	EMBL	AL353806	CA110811.1	JOINED	Genomic DNA
DR	Ensembl	ENSG00000157654	Homo sapiens		
KM	kinase				
SQL	SEQUENCE	1103 AA	122071 MW	B501182135112FE5 CRC64	
Query Match	5.7%	Score 205	DB 2	Length 1103	
Best Local Similarity	19.9%	Pred. No. 0.042			
Matches	155	Conservative 105	Mismatches 228	Indels 292	Gaps 33
QY	100	RDAGQGRPTWALRPEDEGDEKMKTYRLDAGDAP-RRLCDLERRRMVLVIGQAVRKSTV	158		
DB	413	RAFHEDKKPSLTFEDDEHEKQYCR---KVRSEMLELEKRRRLIRSQAVKQKPGI	468		
QY	159	AT-----	174		
DB	469	AAKWMNPQOEKTEIEQDLDEHLSHKYKERKERRAQOEQLLQKOLQOQOQCPSPQLCT	528		
QY	175	PRRSTPLEENVDR-----EQLDPLAAQQLFSLQANKGAPHSRPAETPAGTTP--	225		
DB	529	APASSHERASMTDAKEDIYTEQIDFSAARKQFQLEMNSKQAV---AQQ--STPRL	580		
QY	226	-----GASQAPKAFNKLHANGHVPIKQVGVVAEENKVAIPVPMASQVQVDD	275		
DB	581	FSIRPFRPLGSVNSDKPLNP-----RPSVGGPPEDSGAALGQKS-----	624		
QY	276	PGSLASVESPGTPKREPLERIRLAQERADLRE--QRLGQATVHQELVEIPTRPLITK	333		
DB	625	FGALETSPASGQGNL-----ASQKEGPGYSEPSKRG-----PLSKLMAE	664		
QY	334	LSLITTPRR-----ERGRPSLYQORDIYQETQREDRHRRELHYGRASPDPWSEGR	385		
DB	665	DGEFTSAVAVLTVVKDDHGLDHFSSVNVSLTQEBLSDGLDELVSRSQDTL-----	717		
QY	386	QPGELRALISDSILSPAPDAAPADPAEVEKVNRIIPDAYQVYSPGTPGLE-----	437		
DB	718	---VLEITSNDFSNIDNISDSGASN-----ETTNALQENSLADFLSLPQTPTQDNSEBGE	769		
QY	438	-----FSAFGAFGRSSLSLTA-----EAKVATSPKA-TWSPHLS	471		
DB	770	GVSKSFSDHGFYSPSSTLGDPSLVDPLEYQAGLLVGNALIQALAEQVDDKAVSKTSDGA	829		
QY	472	ESSGKPLSTKQEAS-----KPR-GCP-QANGVVMWEXFLRP-----LRF	511		
DB	830	EQQG-PEATVEAEAAAAFGSEKPSQMEFPQVSSPVEKEDVLP-----KLIPADRLRE	884		
QY	512	RAPDEP-----	531		
DB	885	RGPRQPLPVPVQSPSPIMMEETRRPGSIFSKTSEAAELRSTASLILATDESIV-----MV	937		
QY	532	GAPALRLQKSGSDLLERERESVLRQOEVAEER-----RNALPPEV-----	573		
DB	938	GPFLLRSKKQKTLTSMIEBEIRIAAGEREBELKQGOVLQSTQSPRTKXA--PSLSRPTCYK	995		
QY	574	-----ESPPTDENSDQNSKSSSQASGITGSYSVSESPFSPILHNSVANTVE	621		
DB	996	TAPGKIEKVKRPPPTTEGSLQDLAPBEBAAG-----TORP-----KYLKQTLIM	1040		
QY	622	DPVDSAPRGQKK--EDQVAGINSDGINSFVLEAIRVTRHKXMAERMSRIYASEED	679		
DB	1041	EDYETHKSKRRERDDSSYTSKLSKCVTSFVLEATRVNRRKSKALRLMEAGIYANQDEE	1100		
RESULT 10					
Q7S696_NUCR					
ID	Q7S696_NUCR	PRELIMINARY	PRT	1095 AA	
AC	Q7S696				
DT	01-MAR-2004	(Tremblrel. 26, Created)			
DR	01-MAR-2004	(Tremblrel. 26, Last sequence update)			
DT	01-FEB-2005	(Tremblrel. 29, Last annotation update)			
DE	Predicted protein (Hypothetical protein H4H7.100).				
GN	Name=NCU04757.1; Synonym=H4H7.100;				
OS	Neurospora crassa.				

CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=0874A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 Raife D., Fitchugh W., Ma L.-U., Smirnov S., Percell S., Rehm B.,
 Eklund D., Engels R., Wang S., Nielsen C.B., Butler J., Endtzzi M.,
 Qut D., Imankev P., Pedersen D., Nelson M., Washburne M.,
 Seltrunkoff C.P., Kansey J.A., Braun E.L., Zelter A., Schulte U.,
 Koche G.O., Jedd G., Mewes W., Straben C., Marcotte E., Greenberg D.,
 Roy A., Foley K., Naylor U., Thoman N., Barrett R., Gnerre S.,
 Kamel N., Kamysellis M., Mauceli E., Bielke C., Rudd S., Fishman D.,
 Krysotova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
 Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmati S.A.,
 Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
 Yarden O., Plamann M., Selter S., Dunlap J., Radford A., Armayo R.,
 Naveig D.O., Alex L.A., Mannhaupt G., Ebdole D.J., Freitag M.,
 Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
 RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.",
 RT Nature 0:0-0(2003).
 RL Nature 0:0-0(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Schulte U., Aign V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.,
 RL Submitted (JAN-2004) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA German Neurospora genome project;
 RL Submitted (JAN-2004) to the EMBL/Genbank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL: AABY01000328; RA31054.1; -; Genomic DNA.
 CC EMBL: BX908811; CAF06122.1; -; Genomic DNA.
 CC DR EMBL: BX908811; CAF06122.1; -; Genomic DNA.
 CC DR EMBL: BX908811; CAF06122.1; -; Genomic DNA.
 CC KW Hypothetical protein.
 CC SQ SEQUENCE 1095 AA; 118854 MW; E517G9D5C0385DC8 CRC64;
 Query Match 5.7%; Score 203; DB 2; Length 1095;
 Best Local Similarity 20.9%; Pred. No. 0.052;
 Matches 152; Conservative 96; Mismatches 282; Indels 198; Gaps 33;
 QY 24 DGDTSYTHLVCMGPGASGCODE-----PQWPTDHRAGQGVQGVSVSHVATYQ 76
 DB 491 DAPSTMTVAEVSSTPEPSAEQGEBOQAKQVE-----RGEETPA-QAFARQ 539
 QY 77 PSPRLGSHENRD--EGQVYRLGARDANQGRPTMALRPEDDEKMTYRLDAGDADR 134
 DB 540 QEELA-EKEARENGPDPGFVKSSI PKSSSHQKPSWV---QOQPHLDQVKKAAKARPA 594
 QY 135 RLCDL-EERNAVIOQOAVRKSTVATLCTGDHGRPTGPRSPRLPENVDREQIDF 193
 DB 595 MAQRPSPRVWE-DSPESLQLOTEVSTPOODEQTEATBSPQVSFTE--LPEPKID- 650
 QY 194 LLAAROFSLLEQANKGAPHSPPAGTTPGASQAPAFKXPHLANGVVPPIKPOVG 253
 DB 651 ----ETLQKPELEDKTPPEKPAIPAVVTERKSPPIVAPRPLPSRPSIDPRKXP 706
 QY 254 VVR---EENKRAVPTMASVQVDDPGSLASVESFPTPKETPIEREIRLAQEREDLRQ 310
 DB 707 AAKPAIPARPVKASPT-----SGGLEPESASAPPROKP----- 739
 QY 311 RGRQATDHOELVEITRPLTLTSLTA-----PRERGRPSLVVQGDIVQETOREED 364
 DB 740 -----AVPARPMSKIALQGFPMNDLNNRLGLQPMACKEBAPAEQKX 786
 QY 365 HREGLAV-----GRASDPWVSEGPQGLRRLSSDLSIPAPDARAADPAPEYKVR 419
 DB 787 EKKEKPLDARKGRA-----RGRQ--RRAPAA-----AKAAAAAANP----- 823
 QY 420 IPPDAVQPLSPCTPOLERSA--FGAFKPS-----SLSTVAKAKATSPKATMSPRHS 471

DB 824 -PPAVIEEKEKVAGPKLFSFASISYMAIDPESSEGVSLGVAELKALEKK-----PREKT 878
 QY 472 ESSGKPLSTQOEAKPP-RGCPQANRGVWMEYRRLAPLRAPADEPQAVPVMGMEV 530
 DB 879 EEVASEKTEETEARPFLLENVDEAKAVE-----KLVP-----EPQKEVQV----- 921
 QY 531 AGAPALRLKQSSQDLERERESVTLAREQVAERERNAAPPEVSPPT-----DENS 582
 DB 922 -EAKKEIKERKTS-----EES-----EPSPLPALIPENAPGAPSPPTALIRELKAQET 971
 QY 583 DONSRRSSQASGITGSYSVSESPFSPPIH-----LHSNVATYDEPYD----- 625
 DB 972 EAEFEASSAPADTP--TSTAPAPPEVPAEVAEKAETAASETTEKEDNDATYASAKA 1029
 QY 626 -----SAPPOQRKEQWYAGINSDDGINSVLALIVTRHKMAERME 669
 DB 1030 EAAADTEVTNNSNTGVSVPDEAPAEKYSLVNTAG--ETVAEHVTRDGSNVKPLE 1086
 QY 670 SRIVASEE 677
 DB 1087 AEDKGEH 1094
 RESULT 11
 Q5KDK5_CRYNE PRELIMINARY; PRT; 1978 AA.
 ID Q5KDK5;
 AC 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Protein binding protein, putative.
 GN ORENAME=CNG03630;
 OS Cryptococcus neoformans var. neoformans JE21.
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 CC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=214684;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lofthus B., Amedeo P., Roncaglia P., Vamathevan J., Uterback T.,
 RA Van Aken J., Fraser C.,
 RL Submitted (MAY-2004) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=JE21;
 RC NCBI:15653466; DOI=10.1126/science.1103773;
 RX PubMed:15653466; DOI=10.1126/science.1103773;
 RA Lofthus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
 RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
 RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
 RA D'Souza C.A., Fox D.S., Grindberg V., Fu J., Fukushima M., Haas B.J.,
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Kuyshima M.I.,
 RA Kwon-Chung K.J., Lengeler K.B., Malt R., Marra M.A., Marra R.E.,
 RA Mathewson C.A., Mitchell T.G., Pertea M., Rigg F.R., Salzberg S.L.,
 RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
 RA Sun B.B., Tenney A., Uterback T.R., Wickes B.L., Wortman J.R.,
 RA Wye N.H., Kronstad J.W., Lodge J.K., Heltman J., Davis R.W.,
 RA Fraser C.M., Hyman R.W.,
 RT "The genome of the basidiomycetous yeast and human pathogen
 RT Cryptococcus neoformans."
 RL Science 307:1321-1324(2005).
 DR EMBL: AB017347; AW44761.1; -; Genomic DNA.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR GO: GO:0005085; F:guanylyl-nucleotide exchange factor activity; IEA.
 DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
 DR InterPro: IPR011992; EF-Hand type.
 DR InterPro: IPR002048; EF-hand_Ca_bd.
 DR InterPro: IPR000261; EF5_homo1ogy.
 DR InterPro: IPR001311; GDS_CDC24.
 DR InterPro: IPR001018; Neu_cyt_fact_2.
 DR InterPro: IPR000429; RhGEF.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR003124; WH2_actin_bd.
 DR Pfam: PF00036; ethanol; 1.

DR Pfam; PF00621; Rhogef; 1.
 DR Pfam; PF00018; SH3_1; 2.
 DR Pfam; PF02205; WH2_1.
 DR PRINTS; PR00499; P67PHOX.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR Pfam; PF00066; SH3; 2.
 DR SMART; SM00027; EH; 1.
 DR SMART; SM00325; Rhogef; 1.
 DR SMART; SM00326; SH3; 2.
 DR SMART; SM00246; WH2; 1.
 DR PROSITE; PS00741; DH_1; 1.
 DR PROSITE; PS00010; DH_2; 1.
 DR PROSITE; PS00031; EH; 1.
 DR PROSITE; PS01082; WH2; 1.
 DR Complete proteome.
 KW SEQUENCE 1978 AA; 217438 MW; 7882A93A63A23DB CRC64;
 SQ
 Query Match 5.5%; Score 197.5; DB 2; Length 1978;
 Best Local Similarity 21.2%; Pred. No. 0.19;
 Matches 136; Conservative 63; Mismatches 234; Indels 209; Gaps 25;
 QY 142 ERMAVIGQAVRKSTVATLQGTDPHGDPTGPPRSTPLEENVYDDEQIDFLAQQFL 201
 DB 619 ERKAVIREQARQRIQERLKLGVSE-----DKEREVDTSVQDRLEKKEKKEKSR 670
 QY 202 SLQANKGAPHSPPARGTTPAGTTPGASQAPKFNKPHLANGHVPIKQVGVREENVK 261
 DB 671 KAEPQKQERDEARKRRLAEAG--GAAPKSEKPE-----AEPASLSAMKKAPAP 721
 QY 262 RAVPTWASVQVVDPPGSLA-----SVSPGTPK--ETPIREIRLAQERAD 306
 DB 722 PRATTPPSKAPVPPPSAHAPAPAPAPPTPTQPTPTKPDDEDELELRREBEAAK 781
 QY 307 LREQGLQATDHQELVEIPTRPLTKSLITAPRRERKGRSLYQDVIQETQREEDHR 366
 DB 782 AKARRAR-----LALQKEEERERQ 803
 QY 367 REGHVGK-----ASTPDWSEGPQGLRRLALSDSLSPAPADAPAPAEVKVNR 420
 DB 804 EELLAANKRSLGASPVPAETP--KKEASSAPSPAPPPAPPPAPPPAPPA-- 856
 QY 421 PP----DAYQVYLSFG-----TPOLEFSAFGAGK--PSSLSTAEAKATSPRATWSPR 468
 DB 857 PPASAPAYNPFRKKGAGAPATPPAPAPAGFNPFPKPPAASVSPSAPLAAPR- 915
 QY 469 HLSSESGPLSTKQEASPPRGCPQANRGVVR-----EYFRLRPLRF- 511
 DB 916 ----PPAPPPPADPAFPQPRG-PPSPSEPEMEDIAEKQVDESDDDEYTTSRAGQG 970
 QY 512 -----RAPDEQQAQVPHVGMVAGAPAL-----RL 538
 DB 971 LAQALFGNMGSGSPSTRPGSAPAPQAPKEPPKALANVGAGNPEQAGALLSAIQGAKL 1030
 QY 539 QKSQSDLLERERESVLRREQVAEERNALPPEVFSPTPDENSQNSRSSQASGITGS 598
 DB 1031 KKAQVVD-----KSGPDIQVIGDAAPPSIIRTPRE----- 1063
 QY 599 YSVSESPFSPPIHLSNVAMTVEDPVS-APPQ-----RKQEWYAGI-----NP 643
 DB 1064 YAPSPAPAAP-----GPIEERAPSPAPPESEDSFTSGNPNRQISIMVAGLAADASHP 1115
 QY 644 SDGINSEVL-----EATRVTRHKNAAMERESRYASEDD 679
 DB 1116 AASVGETSMLEPPEEERKEQHYEQLEK--PRVQIEGEDD 1155
 RESULT 12
 OSUTZ4 HUMAN
 ID OSUTZ4 HUMAN PRELIMINARY; PRT; 949 AA.
 AC OSUTZ4;
 DT 10-MAY-2005 (Tremblrel. 30, Created)
 DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
 DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)

DE A kinase (PRKA) anchor protein 2 (Fragment).
 GN Name=AKAP2; ORFNames=RP11-470J20.3-007;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Philimore B.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Kimberley A.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL153598; CA140818.1; -; Genomic DNA.
 DR EMBL; AL158823; CA139562.1; -; Genomic DNA.
 DR EMBL; AL158823; CA140818.1; JOINED; Genomic DNA.
 DR EMBL; AL153598; CA139562.1; JOINED; Genomic DNA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 KW Kinase.
 FT NON TTR
 SQ SEQUENCE 949 AA; 104234 MW; 4B6KAFCA26F2EBD CRC64;
 Query Match 5.5%; Score 195.5; DB 2; Length 949;
 Best Local Similarity 19.5%; Pred. No. 0.11;
 Matches 152; Conservative 104; Mismatches 221; Indels 301; Gaps 33;
 QY 100 RDAHQRPYALPDEDEDEKNTYRLDAGDAP-RLCLLEBRMAVIGQAVRKSTV 158
 DB 272 RAHEDEKPKPEKLPDEDEHEKEQYCIK---KVPSEEMLEKERRRLISQAVKXNPGI 327
 QY 159 AT-----LQGTDPHGDPTG----- 174
 DB 328 AAKWMPDQKTEBQIDESHLSHKYKRRKERRAQEQULLQKLOQQQQQPPSOLCT 387
 QY 175 PPRSTPLEENVDR-----EQIDFLAARQFLSLQANKGAPHSPPARGTTP-- 225
 DB 388 APASSHERAMIDKAKEDYTBQIDFSAARKQQLMENSQAV-----AKGQ--STPRL 439
 QY 226 -----GASQAPKAPKPHLANGHVPIKQVGVREENVKRAVPTWASVQVVD 275
 DB 440 FSIKPFYRPLGVSNSDPLTNP-----PPSVGGEPEDSGASAAKQKS- 483
 QY 276 PGSLASVSPGTPEPTPIEREIRLAQERADLR-ORGLQATDHQELVEIPTRPLTK 333
 DB 484 PGLAETPSAAGSQGT-----ASQKEGPGYSEPSKRG-----PLSKLMAE 523
 QY 334 LSLITAPRR-----ERGRPSLYQDVIQETQREEDHRERGLAHVGRASTPDWSEGP 385
 DB 524 DGEFTSARAVLVTKDDDHILQDFRSVNVSLQELDGLBELSVRSQDTT----- 576
 QY 386 QPGLRRLSSDSILSPAPADAPAEVKNRIPPDAYQPIYLSPTPOLE----- 437
 DB 577 ----VLEITLNDPFSMDNISDSGASN-----ETVNALQENSILADLSLPOTPDNDPSEGRGE 628
 QY 438 -----FSAFGAFGKSSLSLA-----EAKAATSPKA-TWSPPHLS 471
 DB 629 GVSKFSFDHGGYSPSSTLGDSPLYVDPLEYQAGLLVONALQALAEQVDAVAKTSIDGA 688
 QY 472 ESSGKPLSTKQEAS-----KPPR-GCP-QANGVVRMEYFRLLRP-----LRF 511
 DB 689 EQGQ-PEATVEEAAAFAGSEKPKQSMWEPQVSPVQEKDVLDP-----KLIPADRALRE 743
 QY 512 RAPDEP-----QAQVPHVGMVEVA 531
 DB 744 RGPQPLPAVQSPGPINMEETREPGSYFSKYSEAEILRTASLATTQESDV-----MV 796
 QY 532 GAPLRLOKQSSDLLEERESVLRREQVAEER-----RNALPPEY----- 573
 DB 797 GPFTLRGRKORTSMIEEIRLAQEREELKRGQVQVISTQSPPTKKA--PSLSRSTCYK 854
 QY 574 -----FSPTPDENSDQNSRSSQASGITGSYSVSESPFPIHLSNVAMTVE 621

Db 167 RDIEREA-----HROAL-----ARPAVEP 187
Qy 413 EVRKVNRIIPDAVQPYLSPTGPLEFSNF--GARGKSSLSAATAKATSPKATMSPRHL 470
Db 188 RAR-----SPQPLGLBKRFEPFAAGSSSAGAGG-----AGPQRL 224
Qy 471 SESSGKPLSTKOE-----ASKPRGCPQANRGVWWEFRLPLRFPAPDEPQOAVPHV 525
Db 225 PEPGRPRSNVQGGCRVVGSAFPPTP----- 251
Qy 526 GWGEVAGAPALRLKQSSDILLERRESVLRREQVAERENALPEYF--SPYDENSQ 584
Db 252 -----SLEQEVRAVREERQELQRRSVYGTAFFKEPTP----- 286
Qy 585 NSRSSSQASG 594
Db 287 -SLTASRGDG 295

RESULT 15
OSKKE6 CRVNE
ID QSKKE6 CRVNE PRELIMINARY; PRT; 1558 AA.
AC QSKKE6;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CNC03270;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=214684;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Lotfus B., Amedeo P., Roncaglia P., Vamathevan J., Uterback T.,
RA Van Aken S., Frazer C.,
RL Submitted (MAY-2004) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=JEC21;
RX PubMed=15553466; DOI=10.1126/science.1103773;
RA Lotfus B., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA Vamathevan J., Miranda M., Anderson I.J., Frazer J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA Kwon-Chung K.J., Lengele K.B., Maiti R., Maiti M.A., Maiti R.E.,
RA Mathewson C.A., Mitchell T.G., Perlea M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B.B., Tenney A., Uterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronsted J.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.,
RA "The genome of the basidiomycetous yeast and human pathogen
RT Cryptococcus neoformans.";
RT Science 307:1321-1324 (2005).
RL EMBL; AE017343; AAM42345.1.-: Genomic DNA.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 1558 AA; 167093 MW; 09C7C501D033CEBE CRC64;

Query Match 5.4%; Score 192; DB 2; Length 1558;
Best Local Similarity 21.2%; Pred. No. 0.28;
Matches 177; Conservative 81; Mismatches 290; Indels 288; Gaps 36;

Qy 52 PTDHRA--QGGVQGVSYSHVAYTGQSPRGLSHNEDEGMOYRIGADAHQGRPTW 109
Db 777 PIYKALSRKAGSGTGLSVS--DAVETSGSSASSESEDEGSV--GSGSGV----- 826
Qy 110 ALRPEDGDXKMKYTRLADGADPRRLCDLERKAVIQG--AVKKSSTVATLQGTDPHG 168
Db 827 -----GSESE-----TESSEASIQGNAMSRSGSTSTSSPPSS 862
Qy 169 DPTGPRPRSTPLBENVVDREQIDFLARQQLS--LEQANKGAVHSSPAR----- 217

Db 863 SSSPPPP-----DLSKLDPOALRLHFLTAFLSQCRRAABDSAHMQVVDQDV 912
Qy 218 -----GTAG-----TPPASQAPKAFNNCHLA 240
Db 913 EIEBASVESDEDEGTNASFARIMDESEI VGEFEDEKEDEVEDVEEPRDEQPAL- 971
Qy 241 NGHVVPKIPQVK-----GVVREKNVRAVPTVASVQ 271
Db 972 -----PVOQSESDDEMQLDVEGSQVLEBSALQPPAAGGEBEERIRIDVNTAEPM 1023
Qy 272 VVD-----PQS-----LASVESFTP--KETPIREIRLA--QER 303
Db 1024 DVQQRPTLKTQSPRESSPLSFHESGRQSFNLLAALASPTQHRELPCDAAREALAEQ 1083
Qy 304 EADLRERGLRQATDQELVEIPT---RPLTLGLSLTAPRRRGPSLVQGDYQETQ 360
Db 1084 EAPVRD--AMRQDDVHPKQRIPINGVQEPVLTQ--QLMSPSSVAERDEIEPLPATQLVQ 1140
Qy 361 REEDHREGLHVGRASTPDWVSEGP-----QGLRRALSDDSLSP-----APPARA 407
Db 1141 RFEDDEGQ-----EATPLAKSAFPAVRSTRQPSRQPSVARDIIPPRRLASASREPA 1195
Qy 408 ADPAPEVRKYNR-----IPDAVQPYLSPTGPLEFSAFGAFGKPSLSLTAKAATS 460
Db 1196 LVPEPRTMTTRSSQORVVPSPHPV--IRSTRRTVSSQ-----SDVQSSQLLE--PSS 1249
Qy 461 P---KATMSPRHSSSGK---PLSTKQKSKPRGCPQANRGVWWE--YFLRLPLRFR 512
Db 1250 PVQLHATLTATLRRSSRRQTTPLRSSQVDELDPSSPPASQQPIEESPLPIETQLHS 1309
Qy 513 APDEPQOAVPHVWGEVAGA--PALRLQKSO-----SSDLERERESV 554
Db 1310 QPSSQSSQSLNSQRFRIISGEENPLFMSGSQLPQGANLYPNIDSSSDVGETPPGAK 1369
Qy 555 LRRE-----QEAERENAL-----PPEVSPYDENSQ 585
Db 1370 IGIEGSSPNDKQEGGRANYLSVSSPILEDEDEQNALVTEKHEQTSSEGVDEHDDQS 1429
Qy 586 SRSSSQASGITGSYSVESPFSPHLSNVMTVEDPVDVASRPGQKKQWYAGINPSD 645
Db 1430 VDASEASDDEGSSISIPRSPITY-----PSLPRSSLSFSQPVAAASQPT 1476
Qy 646 G---INSEVLEAIR-----VTHKNMAARWESRIYASEDD 679
Db 1477 GFPTLSLPRALRMKSTGTFSSSQPETSKEKTSRHMNGAGSESEETSGDSDE 1532

Search completed: March 3, 2006, 13:26:04
Job time : 265.327 secs

GenCore version 5.1.7
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OW protein - protein search, using SW model

Run on: March 3, 2006, 13:35:46 / Search time 91.0612 Seconds
(without alignments)
616.473 Million cell updates/sec

Title: US-10-646-873-42

Perfect score: 3583

Sequence: 1 MDRVTRYPILGIPQAHRTG.....HKNAWERESRIVASEED 679

Scoring table: BLOSUM62

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

- 1: /cgn2_6/prodata/1/1aa/5_COMB.pep.*
- 2: /cgn2_6/prodata/1/1aa/6_COMB.pep.*
- 3: /cgn2_6/prodata/1/1aa/7_COMB.pep.*
- 4: /cgn2_6/prodata/1/1aa/8_COMB.pep.*
- 5: /cgn2_6/prodata/1/1aa/9_COMB.pep.*
- 6: /cgn2_6/prodata/1/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3583	100.0	679	US-09-050-516-42	Sequence 42, Appl
2	3583	100.0	679	US-10-278-547-42	Sequence 42, Appl
3	1132	31.6	215	US-09-050-516-47	Sequence 47, Appl
4	1132	31.6	215	US-10-278-547-47	Sequence 47, Appl
5	189	5.3	36	US-09-050-516-43	Sequence 43, Appl
6	189	5.3	36	US-10-278-547-43	Sequence 43, Appl
7	175	4.9	35	US-09-050-516-45	Sequence 45, Appl
8	175	4.9	35	US-10-278-547-45	Sequence 45, Appl
9	175	4.9	35	US-09-252-991A-29419	Sequence 29419, A
10	173	4.8	2468	US-09-538-092-1135	Sequence 1135, App
11	173	4.8	2468	US-09-538-092-1135	Sequence 1135, App
12	173	4.8	2522	US-09-949-016-10337	Sequence 10337, A
13	171	4.8	33	US-09-050-516-46	Sequence 46, Appl
14	171	4.8	33	US-10-278-547-46	Sequence 46, Appl
15	168	4.7	2843	US-10-092-138A-30	Sequence 30, Appl
16	168	4.7	2843	US-08-681-219A-30	Sequence 30, Appl
17	166.5	4.6	1308	US-09-862-027-79	Sequence 79, Appl
18	166	4.6	1308	US-09-862-027-79	Sequence 79, Appl
19	166	4.6	2842	US-07-741-940-7	Sequence 7, Appl
20	166	4.6	2842	US-08-289-548A-7	Sequence 7, Appl
21	166	4.6	2842	US-08-452-654-7	Sequence 7, Appl
22	166	4.6	2842	US-08-449-731-7	Sequence 7, Appl
23	166	4.6	2843	US-07-741-940-2	Sequence 2, Appl
24	166	4.6	2843	US-08-289-548A-2	Sequence 2, Appl
25	166	4.6	2843	US-08-452-654-2	Sequence 2, Appl
26	166	4.6	2843	US-08-452-655B-2	Sequence 2, Appl
27	166	4.6	2843	US-08-452-655B-7	Sequence 7, Appl

28	166	4.6	2843	1	US-08-370-235A-2	Sequence 2, Appl
29	166	4.6	2843	2	US-08-450-582-2	Sequence 2, Appl
30	166	4.6	2843	2	US-08-450-582-7	Sequence 7, Appl
31	166	4.6	2843	2	US-08-449-731-2	Sequence 2, Appl
32	166	4.6	2843	2	US-09-538-092-1007	Sequence 1007, Ap
33	166	4.6	2843	1	US-08-821-355A-7	Sequence 7, Appl
34	166	4.6	2973	1	US-09-003-687A-7	Sequence 7, Appl
35	166	4.6	2973	2	US-09-136-605-7	Sequence 7, Appl
36	165.5	4.6	2973	1	US-09-136-605-7	Sequence 17054, A
37	164.5	4.6	1341	2	US-09-252-991A-17054	Sequence 6890, Ap
38	164.5	4.6	1341	2	US-09-949-016-6890	Sequence 10925, A
39	163	4.5	1197	2	US-09-949-016-10925	Sequence 30833, A
40	162	4.5	1197	2	US-09-252-991A-30833	Sequence 10, Appl
41	162	4.5	885	2	US-09-914-259-10	Sequence 615, App
42	161	4.5	904	2	US-09-976-594-615	Sequence 31473, A
43	161	4.5	507	2	US-09-252-991A-31473	Sequence 31894, A
44	158	4.4	588	2	US-09-252-991A-31894	Sequence 30890, A
45	158	4.4	1326	2	US-09-688-188B-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL TRACT
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:
 LENGTH: 679 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 6627414e
 US-09-050-516-42

Query Match 100.0%; Score 3583; DB 2; Length 679;
 Best Local Similarity 100.0%; Pred. No. 5,6e-294;
 Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDRVTRPIIGIQAHRGTGLVLDGDTSTYTHLVCMGPEASGMGODEPQTPDHRQOG 60
DB 1 MDRVTRPIIGIQAHRGTGLVLDGDTSTYTHLVCMGPEASGMGODEPQTPDHRQOG 60
QY 61 VORQGVSYHAAYTGQSPRGLHSENREDEGMQVYRLGARDAHQGRPTMALRPEDGEDXE 120
DB 61 VORQGVSYHAAYTGQSPRGLHSENREDEGMQVYRLGARDAHQGRPTMALRPEDGEDXE 120
QY 121 MKTYRLDAGDADPRRLCDLEREMAVIQQAVKKSSTVATLQGTDPDHGDPRTGPPRSTP 180
DB 121 MKTYRLDAGDADPRRLCDLEREMAVIQQAVKKSSTVATLQGTDPDHGDPRTGPPRSTP 180
QY 181 LEENVVDREQIDFLAARQOFLSLEQANKGAHSSPAGTTPGASQAKFNKPHLA 240
DB 181 LEENVVDREQIDFLAARQOFLSLEQANKGAHSSPAGTTPGASQAKFNKPHLA 240
QY 241 NGHVPIKPOVKGVREENVRAVPTWASVQVDDPGSLASVESPGTPEKTEPIREIRLA 300
DB 241 NGHVPIKPOVKGVREENVRAVPTWASVQVDDPGSLASVESPGTPEKTEPIREIRLA 300
QY 301 QERADLREQRLQATDHQELVEIPTRPLTLTKSLITAPRRERGRPSLYVQORDIVQETO 360
DB 301 QERADLREQRLQATDHQELVEIPTRPLTLTKSLITAPRRERGRPSLYVQORDIVQETO 360
QY 361 REEDHRRGLHVGRASSTPDWVSEGPQGLRRALSSTLSLSPAPARADPAPEYKVNRI 420
DB 361 REEDHRRGLHVGRASSTPDWVSEGPQGLRRALSSTLSLSPAPARADPAPEYKVNRI 420
QY 421 PPDAQPYLSPQTPQLEFSARFAGFQPSLSLTAEKAAATSPKATMSPRHLSSESGKPLST 480
DB 421 PPDAQPYLSPQTPQLEFSARFAGFQPSLSLTAEKAAATSPKATMSPRHLSSESGKPLST 480
QY 481 KOEASKPPRCGPOANRGVVRWEYFRLRLPRAPDEPOQAOVPHWGMEVAGAPALRLQX 540
DB 481 KOEASKPPRCGPOANRGVVRWEYFRLRLPRAPDEPOQAOVPHWGMEVAGAPALRLQX 540
QY 541 SOSDLERERESVLRQOEVAEERRNALPFEVFSPTPDENSDDONSRSQASGITGSYS 600
DB 541 SOSDLERERESVLRQOEVAEERRNALPFEVFSPTPDENSDDONSRSQASGITGSYS 600
QY 601 VSESPFSPILHLSNVATVEDPVDASPPQGRKKEQWYAGINPSDGINSEVLEAIRVTRH 660
DB 601 VSESPFSPILHLSNVATVEDPVDASPPQGRKKEQWYAGINPSDGINSEVLEAIRVTRH 660
QY 661 KNMAAERESRIYASEDD 679
DB 661 KNMAAERESRIYASEDD 679

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RESULT 2

US-10-278-547-42
 Sequence 42, Application US/10278547
 Patent No. 6660834

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
 COHEN, MAURICE
 COLPITTS, TRACEY L.
 FRIEDMAN, PAULA N.
 GORDON, JULIAN
 GRANADOS, EDWARD N.
 HAYDEN, MARK

HODGES, STEVEN C.
 KLAS, MICHAEL R.
 KRATOCHVIL, JON D.
 TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
 FOR DETECTING DISEASES OF THE GASTROINTESTINAL
 TRACT

NUMBER OF SEQUENCES: 49
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547

FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065, US, P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 679 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6660834e

SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

QY 1 MDRVTRPIIGIQAHRGTGLVLDGDTSTYTHLVCMGPEASGMGODEPQTPDHRQOG 60
DB 1 MDRVTRPIIGIQAHRGTGLVLDGDTSTYTHLVCMGPEASGMGODEPQTPDHRQOG 60
QY 61 VORQGVSYHAAYTGQSPRGLHSENREDEGMQVYRLGARDAHQGRPTMALRPEDGEDXE 120
DB 61 VORQGVSYHAAYTGQSPRGLHSENREDEGMQVYRLGARDAHQGRPTMALRPEDGEDXE 120
QY 121 MKTYRLDAGDADPRRLCDLEREMAVIQQAVKKSSTVATLQGTDPDHGDPRTGPPRSTP 180
DB 121 MKTYRLDAGDADPRRLCDLEREMAVIQQAVKKSSTVATLQGTDPDHGDPRTGPPRSTP 180
QY 181 LEENVVDREQIDFLAARQOFLSLEQANKGAHSSPAGTTPGASQAKFNKPHLA 240
DB 181 LEENVVDREQIDFLAARQOFLSLEQANKGAHSSPAGTTPGASQAKFNKPHLA 240
QY 241 NGHVPIKPOVKGVREENVRAVPTWASVQVDDPGSLASVESPGTPEKTEPIREIRLA 300
DB 241 NGHVPIKPOVKGVREENVRAVPTWASVQVDDPGSLASVESPGTPEKTEPIREIRLA 300
QY 301 QERADLREQRLQATDHQELVEIPTRPLTLTKSLITAPRRERGRPSLYVQORDIVQETO 360
DB 301 QERADLREQRLQATDHQELVEIPTRPLTLTKSLITAPRRERGRPSLYVQORDIVQETO 360

```


NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-278-547-47

Query Match 31.6%; Score 1132; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.2e-87;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 MSPRLSSSGKPLSTQKASKPPRGCPQANRGVVRWFYFLRLPFRAPDEPQAOVPH 524
DB 1 MSPRLSSSGKPLSTQKASKPPRGCPQANRGVVRWFYFLRLPFRAPDEPQAOVPH 60
QY 525 VMGMEVAGAPALRLQKSSDLLEERESVLRREQVAEERNNALFPEVFSPTPDENSQ 584
DB 61 VMGMEVAGAPALRLQKSSDLLEERESVLRREQVAEERNNALFPEVFSPTPDENSQ 120
QY 585 NSRSSSQASGITGSYSVESPFSPHLSNVAVTVEDPVDASPPGQKKEQWYAGINPS 644
DB 121 NSRSSSQASGITGSYSVESPFSPHLSNVAVTVEDPVDASPPGQKKEQWYAGINPS 180
QY 645 DGINSEVLEAIRVTRHKNAEMRMSRIYASEED 679
DB 181 DGINSEVLEAIRVTRHKNAEMRMSRIYASEED 215

RESULT 5

US-09-050-516-43
Sequence 43, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-43

Query Match 5.3%; Score 189; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 MSPRLSSSGKPLSTQKASKPPRGCPQANRGVVR 500
DB 1 MSPRLSSSGKPLSTQKASKPPRGCPQANRGVVR 36

RESULT 6

US-10-278-547-43
Sequence 43, Application US/10278547
Patent No. 6660834
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-OCT-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-278-547-43

Query Match 5.3%; Score 189; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 MSRRHSSSGKPLSTKQASRPPRCGPOANRGVVR 500
DB 1 MSRRHSSSGKPLSTKQASRPPRCGPOANRGVVR 36

RESULT 7
US-09-050-516-45
Sequence 45, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-45

Query Match 4.9%; Score 175; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 568 ALFPEVFSPTPDNSDQNSRSSQASGITGSYSVS 602
DB 1 ALFPEVFSPTPDNSDQNSRSSQASGITGSYSVS 35

RESULT 8
US-10-278-547-45
Sequence 45, Application US/10278547
Patent No. 6660834
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-278-547-45

Query Match 4.9%; Score 175; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 568 ALPEVPSPTDENSDONSRSQASGITSYSVS 602
Db 1 ALPEVPSPTDENSDONSRSQASGITSYSVS 35

RESULT 9
US-09-252-991A-29419
; Sequence 29419, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; LENGTH: 1008
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29419

Query Match 4.9%; Score 175; DB 2; Length 1008;
Best Local Similarity 21.9%; Pred. No. 9e-06;
Matches 162; Conservative 57; Mismatches 290; Indels 232; Gaps 33;

Qy 48 PQTWPTDRAQGVQGVSVSHVAYTGQSPRGLSHENRED-EGMUYVRLGARDAGCR 106
Db 295 PAAVYTAGAGAGIIPRDAPRLQA--GDPAGRRARGERRRDVTARQRLAA--LHAGR 350
Qy 107 PTMALRPEDGEDKEMKTYRL--DAGDAPRLCDLERRRMAVVGQAVRKSTVATLQCT 164
Db 351 PA-APAPRLVHRHRLRLRPA--HRL--VRRGRGSRPPVVRAGTGH 396
Qy 165 P-----DHGDRTPGPPRSTPLEENVVDREQIDFLAARQCFLSLEQANKGAPH 212
Db 397 PGRPPAGCPAGADRTDPGSGPAS-----ARPRARRRATGAPG 439
Qy 213 SSPARGTAGTTPGASQAPKAFNKPHLANGVVPIKPOV----- 252
Db 440 TOPAARGAALRPPEAGAGAF-----RLTGPRTAAQAAPGRTGAPGRSRVA 491
Qy 253 ---GVVRENNVRAVPTASVQVVDPGSLASVESPGTPKTPIERETRLAQR--EAD 306
Db 492 AGLGRRRQPARLRPPPT-----QFPG--SSGDPAPARPARTRALPARPELDAD 538
Qy 307 ---LRGRLGRLQATDHOELVEIPTRP-----LITTK 333
Db 539 PARTRRARRAGRRHAGODLAVAGPAGKAGRAAHAGAGDAHQPPOLAGKRALRP 598
Qy 334 LSLTAPRRERGRPSLYVQDIVQTOREEDH-----RREGLVHVGASTPD-----W 380
Db 599 RSARAGPARRRPARLRPBR---RARGADHLCPATRRR--RAGQAAPVADPRGAE 652
Qy 381 VSEGPQELRALSSDSLSPAPDARAD-----PAPEVRKVRIRPPDAVQPTLS 430
Db 653 HOERHHQGRRRRPRAGGTASVPVDRHAAGEPPRTLVAVPPDARLARRRP-----VR 706
Qy 431 PGTQLBESAFGAFGKPSLSLTAEAKA-----ATSPKATWSP 467

Db 707 PGLPHADREA-RRRGTQSPGRAPAAVPAATDQGTGGLGTAABERVHVPVARTQGATRTL 765
Qy 468 RHLSSESG-----KPLSTKQASKPRRCPCPQANGVWKEFRLRLRFPAP---DEP 517
Db 766 RDAAPGAGPQGGPRGDRAPRPAQPHDPKGAQAAPGLRL-HAPAAITPGRRRQRPQAOL 824
Qy 518 QQAQVP--HYWGEVAGAPALRLQKSQSDLEREESVLRREQVEAER-----RNA 568
Db 825 GQAGLPARHARRTRDRGSPGPATLVHLDARADRGPRAPARRRLRAPDRDPPRRPCTA 884
Qy 569 LPPEVPSPTDENSDONSRSQASGITSYSVSSEPFPSPIHLSNVAVTVEDPYDSAP 628
Db 885 LPERQAGVDPDQEGRRGRQPDRCG-----HRDPLSLVPE--GGGE 925
Qy 629 PGQRK---EQWYAGIN-PSD 645
Db 926 PGQRPLPRRPGQAGVRLPAD 946

RESULT 10
US-09-976-594-726
; Sequence 726, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976, 594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 726
; LENGTH: 2468
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 4295277CD1
US-09-976-594-726

Query Match 4.8%; Score 173; DB 2; Length 2468;
Best Local Similarity 20.4%; Pred. No. 5e-05;
Matches 171; Conservative 109; Mismatches 289; Indels 270; Gaps 39;

Qy 31 YHLVCMGPASGWDPEPQTWPTDRAQGVQGVQGVSVSHVAYTGQSPRGLSH----- 84
Db 1044 YVAAVVDKAAEAGAEQVGLFTPTKQLGAQSPGREPASHDET---LFGSSEATA 1100
Qy 85 ---ENREDEGVQVYRLGARDAGQ--RPTMALRPEDGEDKEMKTYRLDAGDADPRRLCDL 139
Db 1101 SDEENREDQPEER-----YATSGYTOSTIEISSEPTPMDEMSTPRVMSDETNNERTES 1154
Qy 140 EREBW-----AVIQAVRKSTVATLQCTD-----HGDRTPGPPRSTP 180
Db 1155 PSQGFVNITYTESLSLSQESYKPADVTPPLNGFSEGSKTDATDGKDYNASASTISPPSS-- 1212
Qy 181 LLENVVDREQIDFLAARQCFLSLEQAN-----KGAPHSPPARCTPA 221
Db 1213 MEEDKPSRS-----ALRDACSEVKASTLTDIKDSTSAVSEKVSPEKSPSLSPSPFL 1267
Qy 222 GTTPGASQADKAFNKPCH---LANGHVPIKPOYKGVVRENNKRAVPTASVQV--- 273
Db 1268 EKTPLGRSVNFTLPTNEIKVSAEAEVAPVSPVTOGVVEEH--CASPEDKTLTEVVSQ 1325
Qy 274 -----DDPGSLASVESPGTPKTPIERETRLAQRADLRREGRLQAT 317
Db 1326 SVTSGAGHTPYQSPTEDEKSSHLPTEVTEKPRVAVPSFER-----SDAKDENERSAVS 1378
Qy 318 DHOELV---EIPRPLITKL-----SLTAPRRERGRPSLYVQDIVQTOREED 361

Query Match 4.8%; Score 173; DB 2; Length 2522;

CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PasteSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-278-547-46
Query Match 4.8%; Score 171; DB 2; Length 33;
Best Local Similarity 97.0%; Pred. No. 1.2e-07;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 EDSVDSAPPGQRKKEQVYAGINSDGINSEVLE 653
QY 621 EDPVDSAPPGQRKKEQVYAGINSDGINSEVLE 653
DB 1 EDSVDSAPPGQRKKEQVYAGINSDGINSEVLE 33
RESULT 15
US-10-092-138A-30
Sequence 30, Application US/10092138A
Patent No. 6743630
GENERAL INFORMATION:
APPLICANT: Sateo, Taka-Aki
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
FILE REFERENCE: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
CURRENT APPLICATION NUMBER: US/10/092,138A
CURRENT FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 2843
TYPE: PRT
ORGANISM: human
US-10-092-138A-30
Query Match 4.7%; Score 168; DB 2; Length 2843;
Best Local Similarity 21.1%; Pred. No. 0.00016;
Matches 138; Conservative 82; Mismatches 272; Indels 162; Gaps 30;
QY 78 SPKGLSENEDSGQVYRIGAR----DAHGKPTWALRPEDGDEKMKYRRDAGDA-- 131

DB 2088 SEHGL-SPDSSEFPMKAIQEGANSIVSLHQAAAACLRSQASDSD-SILSLKSGISLG 2145
QY 132 DPERLC-DLEERAAVIOGAVRKSSTVATLQCPDHGDP-----TPGPPRS 178
DB 2146 SPFHLPDQEEKPPTSNKGPRLIPGKSTLEYTKIISSEKIGIKGVKYSLLTGKRS 2205
QY 179 T-----PLEENVVD-----REQIDFLARQOPLSLQANKGAP-----HSSPARGT 219
DB 2206 NSEISGKQKPLQANMPSISGRMTIHFGVRNSSSSSTSPVSKGPPLKTPASKSPSQ 2265
QY 220 PAGTP-----GASQAP-----KAFKPHLANG 242
DB 2266 TATTSPRKAPSVKSELSPVARQTSQIGSSKASRSGRSDSTSPRPAQPLSRPIOSPQ 2335
QY 243 HVPKPKPVKQVAVREKNVRAVPTWASQVVDGSLASVSPGPKETPIEREIRLQOE 302
DB 2326 R-NSISPRNG-ISPNNKISQLPRTSS-----PSTASTVSSGSKMSTYSPGRQMSQ 2376
QY 303 READREORGRLQATDHOELVEIPTRPLTLKSLITAPRRRGRPSLYQORDIVOETORE 362
DB 2377 ---NLTKGTGLSKNAS-----STPSESASK-GLNOMNNGANKVBLSSMSTKSSGS 2427
QY 363 EDHREGLHVGRASTPDWVSBGPOGLRAL-SSDSILSPADAPADPADEVRKVRIP 421
DB 2428 ESDREERVLVRQST--PIKEAPSPTLRKLEBSAFSLSPSRPASPTRS----- 2477
QY 422 PDAYQPYLSPGTPOLBFSAFGKPSLSLTAELAAATSPRATWPRRLSSSGKPLSTK 481
DB 2478 -QAQTPVLSPLPDMSLSTH-----SSVQAGMKRLPNNLSPT-IEYVDGPPAKRH 2526
QY 482 QEA---SKPPGCPQANRGVVRWEYFRLPLRFAPADBPQAOVPHVWGWEVAGAPALRL 538
DB 2527 DIARSHSESPRLPINRGTWKREHK-----HSSSLRVSTWRTGSSSL 2574
QY 539 Q-KSQSDILEREERESVLRRBOEVAEBRRNALFPE-----VFSPTPDENSQNSRS 588
DB 2575 SASSESSSEKAKSEDEKHVNSISGTQSKENQVSAKGTWKIKENFSPT-----NSTS 2627
QY 589 SSOASGIT-GSYVSSESPFPIHLHSVAWT-VND-----PVDASAP 629
DB 2628 QTVSSGATGAKSKTLYQMAPAVSKTBDVWVRIBDCPINRSGRSPGTGTP 2681

Search completed: March 3, 2006, 13:38:51
Job time : 93.2279 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 14:09:14 ; Search time 298.259 Seconds
(without alignments)
951.209 Million cell updates/sec

Title: US-10-646-873-42

Perfect score: 3563
Sequence: 1 MDVRYRPLIGIPQAHRTG.....HKNAARWESRTYASEDD 679

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main.*
1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep.*
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4: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3563	100.0	679	3	US-09-050-516-42 Sequence 42, App1
2	3563	100.0	679	4	US-10-278-547-42 Sequence 42, App1
3	3563	100.0	679	4	US-10-646-873-42 Sequence 42, App1
4	1132	31.6	215	3	US-09-050-516-42 Sequence 47, App1
5	1132	31.6	215	4	US-10-278-547-47 Sequence 47, App1
6	1132	31.6	215	4	US-10-646-873-47 Sequence 47, App1
7	839	23.4	172	4	US-10-646-873-47 Sequence 47, App1
8	236	6.6	43	4	US-10-129-386-33676 Sequence 33676, A
9	205	5.7	910	4	US-10-087-192-1320 Sequence 1320, App
10	205	5.7	913	4	US-10-408-765A-2018 Sequence 2018, App
11	205	5.7	923	5	US-10-719-993-748 Sequence 748, App
12	205	5.7	923	5	US-10-719-993-749 Sequence 749, App
13	205	5.7	1103	5	US-10-719-993-745 Sequence 745, App
14	205	5.7	1103	5	US-10-756-149-4788 Sequence 4788, App
15	205	5.7	1103	5	US-10-631-467-604 Sequence 604, App
16	205	5.7	1103	5	US-10-631-467-691 Sequence 691, App
17	205	5.7	1337	5	US-10-719-993-742 Sequence 742, App
18	205	5.7	1337	5	US-10-719-993-743 Sequence 743, App
19	205	5.7	1337	5	US-10-719-993-747 Sequence 747, App
20	199.5	5.6	948	4	US-10-094-749-2942 Sequence 2942, App
21	195.5	5.5	1092	5	US-10-719-993-744 Sequence 744, App
22	190	5.3	57	4	US-10-106-698-5845 Sequence 5845, App
23	189	5.3	36	3	US-09-050-516-43 Sequence 43, App1
24	189	5.3	36	4	US-10-278-547-43 Sequence 43, App1
25	189	5.3	36	4	US-10-646-873-43 Sequence 43, App1
26	180	5.0	3149	4	US-10-408-765A-2326 Sequence 2326, App
27	179.5	5.0	5008	4	US-10-051-874-166 Sequence 166, App

28	177	4.9	3262	4	US-10-379-381-4	Sequence 4, App1
29	177	4.9	3262	5	US-10-840-512-161	Sequence 161, App
30	176.5	4.9	1321	5	US-10-840-512-117	Sequence 117, App
31	175	4.9	35	3	US-09-050-516-45	Sequence 45, App1
32	175	4.9	35	4	US-10-278-547-45	Sequence 45, App1
33	175	4.9	35	4	US-10-646-873-45	Sequence 45, App1
34	174	4.9	4322	4	US-10-437-963-104793	Sequence 104793, App
35	173	4.8	2468	4	US-10-755-889-615	Sequence 615, App
36	173	4.8	2468	5	US-10-489-740-216	Sequence 216, App
37	173	4.8	2519	5	US-10-489-763-46995	Sequence 46995, App
38	171	4.8	33	3	US-09-050-516-46	Sequence 46, App1
39	171	4.8	33	4	US-10-278-547-46	Sequence 46, App1
40	171	4.8	33	4	US-10-646-873-46	Sequence 46, App1
41	170.5	4.8	2367	5	US-10-485-006A-6	Sequence 6, App1
42	169	4.7	2527	4	US-10-408-765A-2462	Sequence 2462, App
43	169	4.7	2715	4	US-10-408-765A-866	Sequence 866, App
44	168	4.7	1265	4	US-10-437-963-138094	Sequence 138094, App
45	168	4.7	2843	2	US-08-681-219-32	Sequence 32, App1

ALIGNMENTS

RESULT 1
US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. US20100109041
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL TRACT
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:
 LENGTH: 679 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. US20010010904A1e
 US-09-050-516-42

Query Match 100.0%; Score 3583; DB 3; Length 679;
 Best Local Similarity 100.0%; Pred. No. 7.9e-235;
 Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDRVTRVPIIGIPOAHRGTGLVLDGTSYTHLVCMGPBASGMGODEPOTWPTDHRAQOG 60
DB 1 MDRVTRVPIIGIPOAHRGTGLVLDGTSYTHLVCMGPBASGMGODEPOTWPTDHRAQOG 60
QY 61 VOROGVSYSVHAATGQSPRGLHSENREDEGMQYVRLGARDAHQGRPTWALRPEDGDKX 120
DB 61 VOROGVSYSVHAATGQSPRGLHSENREDEGMQYVRLGARDAHQGRPTWALRPEDGDKX 120
QY 121 MKTYRLDAGDADPRRLCDLERERNAVIOGQAVRKSSTVATLOGTPDHGDRTPGPSTP 180
DB 121 MKTYRLDAGDADPRRLCDLERERNAVIOGQAVRKSSTVATLOGTPDHGDRTPGPSTP 180
QY 181 LEENVVREQIDFLAARQFLSLBOANKGAPHSPPAGTTPGASQAPKAFNKPHLA 240
DB 181 LEENVVREQIDFLAARQFLSLBOANKGAPHSPPAGTTPGASQAPKAFNKPHLA 240
QY 241 NGHVVPKIPQVKGVRENNKRAVPTWASVOVDDPGSLASVESPGTPEKTEPIREIRLA 300
DB 241 NGHVVPKIPQVKGVRENNKRAVPTWASVOVDDPGSLASVESPGTPEKTEPIREIRLA 300
QY 301 QERADLREORGRLQATDHOELVEIPTRPLTLTKSLITAPRRERGRPSLYVORDIVETO 360
DB 301 QERADLREORGRLQATDHOELVEIPTRPLTLTKSLITAPRRERGRPSLYVORDIVETO 360
QY 361 REEDHRRREGLVHGRSTPDWVSEGPQGLRRALSDDSLSPAPARADPAPEYKVNRI 420
DB 361 REEDHRRREGLVHGRSTPDWVSEGPQGLRRALSDDSLSPAPARADPAPEYKVNRI 420
QY 421 PPDAVQPLSPGTQPLEFSAFGAFGKPSLSLTAEKAAATSPKATWSPRHLSSESGKPLST 480
DB 421 PPDAVQPLSPGTQPLEFSAFGAFGKPSLSLTAEKAAATSPKATWSPRHLSSESGKPLST 480
QY 481 KOEASKPRGCGPOANGVVRWEYFRLRPLRPRADPEQOAVPVHWGMEVAGALRLQK 540
DB 481 KOEASKPRGCGPOANGVVRWEYFRLRPLRPRADPEQOAVPVHWGMEVAGALRLQK 540
QY 541 SOSDDLREERESVLRQEVAEERRNALFPEVFSPTPDENSDDNSRSSQASGITGSYS 600
DB 541 SOSDDLREERESVLRQEVAEERRNALFPEVFSPTPDENSDDNSRSSQASGITGSYS 600
QY 601 VSESPFSPILHSHNVATVEDPVDSAPPGQRKKEQWYAGINPSDGINSEVLEAIRVTRH 660
DB 601 VSESPFSPILHSHNVATVEDPVDSAPPGQRKKEQWYAGINPSDGINSEVLEAIRVTRH 660
QY 661 KNMAAERESRIYASEEDD 679
DB 661 KNMAAERESRIYASEEDD 679

```

RESULT 2

US-10-278-547-42
 Sequence 42, Application US/10278547
 Publication No. US20030082619A1

GENERAL INFORMATION:
 APPLICANT: BILLING-MEDLE, PATRICIA

COHEN, MAURICE
 COLPITTS, TRACEY L.
 FRIEDMAN, PAULA N.
 GORDON, JULIAN
 GRANADOS, EDWARD N.
 HAYDEN, MARK

HODGES, STEVEN C.
 KASS, MICHAEL R.
 KRATOCHVIL, JON D.
 TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
 FOR DETECTING DISEASES OF THE GASTROINTESTINAL
 TRACT

NUMBER OF SEQUENCES: 49
 CORRESPONDENCE ADDRESS:
 ADDRESS: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL

COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/278,547
 FILING DATE: 23-Oct-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/050,516
 FILING DATE: <Unknown>
 APPLICATION NUMBER: 08/828,855
 FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Becker, Cheryl L.
 REGISTRATION NUMBER: 35,441
 REFERENCE/DOCKET NUMBER: 6065, US, P1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847/935-1729
 TELEFAX: 847/938-2623
 TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 679 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: No. US20030082619A1e
 SEQUENCE DESCRIPTION: SEQ ID NO: 42:
 US-10-278-547-42

Query Match 100.0%; Score 3583; DB 4; Length 679;
 Best Local Similarity 100.0%; Pred. No. 7.9e-235;
 Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDRVTRVPIIGIPOAHRGTGLVLDGTSYTHLVCMGPBASGMGODEPOTWPTDHRAQOG 60
QY 61 VOROGVSYSVHAATGQSPRGLHSENREDEGMQYVRLGARDAHQGRPTWALRPEDGDKX 120
DB 61 VOROGVSYSVHAATGQSPRGLHSENREDEGMQYVRLGARDAHQGRPTWALRPEDGDKX 120
QY 121 MKTYRLDAGDADPRRLCDLERERNAVIOGQAVRKSSTVATLOGTPDHGDRTPGPSTP 180
DB 121 MKTYRLDAGDADPRRLCDLERERNAVIOGQAVRKSSTVATLOGTPDHGDRTPGPSTP 180
QY 181 LEENVVREQIDFLAARQFLSLBOANKGAPHSPPAGTTPGASQAPKAFNKPHLA 240
DB 181 LEENVVREQIDFLAARQFLSLBOANKGAPHSPPAGTTPGASQAPKAFNKPHLA 240
QY 241 NGHVVPKIPQVKGVRENNKRAVPTWASVOVDDPGSLASVESPGTPEKTEPIREIRLA 300
DB 241 NGHVVPKIPQVKGVRENNKRAVPTWASVOVDDPGSLASVESPGTPEKTEPIREIRLA 300
QY 301 QERADLREORGRLQATDHOELVEIPTRPLTLTKSLITAPRRERGRPSLYVORDIVETO 360
DB 301 QERADLREORGRLQATDHOELVEIPTRPLTLTKSLITAPRRERGRPSLYVORDIVETO 360

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QY 361 REEDHRRGLHVGRASTPDWVSEGPGLRRALSSDSLSPADPAADPAPEVKVRI 420
 DB 361 REEDHRRGLHVGRASTPDWVSEGPGLRRALSSDSLSPADPAADPAPEVKVRI 420
 QY 421 PPDAVQPTLSPTPTOLFSAFGAFKPSLSLTAEEKATSPKATMSPHLSSESGKPLST 480
 DB 421 PPDAVQPTLSPTPTOLFSAFGAFKPSLSLTAEEKATSPKATMSPHLSSESGKPLST 480
 QY 481 KOEASKPPRGCPQANRGVVRWEYFRLRLFRPADEPOQAQVPHVGMGEVAGAPALRLQK 540
 DB 481 KOEASKPPRGCPQANRGVVRWEYFRLRLFRPADEPOQAQVPHVGMGEVAGAPALRLQK 540
 QY 541 SOSDILLERERESVLRREQVVAERNNALFPEVFSPTPDENSQSSSSQASGITGSYS 600
 DB 541 SOSDILLERERESVLRREQVVAERNNALFPEVFSPTPDENSQSSSSQASGITGSYS 600
 QY 601 VSESPFFSPHLSNVAVMTVEDPVDSAPPGQKKQWAGINPSDGINSEVLEAIRVTRH 660
 DB 601 VSESPFFSPHLSNVAVMTVEDPVDSAPPGQKKQWAGINPSDGINSEVLEAIRVTRH 660
 QY 661 KNAAMERWESRIYASEEDD 679
 DB 661 KNAAMERWESRIYASEEDD 679

RESULT 3

US-10-646-873-42
 Sequence 42, Application US/10646873
 Publication No. US20040043406A1

GENERAL INFORMATION:
 APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE
 COLPITTS, TRACEY L.
 FRIEDMAN, PAULA N.
 GORDON, JULIAN
 GRANADOS, EDWARD N.
 HAYDEN, MARK
 HODGES, STEVEN C.
 KLAS, MICHAEL R.
 KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
 FOR DETECTING DISEASES OF THE GASTROINTESTINAL
 TRACT

NUMBER OF SEQUENCES: 49
 CORRESPONDENCE ADDRESS:

ADDRESSER: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL

COUNTRY: USA
 ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/646,873

FILING DATE: 22-Aug-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516
 FILING DATE: 30-MAR-1998
 APPLICATION NUMBER: 08/828,855
 FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Becker, Cheryl L.
 REGISTRATION NUMBER: 35,441
 REFERENCE/DOCKET NUMBER: 6065, US, PI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847/935-1729
 TELEFAX: 847/938-2623

TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 679 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. US20040043406A1
 SEQUENCE DESCRIPTION: SEQ ID NO: 42:
 US-10-646-873-42

Query Match 100.0%; Score 3583; DB 4; Length 679;
 Best Local Similarity 100.0%; Pred. No. 7.9e-235;
 Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRVTRVYILGIPQAHRTGLVLDGDTSTYTHLVCMGEASGKQDEQPTPTDRAQOG 60
 DB 1 MDRVTRVYILGIPQAHRTGLVLDGDTSTYTHLVCMGEASGKQDEQPTPTDRAQOG 60
 QY 61 VORQGVSYVAHYTGQSPRGHSENREDEGMQYRLGARDAHQRPYALRPDEGDK 120
 DB 61 VORQGVSYVAHYTGQSPRGHSENREDEGMQYRLGARDAHQRPYALRPDEGDK 120
 QY 61 VORQGVSYVAHYTGQSPRGHSENREDEGMQYRLGARDAHQRPYALRPDEGDK 120
 DB 61 VORQGVSYVAHYTGQSPRGHSENREDEGMQYRLGARDAHQRPYALRPDEGDK 120
 QY 121 MKTYRLDAGDADPRRLCDLIEREWAIVIGQAVRKSSTVATLQGTPTDHDGPTPGPRSTP 180
 DB 121 MKTYRLDAGDADPRRLCDLIEREWAIVIGQAVRKSSTVATLQGTPTDHDGPTPGPRSTP 180
 QY 121 MKTYRLDAGDADPRRLCDLIEREWAIVIGQAVRKSSTVATLQGTPTDHDGPTPGPRSTP 180
 DB 121 MKTYRLDAGDADPRRLCDLIEREWAIVIGQAVRKSSTVATLQGTPTDHDGPTPGPRSTP 180
 QY 181 LEENVVDEQIDFLAARQFTLSLEQANKGAPHSPPARCTPACTTPGASQAPKAFKPHLA 240
 DB 181 LEENVVDEQIDFLAARQFTLSLEQANKGAPHSPPARCTPACTTPGASQAPKAFKPHLA 240
 QY 241 NGHVPIPIQVKGAVRENNKRAVPTMASVOVVDPSGLASVESGTPETPIEIRILA 300
 DB 241 NGHVPIPIQVKGAVRENNKRAVPTMASVOVVDPSGLASVESGTPETPIEIRILA 300
 QY 241 NGHVPIPIQVKGAVRENNKRAVPTMASVOVVDPSGLASVESGTPETPIEIRILA 300
 DB 241 NGHVPIPIQVKGAVRENNKRAVPTMASVOVVDPSGLASVESGTPETPIEIRILA 300
 QY 301 QERADLREORGLROATDHOELVEIPTRLITKLSLITAPRERGRPSLYVORDIVOETQ 360
 DB 301 QERADLREORGLROATDHOELVEIPTRLITKLSLITAPRERGRPSLYVORDIVOETQ 360
 QY 301 QERADLREORGLROATDHOELVEIPTRLITKLSLITAPRERGRPSLYVORDIVOETQ 360
 DB 301 QERADLREORGLROATDHOELVEIPTRLITKLSLITAPRERGRPSLYVORDIVOETQ 360
 QY 361 REEDHRRGLHVGRASTPDWVSEGPGLRRALSSDSLSPADPAADPAPEVKVRI 420
 DB 361 REEDHRRGLHVGRASTPDWVSEGPGLRRALSSDSLSPADPAADPAPEVKVRI 420
 QY 421 PPDAVQPTLSPTPTOLFSAFGAFKPSLSLTAEEKATSPKATMSPHLSSESGKPLST 480
 DB 421 PPDAVQPTLSPTPTOLFSAFGAFKPSLSLTAEEKATSPKATMSPHLSSESGKPLST 480
 QY 481 KOEASKPPRGCPQANRGVVRWEYFRLRLFRPADEPOQAQVPHVGMGEVAGAPALRLQK 540
 DB 481 KOEASKPPRGCPQANRGVVRWEYFRLRLFRPADEPOQAQVPHVGMGEVAGAPALRLQK 540
 QY 541 SOSDILLERERESVLRREQVVAERNNALFPEVFSPTPDENSQSSSSQASGITGSYS 600
 DB 541 SOSDILLERERESVLRREQVVAERNNALFPEVFSPTPDENSQSSSSQASGITGSYS 600
 QY 601 VSESPFFSPHLSNVAVMTVEDPVDSAPPGQKKQWAGINPSDGINSEVLEAIRVTRH 660
 DB 601 VSESPFFSPHLSNVAVMTVEDPVDSAPPGQKKQWAGINPSDGINSEVLEAIRVTRH 660
 QY 661 KNAAMERWESRIYASEEDD 679
 DB 661 KNAAMERWESRIYASEEDD 679

RESULT 4

US-09-050-516-47
 Sequence 47, Application US/09050516
 Patent No. US20010010904A1

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
 APPLICANT: COHEN, MAURICE
 APPLICANT: COLPITTS, TRACEY L.
 APPLICANT: FRIEDMAN, PAULA N.

Db 181 DGINSEVLEAIRVTRHKNAMERWESRIYASEDD 215

RESULT 6

US-10-646-873-47
; Sequence 47, Application US/10646873
; Publication No. US20040043406A1

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITS, TRACEY L.

FRIEDMAN, PAULA N.

GORDON, JULIAN

GRANADOS, EDWARD N.

HAYDEN, MARK

HODGES, STEVEN C.

KATSOCHVIL, JON D.

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KATSOCHVIL, JON D.

QY 585 NSRSSQASGIGTSYSVSESPFPIHLSNVMTVEDPVDSAPPGORKEQWYAGINPS 644
Db 121 NSRSSQASGIGTSYSVSESPFPIHLSNVMTVEDPVDSAPPGORKEQWYAGINPS 180
QY 645 DGINSEVLEAIRVTRHKNAMERWESRIYASEDD 679
Db 181 DGINSEVLEAIRVTRHKNAMERWESRIYASEDD 215

RESULT 7

US-10-106-698-4761
; Sequence 4761, Application US/10106698
; Publication No. US20030109690A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

FILE REFERENCE: PA005P1

CURRENT FILING DATE: 2002-03-27

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

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PRIOR FILING DATE: 2000-09-28


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QY 276 PGSLSAVSPGTPKPTPIERIRLAQERADLRE--ORGLRQATDHQELVEIPTRPLITK 333
DB 435 FGALETPSAAGSQGNT-----ASQKEGSPSEPSKRG-----PLSKMAE 474
QY 334 LSLITAPRR-----ERGRPSLYVQRDIYQETQREEDHREGHVGRASTPVMVSEGP 385
DB 475 DGEFTSAAVALTVVKDDHGLDQFSRSVNSVLQEBELSGDLDELVSRSQDTT----- 527
QY 386 QPGLRRLSSDLSIPADARAADPAPEVRKVNRIPPDAYOPLYSPGTPOLE----- 437
DB 528 ---VLETISNDPSMDNISDSGASN-----ETTNAQENSLADFSLPQTPQTDNPSGEGR 579
QY 438 ---FSAFGAFGKPSLSSTA-----EAKATSPKA-TYSPRLHS 471
DB 580 GVSXSFSDHGFYSPSTLGDSPLYDDPLEYQAGLLVQNALQQAIAEQVDKAVSKTSRDGA 639
QY 472 ESSGKPLSTKQDAS-----KPPR-GCP-QANRGVWMEYRRLP-----LRF 511
DB 640 EQQG-PEATVEAEAAAFGESEKQPMFEPPQVSSPVQEKRDVLP---KILPAEDRALRE 694
QY 512 RAPDEP-----OOAQVPHWGMEVA 531
DB 695 RGPPEPLPAVOPSGPINMEETPREGSYRSKYSEAAELRSTASLATQESDV-----MV 747
QY 532 GAPALRLQKSSDILLERERESVLRREQVAER-----RNALFPEV----- 573
DB 748 GPFKLRSRQKQTLMSIEEIRIAQEREBELKROQVLOSTQSPRTKNA--PSLPERTCYK 805
QY 574 -----FSTPDENSQNSRSSQASGITSYVSSESPPFSPIHLHSNVAWYVE 621
DB 806 TAPGKIEKYKPPSPTEGPSLQPLAPAEAG-----TORP-----KNIMQTLM 850
QY 622 DAVDAPPGQQRK--EQWYAGINPSDGINSEVLEAIRVTRHKNAAERESRIYASEED 679
DB 851 EDETTHKSKRRERMDSSITSKLSCKVTSEVLEAIRVNRKKSALALRMEAGIYANOEBE 910

```

RESULT 11

```

US-10-719-993-748
; Sequence 748, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 748
; LENGTH: 923
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-719-993-748

```

Query Match 5.7%; Score 205; DB 5; Length 923;

Best Local Similarity 19.9%; Pred. No. 4.5e-05; Indels 292; Gaps 33;

Matches 155; Conservative 105; Mismatches 228;

```

QY 100 RDAHGRPTWALRPEDGEDKEMKTYRLDAGDAP--RLCDLREERNAVILQGAVRKSTV 158
DB 233 RAHEDKKPSKLPEDDEHEKEQYCIK---KVRPEEMLELKERRELIRSGAVKKNPGI 288
QY 159 AT-----LQTPDHGDPRTG----- 174
DB 289 AAKMWNPPQKTIIEQLDEEHLSEHKYKERKERRAQQEQLLQKOLQOQOQOQPPSOLCT 348
QY 175 PRPSTPLEENVDR-----EQIDPLARQOFLSLEQANKGAPHSSPARGTAGTTP-- 225
DB 349 APASSHERASMDKAMEDIVTEQIDFSAARKQFOLMENSQAV---AKGO---STPRL 400

```

```

QY 226 -----GASQAFKAFNPHLANGHVVPKIQVGVVREENKVAVPTWASQVVD 275
DB 401 FSIPTFRPLASVNSDKPLTP-----RPPSGCGPEEDSGAAGQKS----- 444
QY 276 PGSLSAVSPGTPKPTPIERIRLAQERADLRE--ORGLRQATDHQELVEIPTRPLITK 333
DB 445 FGALETPSAAGSQGNT-----ASQKEGSPSEPSKRG-----PLSKMAE 484
QY 334 LSLITAPRR-----ERGRPSLYVQRDIYQETQREEDHREGHVGRASTPVMVSEGP 385
DB 485 DGEFTSAAVALTVVKDDHGLDQFSRSVNSVLQEBELSGDLDELVSRSQDTT----- 537
QY 386 QPGLRRLSSDLSIPADARAADPAPEVRKVNRIPPDAYOPLYSPGTPOLE----- 437
DB 538 ---VLETISNDPSMDNISDSGASN-----ETTNAQENSLADFSLPQTPQTDNPSGEGR 589
QY 438 ---FSAFGAFGKPSLSSTA-----EAKATSPKA-TYSPRLHS 471
DB 590 GVSXSFSDHGFYSPSTLGDSPLYDDPLEYQAGLLVQNALQQAIAEQVDKAVSKTSRDGA 649
QY 472 ESSGKPLSTKQDAS-----KPPR-GCP-QANRGVWMEYRRLP-----LRF 511
DB 650 EQQG-PEATVEAEAAAFGESEKQPMFEPPQVSSPVQEKRDVLP---KILPAEDRALRE 704
QY 512 RAPDEP-----OOAQVPHWGMEVA 531
DB 705 RGPPEPLPAVOPSGPINMEETPREGSYRSKYSEAAELRSTASLATQESDV-----MV 757
QY 532 GAPALRLQKSSDILLERERESVLRREQVAER-----RNALFPEV----- 573
DB 758 GPFKLRSRQKQTLMSIEEIRIAQEREBELKROQVLOSTQSPRTKNA--PSLPERTCYK 815
QY 574 -----FSTPDENSQNSRSSQASGITSYVSSESPPFSPIHLHSNVAWYVE 621
DB 816 TAPGKIEKYKPPSPTEGPSLQPLAPAEAG-----TORP-----KNIMQTLM 860
QY 622 DAVDAPPGQQRK--EQWYAGINPSDGINSEVLEAIRVTRHKNAAERESRIYASEED 679
DB 861 EDETTHKSKRRERMDSSITSKLSCKVTSEVLEAIRVNRKKSALALRMEAGIYANOEBE 920

```

RESULT 12

```

US-10-719-993-749
; Sequence 749, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 749
; LENGTH: 923
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-719-993-749

```

Query Match 5.7%; Score 205; DB 5; Length 923;

Best Local Similarity 19.9%; Pred. No. 4.5e-05; Indels 292; Gaps 33;

Matches 155; Conservative 105; Mismatches 228;

```

QY 100 RDAHGRPTWALRPEDGEDKEMKTYRLDAGDAP--RLCDLREERNAVILQGAVRKSTV 158
DB 233 RAHEDKKPSKLPEDDEHEKEQYCIK---KVRPEEMLELKERRELIRSGAVKKNPGI 288
QY 159 AT-----LQTPDHGDPRTG----- 174
DB 289 AAKMWNPPQKTIIEQLDEEHLSEHKYKERKERRAQQEQLLQKOLQOQOQOQPPSOLCT 348
QY 175 PRPSTPLEENVDR-----EQIDPLARQOFLSLEQANKGAPHSSPARGTAGTTP-- 225

```


Db 349 APASHHERAMIDKXEDIVTEQIDFSAARKQFOLMENSROAV-----AKGQ---STPRL 400
Qy 226 -----GASQAPKAFKPHLANGHVPIKQVGVAREENKRAVPMTASVQVYDD 275
Db 401 FSIKPYRPLGVSNSDKPLTNP-----RPPSVGGPPEDSGASAAGQKS----- 444
Qy 276 PGSIASVESPGTPKEPTIEREIRLAQERADLRE--ORGKQATDHQELVEIPRPLITK 333
Db 445 PGLAETPSAAGSQNT-----ASQKEGYPSEPSKRG-----PLSKLMAB 484
Qy 334 LSLITAPRR-----ERGRPSLVYQRDIYQETQOREDHRRREGIHAVGRASTPDMWSEGP 385
Db 485 DGEFTSARAVALTVYKDDHGLDQFSRSVNSLTQELDGLBELSRSQDTT----- 537
Qy 386 QPGLRRALSDDSIILSPADARAADPAPEVKVNRIPPDAYQPYLSPGTPQLE----- 437
Db 538 ---VLETLSNDPFSMDNISDSGASN-----ETTNAQENSLADPSLPQTPQTDNPSSEGRGE 589
Qy 438 ---FSAFGAFGKPSLSLSTA-----EAKAATSPKA-TMSPRHLS 471
Db 590 GVSXSFSDHGFYSPBSTLGDSPVDDPLEYQAGLLVQNALQALAEQVDAVSKTSRDGA 649
Qy 472 ESSGKPLSTKQOAS-----XPPR-GCP-QANRGVWMEYFRLRP-----LRF 511
Db 650 EQQG-PEATVEAEALAAFGSEKQSMFEPQVSSPVQEKDVLPR---KLIPAEADRLRE 704
Qy 512 RAPDEP-----QAQVPHVMGWMEVA 531
Db 705 RGPQPLPAVQPSGPIINMEETREGSYFSKYSEAAELRSTASLATTQESDV-----MV 757
Qy 532 GAPALRLQKQSSDILERESESVLRBOEVAEER-----RNALPPEV----- 573
Db 758 GPFILRSKQKQTLTSMIEEIRAAQEREELKQROVLOSTQSPRTKNA--PSLSRTCYK 815
Qy 574 -----FSPPTDENSQNSRSSQASGITGSYSSESPPFPIHLSNVAMTVE 621
Db 816 TAPGKIEKVPSPPTTEGSLQPLADPEBAAG-----TORP-----KMLQTLM 860
Qy 622 DPVDSAPPQGRKK--EOMYAGINPSDGINSEVLAIIRVTHKNAAMERWESRIYASEDD 679
Db 861 EDYETHKSKRRERMDSSYTSKLSCKVTSEVLATRVNRKKSALALRWAGIYANQEE 920

RESULT 13
US-10-719-993-745
; Sequence 745, Application US/10719993
; Publication No. US20040265849a1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 745
; LENGTH: 1103
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-719-993-745

Query Match 5.7%; Score 205; DB 5; Length 1103;
Best Local Similarity 19.9%; Pred. No. 5.7e-05;
Matches 155; Conservative 105; Mismatches 228; Indels 292; Gaps 33;

Qy 100 RDAHQGRPTWALRPDEGEDKEMKTYRLDAGDADP--RRLCDLEBRWAVIQGAAVRSSTV 158
Db 413 RAHFEDKKPSKLFEDDEHEKEQYCIIR---KYRPSSEWLEIEKERREILRSQAVKAMPGI 468
Qy 159 AT-----LQSTPDHGDPRTPG----- 174

Db 469 AAKWMPPOEKTIEQLEDEHLESHKKYKERKERRAQOEQLLQKOLQOQOQPPSGLCT 528
Qy 175 PRPSTPLEENVVR-----EQIDFLAAQOFLSLEQANKGAPHSPARGTAGTTP-- 225
Db 529 APASHHERAMIDKXEDIVTEQIDFSAARKQFOLMENSROAV-----AKGQ---STPRL 580
Qy 226 -----GASQAPKAFKPHLANGHVPIKQVGVAREENKRAVPMTASVQVYDD 275
Db 581 FSIKPYRPLGVSNSDKPLTNP-----RPPSVGGPPEDSGASAAGQKS----- 624
Qy 276 PGSIASVESPGTPKEPTIEREIRLAQERADLRE--ORGKQATDHQELVEIPRPLITK 333
Db 625 PGLAETPSAAGSQNT-----ASQKEGYPSEPSKRG-----PLSKLMAB 664
Qy 334 LSLITAPRR-----ERGRPSLVYQRDIYQETQOREDHRRREGIHAVGRASTPDMWSEGP 385
Db 665 DGEFTSARAVALTVYKDDHGLDQFSRSVNSLTQELDGLBELSRSQDTT----- 717
Qy 386 QPGLRRALSDDSIILSPADARAADPAPEVKVNRIPPDAYQPYLSPGTPQLE----- 437
Db 718 ---VLETLSNDPFSMDNISDSGASN-----ETTNAQENSLADPSLPQTPQTDNPSSEGRGE 769
Qy 438 ---FSAFGAFGKPSLSLSTA-----EAKAATSPKA-TMSPRHLS 471
Db 770 GVSXSFSDHGFYSPBSTLGDSPVDDPLEYQAGLLVQNALQALAEQVDAVSKTSRDGA 829
Qy 472 ESSGKPLSTKQOAS-----KPPR-GCP-QANRGVWMEYFRLRP-----LRF 511
Db 830 EQQG-PEATVEAEALAAFGSEKQSMFEPQVSSPVQEKDVLPR---KLIPAEADRLRE 884
Qy 512 RAPDEP-----QAQVPHVMGWMEVA 531
Db 885 RGPQPLPAVQPSGPIINMEETREGSYFSKYSEAAELRSTASLATTQESDV-----MV 937
Qy 532 GAPALRLQKQSSDILERESESVLRBOEVAEER-----RNALPPEV----- 573
Db 938 GPFILRSKQKQTLTSMIEEIRAAQEREELKQROVLOSTQSPRTKNA--PSLSRTCYK 995
Qy 574 -----FSPPTDENSQNSRSSQASGITGSYSSESPPFPIHLSNVAMTVE 621
Db 996 TAPGKIEKVPSPPTTEGSLQPLADPEBAAG-----TORP-----KMLQTLM 1040
Qy 622 DPVDSAPPQGRKK--EOMYAGINPSDGINSEVLAIIRVTHKNAAMERWESRIYASEDD 679
Db 1041 EDYETHKSKRRERMDSSYTSKLSCKVTSEVLATRVNRKKSALALRWAGIYANQEE 1100

RESULT 14
US-10-756-149-4788
; Sequence 4788, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Azite, Natasha
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4788
; LENGTH: 1103
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-4788

Query Match 5.7%; Score 205; DB 5; Length 1103;
Best Local Similarity 19.9%; Pred. No. 5.7e-05;
Matches 155; Conservative 105; Mismatches 228; Indels 292; Gaps 33;

Qy 100 RDAHQGRPTWALRPDEGEDKEMKTYRLDAGDADP--RRLCDLEBRWAVIQGAAVRSSTV 158

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Db      413 RAHFEDKKPSLFPDDEHEKQYCIK-----KVRSEEMLELEKERRRRLISQAVKXNPGI 468
QY      159 AT-----LOCTPDHGPRTPG-----174
Db      469 AAKMNPPEQKTEIEQDLDEHLESHKKYKERRERRAQQEQLLQKOLQOQOQOQPPSOLCT 528
QY      175 PPRSTPLEENVDR-----EQIDFLAARQOFLSLEQANKGAPHSPPARGTPTGP--225
Db      529 APASHERASMTDKAKEDIVTEQIDFSARKQFQLEMENSRQAV-----AKQO---STRRL 580
QY      226 -----GASQAPKAFNKPMLANGHVPIKQVKGVEENKVRAPVTWASVQVVD 275
Db      581 PSIKFTYRPLASVNSDKLTP-----RPSVGGPPEDSGASAAKQKS-----624
QY      276 PGSIASVSPGTPKETPIERIRLAQEREADLRE--QGLRQATDHQELVEIPTRPLLTG 333
Db      625 PQALETPEASQSGNT-----ASQKEGYPSEPSKRG-----PLSKLWAE 664
QY      334 LSLITAPRR-----ERGRPSLYVQRDIYQETQREEDHREGIHYGRASPTDWSBGP 385
Db      665 DGEFTSABAVLTVVDDHGLDQFSRSVNSVLTQEBELSGDELSTVSODTT-----717
QY      386 QPGLRALSISILSPADARAADAPAVRKVNRIPPAVQPYLSPGTPOLE-----437
Db      718 ---VLETISNDFSMNIDSGASN-----ETTNALQENSLADFSLPQTPQTDNPSGKGE 769
QY      438 -----FSAFGAFGKPSLSLTA-----EAKAATSPKA-TMSPRHLS 471
Db      770 GVSXSFSDHGFYSPSTLGDSPLVDDPLEYQAGLLVQNALQQAILEQVDKAVSKTSRQGA 829
QY      472 ESSGKPLSTKQAS-----KPPR-GCP-QANRGVVRMEYRLRP-----LRF 511
Db      830 EQQG-PEATVEBAEAFAFGSEKQPMFEPVSSPVQEKRDVLP---KILPAEDRALRE 884
QY      512 RAPDPR-----OOAQVPHVWGWEVA 531
Db      885 RGPQPLPAVQPSGFINNEETRPBGYSYSKSEAAELASTASLATQESDV-----MV 937
QY      532 GAPALRLQKSSDILLERERESVLAREQVAER-----RNALFPEV-----573
Db      938 GPFKLRSRKQRTLSMIEEIRAAQEREELKROVLQSTQSPRTKNA--PGLPSRTCYK 995
QY      574 -----FSTPDENSQONSRSSQASGITGSYSVSPFSPFIHLHSNVATYVE 621
Db      996 TAPGKIEKVPKPPSPPTTBGPSLOPDLAPEAAG-----TORP-----KNLMQITLM 1040
QY      622 DVIDSAPQQRK--EQWYAGINPSDGINSEVLEAIRVTRHKNAMAKERSRIYASEDD 679
Db      1041 EDYETHKSRKRRERMDSSYTSKLSLCKVTSEVLEATRVNRKRSALALRWEAGIYANQEE 1100

RESULT 15
US-10-631-467-604
/ Sequence 604, Application US/10631467
/ Publication No. US20050208496A1
/ GENERAL INFORMATION:
/ APPLICANT: Genox Research Inc.
/ TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive P
/ FILE REFERENCE: 3462.1005-000
/ CURRENT APPLICATION NUMBER: US/10/631,467
/ PRIOR FILING DATE: 2003-07-31
/ PRIOR APPLICATION NUMBER: JP 2003-077212
/ PRIOR FILING DATE: 2003-03-20
/ PRIOR APPLICATION NUMBER: JP 2002-229312
/ NUMBER OF SEQ ID NOS: 2086
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 604
/ LENGTH: 1103
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-631-467-604

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Query Match      5.7%; Score 205; DB 5; Length 1103;
Beet Local Similarity 19.9%; Pred. No. 5.7e-05;
Matches 155; Conservative 105; Mismatches 228; Indels 292; Gaps 33;

QY      100 RDAHQRPYMLAREPDEDEKEMKTYRLDAGDAD--RRLCDLEREMNAVIOQAVRKSTV 158
Db      413 RAHFEDKKPSLFPDDEHEKQYCIK-----KVRSEEMLELEKERRRRLISQAVKXNPGI 468
QY      159 AT-----LOCTPDHGPRTPG-----174
Db      469 AAKMNPPEQKTEIEQDLDEHLESHKKYKERRERRAQQEQLLQKOLQOQOQOQPPSOLCT 528
QY      175 PPRSTPLEENVDR-----EQIDFLAARQOFLSLEQANKGAPHSPPARGTPTGP--225
Db      529 APASHERASMTDKAKEDIVTEQIDFSARKQFQLEMENSRQAV-----AKQO---STRRL 580
QY      226 -----GASQAPKAFNKPMLANGHVPIKQVKGVEENKVRAPVTWASVQVVD 275
Db      581 PSIKFTYRPLASVNSDKLTP-----RPSVGGPPEDSGASAAKQKS-----624
QY      276 PGSIASVSPGTPKETPIERIRLAQEREADLRE--QGLRQATDHQELVEIPTRPLLTG 333
Db      625 PQALETPEASQSGNT-----ASQKEGYPSEPSKRG-----PLSKLWAE 664
QY      334 LSLITAPRR-----ERGRPSLYVQRDIYQETQREEDHREGIHYGRASPTDWSBGP 385
Db      665 DGEFTSABAVLTVVDDHGLDQFSRSVNSVLTQEBELSGDELSTVSODTT-----717
QY      386 QPGLRALSISILSPADARAADAPAVRKVNRIPPAVQPYLSPGTPOLE-----437
Db      718 ---VLETISNDFSMNIDSGASN-----ETTNALQENSLADFSLPQTPQTDNPSGKGE 769
QY      438 -----FSAFGAFGKPSLSLTA-----EAKAATSPKA-TMSPRHLS 471
Db      770 GVSXSFSDHGFYSPSTLGDSPLVDDPLEYQAGLLVQNALQQAILEQVDKAVSKTSRQGA 829
QY      472 ESSGKPLSTKQAS-----KPPR-GCP-QANRGVVRMEYRLRP-----LRF 511
Db      830 EQQG-PEATVEBAEAFAFGSEKQPMFEPVSSPVQEKRDVLP---KILPAEDRALRE 884
QY      512 RAPDPR-----OOAQVPHVWGWEVA 531
Db      885 RGPQPLPAVQPSGFINNEETRPBGYSYSKSEAAELASTASLATQESDV-----MV 937
QY      532 GAPALRLQKSSDILLERERESVLAREQVAER-----RNALFPEV-----573
Db      938 GPFKLRSRKQRTLSMIEEIRAAQEREELKROVLQSTQSPRTKNA--PGLPSRTCYK 995
QY      574 -----FSTPDENSQONSRSSQASGITGSYSVSPFSPFIHLHSNVATYVE 621
Db      996 TAPGKIEKVPKPPSPPTTBGPSLOPDLAPEAAG-----TORP-----KNLMQITLM 1040
QY      622 DVIDSAPQQRK--EQWYAGINPSDGINSEVLEAIRVTRHKNAMAKERSRIYASEDD 679
Db      1041 EDYETHKSRKRRERMDSSYTSKLSLCKVTSEVLEATRVNRKRSALALRWEAGIYANQEE 1100

Search completed: March 3, 2006, 14:18:08
Job time : 302.258 secs

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Db 437 -----BAPAP-----SLATSP--ALGHESSTPKSLHPWVGITPTSSPKTKK 476
Qy 366 RRE-----GLHVGRASTPDWVSEGPQGLR-RAISSDILSPAPDAPADPADEVR 415
Db 477 RPARAPASAPLALHAGSLSHSEPPSATPSPALSVESISESASQOTGAEILBPPA----- 532
Qy 416 KVNIPDPAYQPYL-SPGTPOLBFSAFGAFGKPSLSSTAEBKAATSPKATWSPHLSSESS 474
Db 533 -----VPSSESEPAVHARPTP-----GNPVSLSINSTSLA-----SS 563
Qy 475 GKPLSTQOASKPPRGCPQANRGVWMEYFRLRLFRAPDEPOQAVPHWGWAVAG 534
Db 564 GELVEPRVEQ-----MPQASPG-----LAP-RTRGSSGQPAK-----PCSGAT 601
Qy 535 ALRLQKQSSDLERERESVTLRQOEVAEERRNALFEVESPPTDENSDQNSRSSQASG 594
Db 602 PTPPL-----LVGDHSPV-----PSRGSSSPOLQVXSSCKE- 632
Qy 595 ITGSYSSESPFSPHLSNVAMTVEDPDVDSAPPGQ-----RKKEQWYAGINPSDGIN 649
Db 633 --NPPNKKPSAPASPA---TKKATKGSKPVPAPRPGHGFPLIKKVKQADQYI-PEEDIHG 686
Qy 650 EV-----LEAIRVTRHKNM-MAERWESRIYASEED 679
Db 687 EMDITERLDMAL---EHRGVLEEKRLGCLNGREDD 720

RESULT 2
US-11-087-099-2391
; Sequence 2391, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087, 099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2391
; LENGTH: 2479
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-11-087-099-2391

Query Match 4.4%; Score 158; DB 7; Length 2479;
Best Local Similarity 20.9%; Pred. No. 0.011;
Matches 132; Conservative 87; Mismatches 222; Indels 192; Gaps 31;

Qy 114 EDGEDKEMKTYRL-----DAGDADPRRLCDL-----ERERWAVIQQOAVRKSSTVATL 161
Db 762 QEADDKAREELRLLELVNQDAVKAQKAKAELGMNNAVANAKAALAEERRIRVRAEATL 821
Qy 162 QGTPDHGDPRT--PGPRSTPLLEENVVDRQ-----IDFLAARQOFLSLERQANKGAPHS 213
Db 822 AKTVTEKTPKTFPTGCKLTVASASRGDVSRTRDHKKFVPLKTSKVAAASEAKKADDRK 881
Qy 214 SPAGTTPAGTTPGASQAKAFNKPFLANGHVPLKPOVKGYVR--EENKVR-AVPTMASV 270
Db 882 HAAAGAERQO---ALEAAGAERKEIKKGNQO-----GVVKASEANVPKSAADPAISKS 932
Qy 271 QVNDPGLSLAVESPGTPEKTEPIEREIRLAQERADLSEORGLQO-----TD 318
Db 933 PEASFTPLTAERKRNRYET-----IRRREWEQREAKKQDEAKIITYPREADISKP 987
Qy 319 HQELVEIPTRBLTKL--SLITAPRERGRPSLY---VQDRIVOTQREEDHREGLHVG 373
Db 988 FEANVPKPADVISKSPASIPTLPLTEVEKPRNFYETIRRRREWEAQREAAKXTD----- 1042
Qy 374 RASTPDWVSEGPQGLRALSSDSLSPAPDAPADP-----APEKRVKRNIPPDAYQ 426
Db 1043 -----BAEKIKIP-PRADISKSPSEANVHKAPE--KINK-PPEA-- 1076

Qy 427 PYLPGTPOLEFSAFGAFGKPSLSLT--AEAKATSPKATWSPHLSSESGKP----- 477
Db 1077 -----DISPSEANVHKPADPAISKSPASI-PTPLTEAKQBNFYEAI 1119
Qy 478 -----LSTKQASKPPRGCPQANRGVWMEYFRLRLFRAPDEP---QOAVPHWGW 528
Db 1120 RRRREWEAKREAAKKQDE-----ETRRDMLBEKKKQWANDKPSATQOAVBEAWPS 1171
Qy 529 -----EVAGA--PALRL-----OKSSDDL--ERERESVTLRQOEVAEE 564
Db 1172 LPSTQVQKPEALGAAPSVKLPKIKIAPPKPKESQSAKANPOQKQSPTRKRPQOAWSQ 1231
Qy 565 RNALFPEVYSPPTDEN-----SDQNSRSSQASGITGSYSVE-----SP 606
Db 1232 -----PKPDGNDREKQTGLVQVKSQEKTOGQAQASALENTQGSQKTMKGPAK 1280
Qy 607 FSPHLSHN---VAMTVEDPDVDSAPPGQKKE 635
Db 1281 THVPKAEKPPQPAOKKPODPVKKQPOSQOAKK 1313

RESULT 3
US-11-080-991-54
; Sequence 54, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:

; APPLICANT: Veiblv, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FaestSeq for windows Version 4.0
; SEQ ID NO 54
; LENGTH: 2828
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-54

Query Match 4.4%; Score 156.5; DB 7; Length 2828;
Best Local Similarity 19.6%; Pred. No. 0.016;
Matches 167; Conservative 85; Mismatches 305; Indels 293; Gaps 35;

Qy 10 LGIPQAHRTGLV--LDGDTSTYTHLVCMGPASGWDGDEPQTWPTD--HRA---QQ 59
Db 602 LAIPFAHLSWILPNRRIINDLANTSH-VVYLPMGT--LSIPKVQVSDSGYRCVAVNQ 657
Qy 60 GVGQRCYSYIV-HAYIGQSPERG-----LHSENREDQWQVRLGARAHQORPT 108
Db 658 GADHFTVGTIVTKGSLPKRGRRPKAKALSHVEDIVDEGGS---QMGD-EENTSR 712
Qy 109 WALRPEDGE-----DKEMKTYRL-----DAGDADPRRLCDLER--- 141
Db 713 RLHPHQDEVPLTKDQANGDKAKKGRKLLKMGHSEKEPETNNAVEGRVRESRRIN 772
Qy 142 -----ERW-----AVIQOAVRKSSTVATLQGTPDHGDPRTPGPRSTPLLEENVVDR 189
Db 773 MANKQINERHADIILAKVRGKNLPKGTVEVPL-----IKTSPSPS----- 812
Qy 190 QIDFLAARQOFLSLERQANKAPHSPPARGTTPAGTTPGASQAPAFNKPFLANGHVPIKP 249
Db 813 -----LSLE-VTPFPVAVSPSASPVOVTVAESASAD-----VPL-- 847
Qy 250 QVGVVNEENKRAVPTMASVOVDDPGSLASYESPCTPPTPIEREIRLAQERADLRE 309
Db 848 -----LGEENHVLGTISSASMGLEHNHNGVILVEPVT--STPLEBVDVLDSETEITS 900
Qy 310 QRGRLQATDHOELVEIPTRBLTKLSLITA--PRRE----- 343

Db 901 TEGDLKTAAPTLISEPESPFTLHTLDVTEKPHETATEGWSADVSSPEPTSEY 960
 Qy 344 -----NGRPSLYQARDIVQETQREDBHREGLVGRASPFD-WVSEGP----- 385
 Db 961 EPPDAVSLASEBPMQVFPDLETKSDPDEDMKEDTFAHLPTFTIWNDSSTSQLPED 1020
 Qy 386 ----OPG-----LRRALSSDSILSPAP-DA 405
 Db 1021 STIGEPGVPGQSHLQGLTDNIHLVKSLSSTQDTLLIKKMKMSQTLQGGNNLEBDPTHS 1080
 Qy 406 RAADPAPEVRKYNRPDP--AYQPYLSPGTQLEFSAGFAGKPSLSLTAEKATSPKA 463
 Db 1081 RSSEBEGESKSTLPDSTLIGMSMSVKKPAETVTGLDKQTTVTTPROKVAASS 1140
 Qy 464 TMSPRHLSESSGKPLSTKQEASKPRGCPQANRGVMEYFRLRPLRFR----- 512
 Db 1141 TMS-----THPRRRPNGR-----RLRNNKFRHHRKQPTPTTF 1174
 Qy 513 APDEPQQAQVPHVWGEVAGAPALRLQKSQSDLL-----ERRESVLRBQ 559
 Db 1175 APSEFPSTQPTQ-----APDIKISSQVESLVPMTAVDNTVNTPKOLEMKNAEPTS 1226
 Qy 560 EVAERERNAALPEVFSPTPDENSQNSRSSQASGITGSYSVE-----SPFSPILH 613
 Db 1227 KGTPRKKGKRNKRYTP-----STVSSPASGSKSPSPENKRNIVTPSSSTILLP 1279
 Qy 614 SNVAMTVEDPVDSA-----PPGQRKKEQWYAGINPSDGINSEVLEAIRVTRH 660
 Db 1280 RTVSLKTBGPYDSLDMYMTTRKIYSSYPKVQETLVTYTKPISDGEIKDDV--AINVDKH 1337
 Qy 661 KNAMARWES 670
 Db 1338 KSDILVTGES 1347

RESULT 4

US-11-186-284-49
 ; Sequence 49, Application US/11186284
 ; Publication No. US2005026493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Berger, Allison
 ; APPLICANT: Guillemette, Tracy L.
 ; APPLICANT: Kametkar, Shubhang
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Monahan, John E.
 ; APPLICANT: Thibodeau, Stephen N.
 ; APPLICANT: Burgart, Lawrence J.
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
 ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; FILE REFERENCE: MP001-029P2RNM
 ; CURRENT APPLICATION NUMBER: US/11/186,284
 ; CURRENT FILING DATE: 2005-07-21
 ; PRIOR APPLICATION NUMBER: US/10/301,822
 ; PRIOR FILING DATE: 2002-11-21
 ; PRIOR APPLICATION NUMBER: US 60/339,971
 ; PRIOR FILING DATE: 2001-12-10
 ; PRIOR APPLICATION NUMBER: US 60/361,978
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: US 60/381,988
 ; PRIOR FILING DATE: 2002-05-20
 ; NUMBER OF SEQ ID NOS: 228
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 49
 ; LENGTH: 2828
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-11-186-284-49
 Query Match 4.4%; Score 156.5; DB 7; Length 2828;
 Best Local Similarity 19.6%; Pred. No. 0.016;
 Matches 167; Conservative 85; Mismatches 305; Indels 293; Gaps 35;

Qy 10 LGIPQARHGTCLV---LDGTSYTYHLVCKGPEASGCODEPQWPTD---HRA-----QQ 59
 Db 602 LAIEAHLSWILPNRRRIINDLANTSH-VTNLPNCT---LSLPKQVDSGTCRYAVANQ 657
 Qy 60 GVRQGVSYSV-AHYTCQPSPRG-----LHSENRDEGQVYRLGARDAHQHPT 108
 Db 658 GADHPTVGIYTKKSGSLPSKRGRRPGAKALSRREDIVDEGGS---GWGD--EENTSR 712
 Qy 109 WALPDEGE-----DKEMKTYRL-----DAGDADPRRLCDLER--- 141
 Db 713 RLHPKQEVFLKTKDPAINDGKAKKRRQLKMKSEKPEENVAEGRAVFSRRRN 772
 Qy 142 -----ERW-----AVIQQAVKSSVTATLQGTDPHGDPRTPGPSPSTLEENVVDRE 189
 Db 773 MANKQINFERWADILAKRGKLPKGTVEPPL-----IKTSPBS----- 812
 Qy 190 QIDFLAARQFLSTEQANKGAPHSSPARGTPAGTTPGASQA PKAKNPKHLANGHVPIKP 249
 Db 813 -----LSLE-VTPFPVAVSPASVQVYTSASESSAD-----VPL-- 847
 Qy 250 QVKGVREENVKRAVPTVASVQVDDPGSLASVESPGTPEKTPIEREIRLAQERADIRE 309
 Db 848 -----LGEENHVLGTSISASWGLHNHNGVILVEBEVT--STPLEEVVDLSEKTEBTS 900
 Qy 310 QRLGRQADHQBELVEIPRPLTLKSLTLA---PRR----- 343
 Db 901 TEGDLKTAAPTLISEPESPFTLHTLDVTEKPHETATEGWSADVSSPEPTSEY 960
 Qy 344 -----NGRPSLYQARDIVQETQREDBHREGLVGRASPFD-WVSEGP----- 385
 Db 961 EPPDAVSLASEBPMQVFPDLETKSDPDEDMKEDTFAHLPTFTIWNDSSTSQLPED 1020
 Qy 386 ----OPG-----LRRALSSDSILSPAP-DA 405
 Db 1021 STIGEPGVPGQSHLQGLTDNIHLVKSLSSTQDTLLIKKMKMSQTLQGGNNLEBDPTHS 1080
 Qy 406 RAADPAPEVRKYNRPDP--AYQPYLSPGTQLEFSAGFAGKPSLSLTAEKATSPKA 463
 Db 1081 RSSEBEGESKSTLPDSTLIGMSMSVKKPAETVTGLDKQTTVTTPROKVAASS 1140
 Qy 464 TMSPRHLSESSGKPLSTKQEASKPRGCPQANRGVMEYFRLRPLRFR----- 512
 Db 1141 TMS-----THPRRRPNGR-----RLRNNKFRHHRKQPTPTTF 1174
 Qy 513 APDEPQQAQVPHVWGEVAGAPALRLQKSQSDLL-----ERRESVLRBQ 559
 Db 1175 APSEFPSTQPTQ-----APDIKISSQVESLVPMTAVDNTVNTPKOLEMKNAEPTS 1226
 Qy 560 EVAERERNAALPEVFSPTPDENSQNSRSSQASGITGSYSVE-----SPFSPILH 613
 Db 1227 KGTPRKKGKRNKRYTP-----STVSSPASGSKSPSPENKRNIVTPSSSTILLP 1279
 Qy 614 SNVAMTVEDPVDSA-----PPGQRKKEQWYAGINPSDGINSEVLEAIRVTRH 660
 Db 1280 RTVSLKTBGPYDSLDMYMTTRKIYSSYPKVQETLVTYTKPISDGEIKDDV--AINVDKH 1337
 Qy 661 KNAMARWES 670
 Db 1338 KSDILVTGES 1347

RESULT 5

US-11-072-175-242
 ; Sequence 242, Application US/11072175
 ; Publication No. US20060029944A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
 ; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
 ; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
 ; FILE REFERENCE: D0273A CIP
 ; CURRENT APPLICATION NUMBER: US/11/072,175

APPLICANT: Fiddie, Carl Johan
 TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
 FILE REFERENCE: LEX-0281-USA
 CURRENT APPLICATION NUMBER: US/11/114,906
 PRIOR FILING DATE: 2005-04-26
 PRIOR APPLICATION NUMBER: US/10/413,437
 PRIOR FILING DATE: 2003-04-11
 PRIOR APPLICATION NUMBER: US/10/020,079
 PRIOR FILING DATE: 2001-12-12
 PRIOR APPLICATION NUMBER: US 60/255,103
 PRIOR FILING DATE: 2000-12-12
 PRIOR APPLICATION NUMBER: US 60/289,422
 PRIOR FILING DATE: 2001-05-08
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 6
 LENGTH: 764
 TYPE: PRT
 ORGANISM: homo sapiens
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1)...(764)
 OTHER INFORMATION: Xaa = Any Amino Acid
 US-11-114-906-6

Query Match 4.2%; Score 149; DB 7; Length 764;
 Best Local Similarity 21.8%; Pred. No. 0.0099;
 Matches 124; Conservative 44; Mismatches 203; Indels 198; Gaps 25;

39 EASG---GDEPQTPDHRAGQGVQGVSYSHATGQSPGHLSENREDEGMQVY 95
 306 EAFDEKAGTDALSTSTSTPPQNTQTAMFGVNT--VPEDLLRENTED----- 357
 96 RIGANDAGGRTWALRPDEDEKEMKTYRLDAGDAPRLCDLREHNAVIGQAVRKS 155
 358 -----VLOEHLSDOE-----NAPP----- 372
 156 STVATLQTPDHG---DPR---PGPRSTPLEENVVREQIDFLAARQFSLDAQNG 209
 373 ----ILPGPSSGLGSPHLVPHPGPGLAEWEETDVNRNKLRIINGKSPCEEBSQSGM 428
 210 APHSSPARGTP-AGTTGASQAPKAFNKH-----LANGHV-----VPIKP----- 249
 429 GVPSSPVAPADSPPTTPVRSILRYRVNSPESERLSTADGRVELPERRSRMDLPGSPSRQA 488
 250 -----QYKGVVREE---NKYRAVP-----TNASVQV 272
 489 CSSQAPQMLSVDTGHADROASGRMDVSASVEQALSNFRSVPFLAEEDFDSKEV---I 545
 273 VD-----DPSGLASV-----ESPQPKETPIEREIRLAQERADLREORGLRQATDH 319
 546 IKTETELKDFPGAGPSTSGTTDEEPEELRPLPEGEERRRRLGAPTVAPRGSMQALAE 605
 320 QELVEIPTPLTKLSLITAPRRERGRPSLYVQORDIVQETQREEDHRRGLHVGASTPD 379
 606 EDLQHLPPQPLPQLS-----QXD-----GRSET-- 629
 380 WSESGPQGLRRLASDSTL--SPAPDARAADPAEVRKVRNIPPDAYQPYLSPGTPOLE 437
 630 --SQPTPG---SPHSPLHSGPRRRRRESDDTPQRLER--DRLSGHSLPRYSPLR 680
 438 FSAFGAFGKPSLSLTAAGAATSPKATWSFRILSSSGKPLSTKQASKPPGCCPOANG 497
 681 RLASSVF-----SSSTLETHYHPHGGGS-----SGSSGLLQSRSAESSPVRAHRRRA 732
 498 VVRWEYFRLRLFRAPDEPQQAQVPHV 526
 733 PLAGNHRILMPSVLRI-----SRSLQLOQVW 757

RESULT 8
 US-11-114-906-4
 ; Sequence 4, Application US/11114906

Publication No. US20050266452A1
 GENERAL INFORMATION:
 APPLICANT: Turner, C. Alexander Jr.
 APPLICANT: Mathur, Brian
 TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
 FILE REFERENCE: LEX-0281-USA
 CURRENT APPLICATION NUMBER: US/11/114,906
 PRIOR FILING DATE: 2005-04-26
 PRIOR APPLICATION NUMBER: US/10/413,437
 PRIOR FILING DATE: 2003-04-11
 PRIOR APPLICATION NUMBER: US/10/020,079
 PRIOR FILING DATE: 2001-12-12
 PRIOR APPLICATION NUMBER: US 60/255,103
 PRIOR FILING DATE: 2000-12-12
 PRIOR APPLICATION NUMBER: US 60/289,422
 PRIOR FILING DATE: 2001-05-08
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 864
 TYPE: PRT
 ORGANISM: homo sapiens
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1)...(864)
 OTHER INFORMATION: Xaa = Any Amino Acid
 US-11-114-906-4

Query Match 4.2%; Score 149; DB 7; Length 864;
 Best Local Similarity 21.8%; Pred. No. 0.012;
 Matches 124; Conservative 44; Mismatches 203; Indels 198; Gaps 25;

39 EASG---GDEPQTPDHRAGQGVQGVSYSHATGQSPGHLSENREDEGMQVY 95
 406 EAFDEKAGTDALSTSTSTPPQNTQTAMFGVNT--VPEDLLRENTED----- 457
 96 RIGANDAGGRTWALRPDEDEKEMKTYRLDAGDAPRLCDLREHNAVIGQAVRKS 155
 458 -----VLOEHLSDOE-----NAPP----- 472
 156 STVATLQTPDHG---DPR---PGPRSTPLEENVVREQIDFLAARQFSLDAQNG 209
 473 ----ILPGPSSGLGSPHLVPHPGPGLAEWEETDVNRNKLRIINGKSPCEEBSQSGM 528
 210 APHSSPARGTP-AGTTGASQAPKAFNKH-----LANGHV-----VPIKP----- 249
 529 GVPSSPVAPADSPPTTPVRSILRYRVNSPESERLSTADGRVELPERRSRMDLPGSPSRQA 588
 250 -----QYKGVVREE---NKYRAVP-----TNASVQV 272
 589 CSSQAPQMLSVDTGHADROASGRMDVSASVEQALSNFRSVPFLAEEDFDSKEV---I 645
 273 VD-----DPSGLASV-----ESPQPKETPIEREIRLAQERADLREORGLRQATDH 319
 646 IKTETELKDFPGAGPSTSGTTDEEPEELRPLPEGEERRRRLGAPTVAPRGSMQALAE 705
 320 QELVEIPTPLTKLSLITAPRRERGRPSLYVQORDIVQETQREEDHRRGLHVGASTPD 379
 706 EDLQHLPPQPLPQLS-----QXD-----GRSET-- 729
 380 WSESGPQGLRRLASDSTL--SPAPDARAADPAEVRKVRNIPPDAYQPYLSPGTPOLE 437
 730 --SQPTPG---SPHSPLHSGPRRRRRESDDTPQRLER--DRLSGHSLPRYSPLR 780
 438 FSAFGAFGKPSLSLTAAGAATSPKATWSFRILSSSGKPLSTKQASKPPGCCPOANG 497
 781 RLASSVF-----SSSTLETHYHPHGGGS-----SGSSGLLQSRSAESSPVRAHRRRA 832
 498 VVRWEYFRLRLFRAPDEPQQAQVPHV 526
 833 PLAGNHRILMPSVLRI-----SRSLQLOQVW 857

```
RESULT 9
US-11-114-906-2
; Sequence 2, Application US/11114906
; Publication No. US20050266452A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Machur, Brian
; APPLICANT: Frittle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinasee and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/11/114,906
; PRIOR FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: US/10/413,437
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 870
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(870)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-114-906-2

Query Match      4.2%; Score 149; DB 7; Length 870;
Best Local Similarity 21.8%; Pred. No. 0.012;
Matches 124; Conservative 44; Mismatches 203; Indels 198; Gaps 25;

Qy 39 BASGM---GDEPOTWPTDRAQOVQGVSVYAVTQGPSRGLSEKREDEGQVY 95
Db 412 BAFDEKATDALLSTSTSTPQOVTROTAMFGVAVNT--PVGGDLIRENTED----- 463
Qy 96 RLAGARDAHQGRPTWALRPEDEDEKEMKTYRLDAGDADPRRLCDLEREMAVIQOAVRKS 155
Db 464 -----VLQGEHLSDGE-----NAP----- 478
Qy 156 STVATLQCTPDHG---DPR---PEPPSTLEENVVDREQIDPLARQOFLSLEQANKG 209
Db 479 ----ILPGRPEBGIGPSPHLVPHPGPEAEVWEETDVNRKLRINTGKSPCVEEESGRGM 534
Qy 210 APHSSPAGTP-AGTTPGASQAQKAFNKP-----LANGHY-----VPIKP----- 249
Db 535 GVSPSPVADAPPDSFTTPVRSILRYRKVNSPSEERLSTADGRVLEPERSRMDLPSPSRQA 594
Qy 250 -----OVKGVVEE--NKVRAVP-----TWASVOV 272
Db 595 CSSQPAQMLSDVTGHDARQASGRMDVSASVGEALSNAFRSVPLAEEEDPDSKEMV---I 651
Qy 273 VD-----DPGLASV-----ESPSTPKETPIREIRLAQOEADLREGRGLRQATDH 319
Db 652 IDKETELKDFPGAEPTSGTTDEDEBELRPLPEEGERRRLGABPTVRPRGRSMQALAE 711
Qy 320 QELVEIPRPLLTKLSTLTAPRRERGRSLVQORDIVQETQREBDHREGLHVGRASTPD 379
Db 712 EDLQHLRPPQLRPPQS-----QXD-----GRSET-- 735
Qy 380 WVESEPPQGLRRALSSDSIL--SPAADARAADPAPEVKVNRIRPDAPQYLSFGTPOLE 437
Db 736 --SQEPTTG---SPSHPLHSGPRRRRSDPTGPOQLBE---DRLSGHSLRPSPLR 786
Qy 438 FSAFGAFKPSGLSTAEAKAATSPKATMSPRHLSSSGKPLSTKQESKAPRGCPQANRG 497
Db 787 RLASAVF---SSSTLETEHYPHPGGGS---SGSSGSLTIQSRSSASSSVRAVPHRHA 838
```

```
Qy 498 VVRWEYFRLRLFRAPDEPOQAQVPHW 526
Db 839 PLAGNHRRLMPSVLRI-----SRQLQGVW 863

RESULT 10
US-11-241-056-14
; Sequence 14, Application US/11241056
; Publication No. US20060024807A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-US
; CURRENT APPLICATION NUMBER: US/11/241,056
; PRIOR FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/09/980,464
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 1360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-241-056-14

Query Match      4.1%; Score 148.5; DB 7; Length 1360;
Best Local Similarity 20.3%; Pred. No. 0.022;
Matches 144; Conservative 87; Mismatches 251; Indels 227; Gaps 33;

Qy 97 LGARDAHQGRPTWALRPEDEDEKEMKTYRLDAGDADPRRLCDLEREMAVIQOAVRKS 156
Db 182 VGRNRFTFGTPV-MAPD-----VLACDENPDATYDKSDLSL-----GIT 222
Qy 157 TVATTLQCTPDHGD-----PRTGP-----PRSTP 180
Db 223 AISMAGAPRLCMHMRBALFLPRNPAPRLSKKSKKQOSFIESGLVKNHSORPATEQ 282
Qy 181 LEEENVQREQIDPLARQOQF-----LSLEQANKGAPHSSPARGTPEG-- 222
Db 283 LMGHPFIRDPNBRQVRIQLKDHIDRTKKRGKEDETEYVSGSEEEBENDSGEPSSIL 342
Qy 223 TTGASQAPRAFKPHLANHVPIKQVGVVR-----EENKVAVVTWASVOV 272
Db 343 NLPGEESTLRDFFRLQLAN-----KERSEALRQOLEQOQRENEEHK-RQLAEROKRI 395
Qy 273 VDDPGSLASVSGPTPEPIREIRLAQER-----EADLREORGIGRQATDHQELV--- 323
Db 396 EEOKEQRRLE-----EQQRREKELKQDEREGRRHYEEOGMRBEERRRAHDEYIRRQ 450
Qy 324 -----EIPTPLLTKLSTLTAPRR--ERGRPSLYQORDIVQET-----QREED 364
Db 451 LEEBQRLITLQOQLLHEQALLLEYKRLQLEBQROERLQROKQERDYLVSLOHCRQEQ 510
Qy 365 -----HRRGLHVGRASTPDWVSEGPQGLRRALSSDSILSPADRAAD----- 409
Db 511 RVEKKELVHYKKGK--SPSEKPAWAKEVE---RSRLNQS--SPMPHKVANRISDPN 563
Qy 410 --PAPEVRKYNRIIPDAVQYLSFGTPOLE-EFSAFGAFGRPSLSLSTA----- 453
Db 564 LPRSEBSFISGQVAPARTPMLRPVDPQIPIHLVAVVSGFALVLAASGVHROPTKGLSGFQ 623
Qy 454 EAAKAATSPKATMSPRHLSE--SSGKPLST-----KQESKAPRGCPQANRGVVR 500
Db 624 EALNVTSRIVEM-PRQNSDPTSENPLPTRIIEKFDRESMWLRQEBDIPPK-VPORRTTSI-- 679
Qy 501 WEYFRLRLFRAPDEPOQAQVPHWQMEVAGAPALRLQSSGSDLLERREESTLREOE 560
Db 680 -----SPALARKNSPENGSLG--PRLSGQPTIRASN-----DQLRRTPEP 716
```

QY 561 VAERERNAALFPEVSP---TPDENSDONSRSSQASGITSYSVSESPFPIHLHVA 617
 Db 717 ILF-----SPLORTSSSSSSSTPSSOPSSQSGOPGSOQASSERTVRAN-S 764
 QY 618 WTVEDPVASAPGCKEOWAGINPSGINSVEALIRVTRKXNAME 666
 Db 765 KSEGSFVLPHPEAKVKEE-----SBDITRPSRPSYKALIDE 802

RESULT 11

US-11-124-368A-305
 ; Sequence 305, Application US/11124368A
 ; Publication No. US20050287559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; APPLICANT: James J. Devlin
 ; APPLICANT: May Luke
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Use Thereof
 ; FILE REFERENCE: CL001524
 ; CURRENT APPLICATION NUMBER: US/11/124,368A
 ; PRIOR FILING DATE: 2005-05-09
 ; PRIOR APPLICATION NUMBER: US 60/568,845
 ; PRIOR FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: US 60/625,936
 ; PRIOR FILING DATE: 2004-11-09
 ; NUMBER OF SEQ ID NOS: 21112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 305
 ; LENGTH: 2801
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-124-368A-305

Query Match 4.1%; Score 148; DB 7; Length 2801;

Best Local Similarity 19.6%; Pred. No. 0.059; Indels 238; Gaps 38;

Matches 142; Conservative 95; Mismatches 251;

QY 44 GODEPQPTDTHRAQGVQROGVSVHAYTCQSPRGHSHNRDEBGMQVYRLGARD-- 101
 Db 527 GONLQOT--QDH-AKAPKSEKKGITKMPQOSLOPBPINTPTTKQOLKASLGKVGKEL 583
 QY 102 -----AHQGRPTALRPDEGDEKEMKTYRLDAGDAPRLCD-----LEBERNAVI-- 147
 Db 584 LAVGKFTRTSGRTTHREBPAGDGKSIRTFK-----ESPQQLDPAARVTKKKMPRTPK 638
 QY 148 -OGQAVKRSYVATLQGTDPHDP-----RTGPPRS--TPIENVVNDREQD 192
 Db 639 EEAQSLIEDLAGFKELFQTPGPSEESMTDEKTKIACKSP--PESVDTPSTQWPKRSIR 697
 QY 193 FLAARQPTLSLEO---ANKGAPHSSPA-----RGTP-----AGTTPGAS---Q 229
 Db 698 KADVEEFLAKKLTPSAGKAMLTTPKPAAGDEKDIKAFMGTVQKLDLAGTLPSSGRQIQ 757
 QY 230 APK-----AFNKPHLANGHVPIKQYGVVREE---NKVRAVPTWASVQVVD 275
 Db 758 TPEKKAQALIEDLAGFKELFQTPGHT-----EELVAAGTKTKIP-----CDS 798
 QY 276 PGSLSVSPGTPKTPIEREIRLQERADLREQGLAQAT-----DHQELV 323
 Db 799 POS-DEVDTPSTQORP-KRSIRKA-DVEGELLACRNLMPSAGKAMHTPKPSVGEKDI 855
 QY 324 EIPTRPLTLKLSL---ITAPRRERGRPSLYVQRDIVQETQORED-----HRRE 368
 Db 856 IPIGTR-VQKLDLNTLTSKRPQTPK-----EEAQALEDLGFKELFQTPGHTHE 906
 QY 369 GLHVGASTPDDVWSEGPQGLRPLALSSDILS---PADPARADPAPEYKVNRIIPDA 424
 Db 907 AVAAGKTKTKMPCESSPPE-----SADPTSTRQPKTPLEKRDVQKEISALKULTQTS 959
 QY 425 YQPYLSPTGPQLEFSAFGAFGKSSLSLTAEAKAATPKATMSPRH--LSSSSGKEL----- 478
 Db 960 GETTHTDVQVGGDKSINAFRE-----TAKQKLDPAASVTSGRHRTKEKQAQPLEDL 1014

QY 479 -----STQOASK-----PPRGCPQANRGV-----VRWEYPLRLP 508
 Db 1015 LKELFQTPVCTDKTTHREKTKIACRSQDPDPTTSSQKSLKRVNDVEEFPALRK 1074
 QY 509 LRFAPDEPQOAVPHWGWGVAGAPALRLQKS-----QSSDLERERESVLRREQ 559
 Db 1075 ---RTPSAGKAMHTP-----KPAVSGEKNIYAMGTFVQKLDLNTLTS--KRL 1120
 QY 560 EVAERERNAAL-----PPEVFP-----SPTDENSDONSRSSSQ 591
 Db 1121 QTPPEKAQALIEDLAGFKELFQTRGHTESMTNDTKAVACRSQPDDEKXNPASSKRRUKT 1180
 QY 592 ASGITG 597
 Db 1181 SLGKVG 1186

RESULT 12

US-11-124-367A-433
 ; Sequence 433, Application US/11124367A
 ; Publication No. US20060024700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hongjin Huang
 ; APPLICANT: Michele Cargill
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; TITLE OF INVENTION: Fibrosis Methods of Detection and Use Thereof
 ; FILE REFERENCE: CL001519.ORD
 ; CURRENT APPLICATION NUMBER: US/11/124,367A
 ; PRIOR FILING DATE: 2005-05-09
 ; PRIOR APPLICATION NUMBER: US 60/568,846
 ; PRIOR FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: US 60/582,609
 ; PRIOR FILING DATE: 2004-06-25
 ; PRIOR APPLICATION NUMBER: US 60/599,554
 ; PRIOR FILING DATE: 2004-08-09
 ; NUMBER OF SEQ ID NOS: 34460
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 433
 ; LENGTH: 2801
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-124-367A-433

Query Match 4.1%; Score 148; DB 7; Length 2801;

Best Local Similarity 19.6%; Pred. No. 0.059; Indels 238; Gaps 38;

Matches 142; Conservative 95; Mismatches 251;

QY 44 GODEPQPTDTHRAQGVQROGVSVHAYTCQSPRGHSHNRDEBGMQVYRLGARD-- 101
 Db 527 GONLQOT--QDH-AKAPKSEKKGITKMPQOSLOPBPINTPTTKQOLKASLGKVGKEL 583
 QY 102 -----AHQGRPTALRPDEGDEKEMKTYRLDAGDAPRLCD-----LEBERNAVI-- 147
 Db 584 LAVGKFTRTSGRTTHREBPAGDGKSIRTFK-----ESPQQLDPAARVTKKKMPRTPK 638
 QY 148 -OGQAVKRSYVATLQGTDPHDP-----RTGPPRS--TPIENVVNDREQD 192
 Db 639 EEAQSLIEDLAGFKELFQTPGPSEESMTDEKTKIACKSP--PESVDTPSTQWPKRSIR 697
 QY 193 FLAARQPTLSLEO---ANKGAPHSSPA-----RGTP-----AGTTPGAS---Q 229
 Db 698 KADVEEFLAKKLTPSAGKAMLTTPKPAAGDEKDIKAFMGTVQKLDLAGTLPSSGRQIQ 757
 QY 230 APK-----AFNKPHLANGHVPIKQYGVVREE---NKVRAVPTWASVQVVD 275
 Db 758 TPEKKAQALIEDLAGFKELFQTPGHT-----EELVAAGTKTKIP-----CDS 798
 QY 276 PGSLSVSPGTPKTPIEREIRLQERADLREQGLAQAT-----DHQELV 323
 Db 799 POS-DEVDTPSTQORP-KRSIRKA-DVEGELLACRNLMPSAGKAMHTPKPSVGEKDI 855
 QY 324 EIPTRPLTLKLSL---ITAPRRERGRPSLYVQRDIVQETQORED-----HRRE 368

```

Db      856 IFVGTG-VQKLDLTENLTGSKRRPQTPK-----BEAQLEBDLTGFKELFQTPGHTEE 906
Qy      369 GLHVGRASTPDWSEGPQGLRRLSSDSILS-----PAPDARAADPAEYRKVNRIPDDA 424
Db      907 AVAAGKTTKMPCESSPPE-----SADTPTSTRQPTPLEKRDVQKEKLSALKKLTQTS 959
Qy      425 YQPLSGTTPQLEFSAFGAFGKPSLSLTAEKAATSPKATWSPRH--LSBSGKPL----- 478
Db      960 GETTHDVKVPGEGSKINAFRE-----TAKQKLDPAASVYGSKRHPKTKKQAQPLDLAAG 1014
Qy      479 -----STKQASK-----PRGCPQANRGV-----VRWEYFLRLP 508
Db      1015 LKELFQTPVCTDKPTTHEKTKTKIACRSQDPDPTPTSSKPSKSLRKVDVEEFPALRK 1074
Qy      509 LRFAPDEPQOAVPHVWGMEVAGAPALRLQKS-----QSDLLERERESVLRREQ 559
Db      1075 ---RTPSAGKAMHTP-----KPAVSGEKNIYAFMGTPVQKLDLTENLTGS--KRRL 1120
Qy      560 EVABERRNAL-----PPEVF-----SPTPDENSQNSRSSQ 591
Db      1121 QTPKEKAQLEBDLAGFKELFQTRGHTESMTNDKTAACKSSQPPDDKNPASKRLKLT 1180
Qy      592 ASGITG 597
Db      1181 SLGKVG 1186

```

```

RESULT 13
US-11-124-368A-306
; Sequence 306, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: C0001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 306
; LENGTH: 2896
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-306

```

```

Query Match      4.1%, Score 148; DB 7; Length 2896;
Best Local Similarity 19.6%; Pred. No. 0.061;
Matches 142; Conservative 95; Mismatches 251; Indels 238; Gaps 38;

```

```

Qy      44 GQDEPQWPTTHRAQGVQROGVSYVHAATGQPSRGLSENREDEGMOVYRLGAD-- 101
Db      622 GQNLQGT--QDH-AKAPKSEKGIITKMPQCSLOPEINTPTTHKQQLKASLGKGVXEL 678
Qy      102 -----AHQGRPTMALRPDEGDEKEMKTYRLDAGDAPRLCD-----LERERAVI-- 147
Db      679 LAVGKPTRTSGEHTHREBPAGDGSITFK-----ESPKILDPAAAVTMKMPRTPK 733
Qy      148 -QCGAVRKSSTVATLQGTDPDHDGDP-----RTGPPRS--TPLEENVVDRQID 192
Db      734 BEAGSLIEDIAGFKELFQTPGSEBSMTDEKTKIACKSP--PPESVDPPTSTKQWPKSLR 792
Qy      193 FLARQQTLSLSEQ-----ANKAPHSSPA-----KGTTP-----AGTTPAS--Q 229
Db      793 KADVEEFLARLKLTPSAGKMLTPKPAQDEKDIKAFMGTPVQKLDLAGTLPSKQLOQ 852

```

```

Qy      230 APR-----AFNKPILANGHVVPKIQVKNVREE-----NKRAVPTMASVOVVD 275
Db      853 TPKEKAQLEBDLAGFKELFQTPGHT-----BEIYVAGKTTKLP-----CDS 893
Qy      276 PGSLAVESPGTKEPIERITRLAERADLREQGLAQAT-----DHQELV 323
Db      894 PQS-DEVDPTSTRQRP-KRSIRKA-DVEGELLACNLMPSAGKAMHTPKPSVGEKDI 950
Qy      324 EITPRLTLTSL-----ITAPRRERGRPSLYVQDVIQETQREED-----HRR 368
Db      951 IFVGTG-VQKLDLTENLTGSKRRPQTPK-----BEAQLEBDLTGFKELFQTPGHTEE 1001
Qy      369 GLHVGRASTPDWSEGPQGLRRLSSDSILS-----PAPDARAADPAEYRKVNRIPDDA 424
Db      1002 AVAAGKTTKMPCESSPPE-----SADTPTSTRQPTPLEKRDVQKEKLSALKKLTQTS 1054
Qy      425 YQPLSGTTPQLEFSAFGAFGKPSLSLTAEKAATSPKATWSPRH--LSBSGKPL----- 478
Db      1055 GETTHDVKVPGEGSKINAFRE-----TAKQKLDPAASVYGSKRHPKTKKQAQPLDLAAG 1109
Qy      479 -----STKQASK-----PRGCPQANRGV-----VRWEYFLRLP 508
Db      1110 LKELFQTPVCTDKPTTHEKTKTKIACRSQDPDPTPTSSKPSKSLRKVDVEEFPALRK 1169
Qy      509 LRFAPDEPQOAVPHVWGMEVAGAPALRLQKS-----QSDLLERERESVLRREQ 559
Db      1170 ---RTPSAGKAMHTP-----KPAVSGEKNIYAFMGTPVQKLDLTENLTGS--KRRL 1215
Qy      560 EVABERRNAL-----PPEVF-----SPTPDENSQNSRSSQ 591
Db      1216 QTPKEKAQLEBDLAGFKELFQTRGHTESMTNDKTAACKSSQPPDDKNPASKRLKLT 1275
Qy      592 ASGITG 597
Db      1276 SLGKVG 1281

```

```

RESULT 14
US-11-124-367A-434
; Sequence 434, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: C0001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 434
; LENGTH: 2896
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-434

```

```

Query Match      4.1%, Score 148; DB 7; Length 2896;
Best Local Similarity 19.6%; Pred. No. 0.061;
Matches 142; Conservative 95; Mismatches 251; Indels 238; Gaps 38;

```

```

Qy      44 GQDEPQWPTTHRAQGVQROGVSYVHAATGQPSRGLSENREDEGMOVYRLGAD-- 101
Db      622 GQNLQGT--QDH-AKAPKSEKGIITKMPQCSLOPEINTPTTHKQQLKASLGKGVXEL 678
Qy      102 -----AHQGRPTMALRPDEGDEKEMKTYRLDAGDAPRLCD-----LERERAVI-- 147

```

```

Db 679 LAVGKFTRTSGTTHHEBPADGKSINTFK-----ESPQILDPAARVGMKKMPRPK 733
Qy 148 -OGQAVRKSTVATLQGTDPDHGP-----RTPGPPRS--TLEENVVDREQID 192
Db 724 EBAQSLBDAAGFKELFOTPGSEESMTDEKTKIACKSP--PPESVDPTSTKQMPKRSIR 792
Qy 193 FLAAQOFLSLSEQ-----ANKAPHSSPA-----RGRP-----AGTTPGAS---Q 229
Db 793 KADVEEELALRKLTPPSAGKAMLTPEKPGDGDEKDIKAFMGTPVQKLDLAGTLPGSKROLQ 852
Qy 230 APK-----AFNKHPLANGHVPIKPVKGVVREE---NKVRAVPTWASVQVVD 275
Db 833 TPKEKAQALBDAAGFKELFOTPGHT-----BELVAGKTTKIP-----CDS 893
Qy 276 PGSLASVSPGTPKETPIEREIRLAQERADLREGRLQAT-----DHQELV 323
Db 894 PQS-DPVDTPSTKQRP--KRSIRKA--DVEGELLACRNIMPAGKAMHTPKPSVGEKDI 950
Qy 324 EIPTRPLTLKSL---ITAPRERGRPSLYVORDIVQETOREED-----HRE 368
Db 951 IFVGTTP-VQKLDLTENLTGSKRRPQTPK-----EBAQLEDLTGFEKELFOTPGHTEE 1001
Qy 369 GLHVRASPTDPMVSSGPGQGLRRLSSDSILS---PAPDARAADPAPEVRKVNIPDA 424
Db 1002 AVAAGKTTKMPCESSPP-----SADTPTSTRQOPTPEKRDVQKELSLAKLTOTS 1054
Qy 425 YOPVLSPTGPOLFSAFGAFGKPSLSSTAACAATSPKATMSPRH--LSSESGKPL----- 478
Db 1055 GETHTDVKPGGEDSKSINAFRE---TAKQKLDPAASVTGSKRHPKTEKAQPLEDLAG 1109
Qy 479 -----STQOASK-----PPRCGPQANRGV---VMEYFRLRP 508
Db 1110 LKELFQTPVCTDKPTTHEKTKIACRSQDPVDPTPTSSKPSKRSIRKVDVEEELALRK 1169
Qy 508 LAFRAPDEPQOAVPHVWGMVAGAPALALOKS-----QSSDLEREESVLRREQ 559
Db 1170 ---RTPSAGKAMHTP-----KPAVSGEKNIYAFMGTPVQKLDLTENLTGS--KRL 1215
Qy 560 EVAERBNAL-----PPEVF-----SPTPENSQNSRSSQ 591
Db 1216 QTPKEKAQALBDAAGFKELFOTRGHTESMTNDKTAQVACKSQSDPDKNPASSKRLKT 1275
Qy 592 ASGITG 597
Db 1276 SLGXVG 1281

RESULT 15
US-11-124-368A-304
Sequence 304, Application US/11124368A
Publication No. US20050287559A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: James J. Devlin
TITLE OF INVENTION: Genetic Polymorphisms Associated with
FILE REFERENCE: C1001524
CURRENT APPLICATION NUMBER: US/11/124,368A
PRIOR FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 304
LENGTH: 3256
TYPE: PRT
ORGANISM: Homo sapiens
US-11-124-368A-304
Query Match 4.1%; Score 148; DB 7; Length 3256;

```

```

Best Local Similarity 19.6%; Pred. No. 0.071;
Matches 142; Conservative 95; Mismatches 251; Indels 238; Gaps 38;
Qy 44 GODEPQTPWDHRAQGVQVQGVSYHAATYGQSPGSLHSENRDEGMQVYRLGARD-- 101
Db 982 GQNLQGT--QDH-AKAPKSEKGIITKMPCCSLQPEPINTPHTQQLKASIGKGVKEL 1038
Qy 102 -----AHQGRPTWALRPEDGEDKEMKTYLDAGDDAPRLCD-----LBERAVI-- 147
Db 1039 LAVGKFTRTSGTTHHEBPADGKSINTFK-----ESPQILDPAARVGMKKMPRPK 1093
Qy 148 -OGQAVRKSTVATLQGTDPDHGP-----RTPGPPRS--TLEENVVDREQID 192
Db 1094 EBAQSLBDAAGFKELFOTPGSEESMTDEKTKIACKSP--PPESVDPTSTKQMPKRSIR 1152
Qy 193 FLAAQOFLSLSEQ-----ANKAPHSSPA-----RGRP-----AGTTPGAS---Q 229
Db 1153 KADVEEELALRKLTPPSAGKAMLTPEKPGDGDEKDIKAFMGTPVQKLDLAGTLPGSKROLQ 1212
Qy 230 APK-----AFNKHPLANGHVPIKPVKGVVREE---NKVRAVPTWASVQVVD 275
Db 1213 TPKEKAQALBDAAGFKELFOTPGHT-----BELVAGKTTKIP-----CDS 1253
Qy 276 PGSLASVSPGTPKETPIEREIRLAQERADLREGRLQAT-----DHQELV 323
Db 1254 PQS-DPVDTPSTKQRP--KRSIRKA--DVEGELLACRNIMPAGKAMHTPKPSVGEKDI 1310
Qy 324 EIPTRPLTLKSL---ITAPRERGRPSLYVORDIVQETOREED-----HRE 368
Db 1311 IFVGTTP-VQKLDLTENLTGSKRRPQTPK-----EBAQLEDLTGFEKELFOTPGHTEE 1361
Qy 369 GLHVRASPTDPMVSSGPGQGLRRLSSDSILS---PAPDARAADPAPEVRKVNIPDA 424
Db 1362 AVAAGKTTKMPCESSPP-----SADTPTSTRQOPTPEKRDVQKELSLAKLTOTS 1414
Qy 425 YOPVLSPTGPOLFSAFGAFGKPSLSSTAACAATSPKATMSPRH--LSSESGKPL----- 478
Db 1415 GETHTDVKPGGEDSKSINAFRE---TAKQKLDPAASVTGSKRHPKTEKAQPLEDLAG 1469
Qy 479 -----STQOASK-----PPRCGPQANRGV---VMEYFRLRP 508
Db 1470 LKELFQTPVCTDKPTTHEKTKIACRSQDPVDPTPTSSKPSKRSIRKVDVEEELALRK 1529
Qy 508 LAFRAPDEPQOAVPHVWGMVAGAPALALOKS-----QSSDLEREESVLRREQ 559
Db 1530 ---RTPSAGKAMHTP-----KPAVSGEKNIYAFMGTPVQKLDLTENLTGS--KRL 1575
Qy 560 EVAERBNAL-----PPEVF-----SPTPENSQNSRSSQ 591
Db 1576 QTPKEKAQALBDAAGFKELFOTRGHTESMTNDKTAQVACKSQSDPDKNPASSKRLKT 1635
Qy 592 ASGITG 597
Db 1636 SLGXVG 1641

Search completed: March 3, 2006, 14:19:02
Job time : 36.3333 secs

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GenCore version 5.1.7
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OW protein - protein search, using sw model

Run on: March 3, 2006, 14:18:31 ; Search time 245.321 Seconds
(without alignments)
1216.113 Million cell updates/sec

Title: US-10-646-873-42

Perfect score: 679
Sequence: 1 MDRVTRYPILGIPQAHRCGTG.....HKMAAEKRESRIYASEDD 679

Scoring: Gapped 60.0, Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 20
Total number of hits satisfying chosen parameters: 31

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

- Database: A_Geneseq_21.*
- 1: geneseqp1980a:*
 - 2: geneseqp1990a:*
 - 3: geneseqp2000a:*
 - 4: geneseqp2001a:*
 - 5: geneseqp2002a:*
 - 6: geneseqp2003a:*
 - 7: geneseqp2003b:*
 - 8: geneseqp2004a:*
 - 9: geneseqp2005a:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	679	100.0	679	2	AAW79676 Human CS1
2	679	100.0	679	4	AAE07319 Human CS
3	679	100.0	679	6	ADA26379 Predicted
4	679	100.0	679	8	ADN17172 CS198 pro
5	679	100.0	679	8	ADX97562 Pancreat
6	625	92.0	672	4	AAW79574 Human pro
7	580	85.4	679	4	AAW78590 Human NC2
8	264	38.9	679	7	ADG14341 Human
9	215	31.7	215	2	AAW79681 Human CS1
10	215	31.7	215	4	AAE07324 Human CS
11	215	31.7	215	6	ADA26384 Synthetic
12	215	31.7	215	8	ADN17177 CS198 pro
13	60	8.8	172	4	AAW73987 Human col
14	43	6.3	43	8	ABO60042 Human gen
15	38	5.6	57	4	AAW75071 Human col
16	36	5.3	36	2	AAW79677 Synthetic
17	36	5.3	36	4	AAE07320 Human CS
18	36	5.3	36	6	ADA26380 Synthetic
19	36	5.3	36	8	ADN17173 CS198 pep
20	35	5.2	35	2	AAW79679 Synthetic
21	35	5.2	35	4	AAE07322 Human CS
22	35	5.2	35	6	ADA26382 Synthetic
23	35	5.2	35	8	ADN17175 CS198 pep
24	31	4.6	31	2	AAW79678 Synthetic

25	31	4.6	31	4	AAE07321 Human CS
26	31	4.6	31	6	ADA26381 Synthetic
27	31	4.6	31	8	ADN17174 CS198 pep
28	30	4.4	30	2	AAW79680 Synthetic
29	30	4.4	30	4	AAE07323 Human CS
30	30	4.4	30	6	ADA26383 Synthetic
31	30	4.4	30	8	ADN17176 CS198 pep

ALIGNMENTS

RESULT 1
AAW79676 standard; protein; 679 AA.
AAW79676;
11-JAN-1999 (first entry)
Human CS198 protein.
Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
pancreatitis.
Homo sapiens.
WO9844159-A1.
08-OCT-1998.
30-MAR-1998; 98WO-US006251.
PR 31-MAR-1997; 97US-00828855.
(ABBO) ABBOTT LAB.
Billing-Medel PA, Cohen M, Colpitta TL, Friedman EN, Gordon J;
Granados EN, Hayden M, Hodges SC, Klaes MR, Kratochvil JD;
Roberts-Rapp L, Russell JC, Stroupe SD;
WPI; 1998-542714/46.
New gastrointestinal polynucleotides, CS198, and their detection - used
for developing products for the diagnosis and treatment of
gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
Claim 26; Page 100-102; 127pp; English.
This sequence represents the human CS198 protein which is used in a
method to detect the presence of a target CS198 polynucleotide in a test
sample. The CS198 gene is useful as a marker for gastrointestinal (GI)
tract disorders. The methods and products can be used in detecting,
diagnosing, staging, monitoring, prognosticating, preventing or treating,
or determining the predisposition to diseases and conditions of the GI
tract, such as GI tract cancer, Barrett's oesophagus, gastric ulcer,
gastritis, leiomyoma, polyps, Crohn's disease, ulcerative colitis, and
pancreatitis
Sequence 679 AA;
Query Match 100.0%; Score 679; DB 2; Length 679;
Best local Similarity 100.0%; Pred. No. 0;
Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDRVTRYPILGIPQAHRCGTGLDGTSTYTHLVCMGPASGWDPEPTWTDHRAOOG 60
DB 1 MDRVTRYPILGIPQAHRCGTGLDGTSTYTHLVCMGPASGWDPEPTWTDHRAOOG 60
QY 61 VORQGVSVHAYTGQSPRGLHSENRDEGMYVRLGARDHOSPTALRPDCEGDE 120


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Db      61  VOROGVSVAHYATGQSPRGLSHSENREDEGMQVYRLGARDADHOGRPTMALRPEDEGKE 120
Qy      121  MKTYRLDAGDADPRRLCDLERERNAVIOGQAVRKSSTVATIGTPDHGDPTPGPPSTP 180
Db      121  MKTYRLDAGDADPRRLCDLERERNAVIOGQAVRKSSTVATIGTPDHGDPTPGPPSTP 180
Qy      181  LEENVVDREQIDFLAARQOFLSLERQANKGAPHSPPARGTTPGASQAPKANKPHLA 240
Db      181  LEENVVDREQIDFLAARQOFLSLERQANKGAPHSPPARGTTPGASQAPKANKPHLA 240
Qy      241  NGHVVPPIKPOVKGVREENKRAVPTWASVOVDDPGSLASVSPGPKETPIREIRLA 300
Db      241  NGHVVPPIKPOVKGVREENKRAVPTWASVOVDDPGSLASVSPGPKETPIREIRLA 300
Qy      301  QERADLREQRLQATDHOELVEIPTRPLTKSLITAPRRERGRPSLYVQBDIVQETQ 360
Db      301  QERADLREQRLQATDHOELVEIPTRPLTKSLITAPRRERGRPSLYVQBDIVQETQ 360
Qy      361  REEDHRRREGLVHGRASPTPDWVSEGPQGLRRALSSDSITLSPAPDARAADPAPEVRKYNRI 420
Db      361  REEDHRRREGLVHGRASPTPDWVSEGPQGLRRALSSDSITLSPAPDARAADPAPEVRKYNRI 420
Qy      421  PPDAVQPYLSPTQPLEFSAFGAFGKPSLSLTAEKAAATSPKATWSPRHLSSESGKPLST 480
Db      421  PPDAVQPYLSPTQPLEFSAFGAFGKPSLSLTAEKAAATSPKATWSPRHLSSESGKPLST 480
Qy      481  KOEASKEPRGCPQANRGVNRWEYFRLRPLRRADEPOQAVPYWGVMEVAGALRLQK 540
Db      481  KOEASKEPRGCPQANRGVNRWEYFRLRPLRRADEPOQAVPYWGVMEVAGALRLQK 540
Qy      541  SOSDDLREERESVLRERQEAERERNALFPEVSPTEPDENSDQNSRSSQASGITGSYS 600
Db      541  SOSDDLREERESVLRERQEAERERNALFPEVSPTEPDENSDQNSRSSQASGITGSYS 600
Qy      601  VSESPFPEPIHLHSNVAVTVEDPVDSAPPGQKKEQWYAGINPSDGINSEVLAIKRYTRH 660
Db      601  VSESPFPEPIHLHSNVAVTVEDPVDSAPPGQKKEQWYAGINPSDGINSEVLAIKRYTRH 660
Qy      661  KNAMAEWESRIRYASEED 679
Db      661  KNAMAEWESRIRYASEED 679

RESULT 2
AAE07319 standard; protein; 679 AA.
ID      AAE07319
AC      AAE07319;
XX      AAE07319;
XX      06-NOV-2001 (first entry)
DT      06-NOV-2001 (first entry)
XX      Human CS 198 protein.
DE      Human CS 198 protein.
XX      CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
KW      gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
KW      Barrett's oesophagus; gene therapy; drug screening; human.
XX      Homo sapiens.
OS      Homo sapiens.
XX      Key Location/Qualifiers
FH      Misc-difference 353
FT      /note= "Encoded by CGGN"
XX      US2001010904-A1.
XX      02-AUG-2001.
XX      30-MAR-1998; 98US-00050516.
XX      31-MAR-1997; 97US-00028855.
XX      (BILL/) BILLINGEL P A.
XX      (COHE/) COHEN M.

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PA      (COLP/) COLPITTS T L.
PA      (FRIE/) FRIEDMAN P N.
PA      (GORD/) GORDON J.
PA      (GRAN/) GRANADOS E N.
PA      (HAYD/) HAYDEN M.
PA      (HODG/) HODGES S C.
PA      (KLAS/) KLAS M R.
PA      (KRAT/) KRATOCHVIL J D.
PA      (ROBE/) ROBERTS-RAPP L.
PA      (RUSSE/) RUSSELL J C.
PA      (STRO/) STROUPE S D.
XX      Billingel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI      Granados EN, Hayden M, Hodges SC, Kلاس MR, Kratochvil JD;
PI      Roberts-Rapp L, Russell JC, Stroupe SD;
XX      WPI; 2001:496163/54.
DR      N-PSDB; AAD13637.
XX      Claim 17; Page 49-51; 68pp; English.
XX      The invention relates to a method of detecting the presence of a target
CC      CS 198 polynucleotide comprising contacting the test sample with at least
CC      one CS 198-specific polynucleotide. The method is useful for detecting
CC      diseases of the gastrointestinal (GI) tract organs, particularly cancer.
CC      The CS 198 polynucleotides, polypeptides and antibodies are useful for
CC      detecting, diagnosing, staging, monitoring, prognosticating, preventing,
CC      treating or determining predisposition to diseases and conditions of the
CC      GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
CC      ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
CC      polypeptides are useful as standards or reagents in diagnostic
CC      immunoassays, as components or as target sites for various therapies.
CC      Antibodies directed against at least one epitope contained within these
CC      polypeptides are useful as delivery agents for therapeutic agents. In
CC      diagnostic tests and for screening for conditions or diseases associated
CC      with CS 198, particularly cancer. Monoclonal antibodies may also be used
CC      for the generation of chimeric antibodies for therapeutic use. The CS 198
CC      polynucleotide is also useful in gene therapy and drug screening. The
CC      method of the invention provides an alternative, non-surgical diagnostic
CC      method capable of detecting early stage GI tract disease such as cancer.
CC      The present sequence is human CS 198 polypeptide
XX      Sequence 679 AA:
SQ      Query Match 100.0%; Score 679; DB 4; Length 679;
          Best Local Similarity 100.0%; Pred. No. 0;
          Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1  MDRVTRPIIGIPQAHRTGLVLDGTSYTHLVCKGPEASGNGDEPQTWPTDHRAQOG 60
Db      1  MDRVTRPIIGIPQAHRTGLVLDGTSYTHLVCKGPEASGNGDEPQTWPTDHRAQOG 60
Qy      61  VOROGVSVAHYATGQSPRGLSHSENREDEGMQVYRLGARDADHOGRPTMALRPEDEGKE 120
Db      61  VOROGVSVAHYATGQSPRGLSHSENREDEGMQVYRLGARDADHOGRPTMALRPEDEGKE 120
Qy      121  MKTYRLDAGDADPRRLCDLERERNAVIOGQAVRKSSTVATIGTPDHGDPTPGPPSTP 180
Db      121  MKTYRLDAGDADPRRLCDLERERNAVIOGQAVRKSSTVATIGTPDHGDPTPGPPSTP 180
Qy      181  LEENVVDREQIDFLAARQOFLSLERQANKGAPHSPPARGTTPGASQAPKANKPHLA 240
Db      181  LEENVVDREQIDFLAARQOFLSLERQANKGAPHSPPARGTTPGASQAPKANKPHLA 240
Qy      241  NGHVVPPIKPOVKGVREENKRAVPTWASVOVDDPGSLASVSPGPKETPIREIRLA 300
Db      241  NGHVVPPIKPOVKGVREENKRAVPTWASVOVDDPGSLASVSPGPKETPIREIRLA 300
Qy      301  QERADLREQRLQATDHOELVEIPTRPLTKSLITAPRRERGRPSLYVQBDIVQETQ 360

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DB 301 OERADLRQRLRQATDHQELVEIPTRLTKLSLITAPRERGRPSLYVORDIVOETQ 360
QY 361 REEDHRRREGIAVGRASTPDWVSEGPQGLRRALSSDSILSPADARAADPAPEVRKVNRI 420
DB 361 REEDHRRREGIAVGRASTPDWVSEGPQGLRRALSSDSILSPADARAADPAPEVRKVNRI 420
QY 421 PPDAYQPYLSPTPTOLEFSAFGAFGKPSLSLTAEKAAATSPKATMSPRILSSSGKPLST 480
DB 421 PPDAYQPYLSPTPTOLEFSAFGAFGKPSLSLTAEKAAATSPKATMSPRILSSSGKPLST 480
QY 481 KOEAKPRPGGCPQANRGVVRWMEYFRLRPLRFRAPDEPOQAVPHVGMGEVAGAPALRLQK 540
DB 481 KOEAKPRPGGCPQANRGVVRWMEYFRLRPLRFRAPDEPOQAVPHVGMGEVAGAPALRLQK 540
QY 541 SOSDLLERRERSVLRREQVVAERNNALFPEVFSPTPDENSQNSRSSQASGITGSYS 600
DB 541 SOSDLLERRERSVLRREQVVAERNNALFPEVFSPTPDENSQNSRSSQASGITGSYS 600
QY 601 VSESPPFSPIHLHSNVAMTWEDPVDSPAPGQKKEQWAGINPSDGINSEVLEAIRVTRH 660
DB 601 VSESPPFSPIHLHSNVAMTWEDPVDSPAPGQKKEQWAGINPSDGINSEVLEAIRVTRH 660
QY 661 KNAMAEWRMSRIYASEDD 679
DB 661 KNAMAEWRMSRIYASEDD 679

RESULT 3
ID ADA26379 standard; protein; 679 AA.
AC ADA26379;
XX
DT 20-NOV-2003 (first entry)
XX
DE Predicted amino acid sequence of the CS198 protein.
XX
KM CS198; cancer diagnosis; cancer staging; cancer monitoring;
KM cancer prognosticating; cancer prevention; cancer;
KM gastrointestinal tract disorder; gene therapy.
XX
OS Synthetic;
XX
PN US2003082619-A1.
XX
PD 01-MAY-2003.
XX
PF 23-OCT-2002; 2002US-00278547.
XX
PR 31-MAR-1997; 97US-00828855-
PR 30-MAR-1998; 98US-00050516.
XX
PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORO/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M A.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUSSE/) RUSSELL J C.
PA (STROU/) STROUPE S D.
XX
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 2003-596961/56.
XX
```

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PT Detecting the presence of a target CS198 polynucleotide in a test sample
PT comprises contacting the sample with a CS198 specific polynucleotide and
PT detecting the presence of the target CS198 polynucleotide in the test
PT sample.
XX
PS Claim 17; Page 49-50; 67pp; English.
XX
CC The invention describes a method of detecting the presence of a target
CC CS198 polynucleotide in a test sample. The method comprises contacting
CC the test sample with at least one CS198 specific polynucleotide or its
CC complement, and detecting the presence of the target CS198 polynucleotide
CC in the test sample, where the CS198-specific polynucleotide has at least
CC 50% identity to a polynucleotide having any of the 27 fully defined
CC sequences of 34-2894 bp (51-27) given in the specification, or their
CC fragments or complements. The composition and methods are useful in
CC diagnosis, staging, monitoring, prognosticating, preventing or treating,
CC or determining the predisposition of an individual to, diseases and
CC conditions of the gastrointestinal tract, e.g. cancer and in gene
CC therapy. This is the predicted amino acid sequence of the human CS198
CC protein derived from the CS198 consensus sequence shown in seq id 27.
XX
SQ Sequence 679 AA;
XX
Query Match 100.0%; Score 679; DB 6; Length 679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDRVTRYPILGIPOAHRTGTLVDGTSYTHLVCMGPBAGWGQDEPQWPTDRAQOG 60
DB 1 MDRVTRYPILGIPOAHRTGTLVDGTSYTHLVCMGPBAGWGQDEPQWPTDRAQOG 60
QY 61 VORQGVSYVAHYTCQSPRGHSENREDEGQVYRLGARDAHQGRPTMALRPEDEGKE 120
DB 61 VORQGVSYVAHYTCQSPRGHSENREDEGQVYRLGARDAHQGRPTMALRPEDEGKE 120
QY 61 VORQGVSYVAHYTCQSPRGHSENREDEGQVYRLGARDAHQGRPTMALRPEDEGKE 120
DB 61 VORQGVSYVAHYTCQSPRGHSENREDEGQVYRLGARDAHQGRPTMALRPEDEGKE 120
QY 121 MKTYRLDAGDADPRRLCDLERRERNAVIOGAVRKSTVATLQGTDPDHGDPRTGPBRSTP 180
DB 121 MKTYRLDAGDADPRRLCDLERRERNAVIOGAVRKSTVATLQGTDPDHGDPRTGPBRSTP 180
QY 121 MKTYRLDAGDADPRRLCDLERRERNAVIOGAVRKSTVATLQGTDPDHGDPRTGPBRSTP 180
DB 121 MKTYRLDAGDADPRRLCDLERRERNAVIOGAVRKSTVATLQGTDPDHGDPRTGPBRSTP 180
QY 181 ILENVVDREQIDFLAARQOFLSLBOANKGAPHSSPARGTACTTGASQAPAFKPHIA 240
DB 181 ILENVVDREQIDFLAARQOFLSLBOANKGAPHSSPARGTACTTGASQAPAFKPHIA 240
QY 181 ILENVVDREQIDFLAARQOFLSLBOANKGAPHSSPARGTACTTGASQAPAFKPHIA 240
DB 181 ILENVVDREQIDFLAARQOFLSLBOANKGAPHSSPARGTACTTGASQAPAFKPHIA 240
QY 241 NGHVVPPIKQVGVVREENKRAVPTWASVOVVDPGSLASVESGTPKEPTIEREIRLA 300
DB 241 NGHVVPPIKQVGVVREENKRAVPTWASVOVVDPGSLASVESGTPKEPTIEREIRLA 300
QY 241 NGHVVPPIKQVGVVREENKRAVPTWASVOVVDPGSLASVESGTPKEPTIEREIRLA 300
DB 241 NGHVVPPIKQVGVVREENKRAVPTWASVOVVDPGSLASVESGTPKEPTIEREIRLA 300
QY 301 OERADLRQRLRQATDHQELVEIPTRLTKLSLITAPRERGRPSLYVORDIVOETQ 360
DB 301 OERADLRQRLRQATDHQELVEIPTRLTKLSLITAPRERGRPSLYVORDIVOETQ 360
QY 301 OERADLRQRLRQATDHQELVEIPTRLTKLSLITAPRERGRPSLYVORDIVOETQ 360
DB 301 OERADLRQRLRQATDHQELVEIPTRLTKLSLITAPRERGRPSLYVORDIVOETQ 360
QY 361 REEDHRRREGIAVGRASTPDWVSEGPQGLRRALSSDSILSPADARAADPAPEVRKVNRI 420
DB 361 REEDHRRREGIAVGRASTPDWVSEGPQGLRRALSSDSILSPADARAADPAPEVRKVNRI 420
QY 361 REEDHRRREGIAVGRASTPDWVSEGPQGLRRALSSDSILSPADARAADPAPEVRKVNRI 420
DB 361 REEDHRRREGIAVGRASTPDWVSEGPQGLRRALSSDSILSPADARAADPAPEVRKVNRI 420
QY 421 PPDAYQPYLSPTPTOLEFSAFGAFGKPSLSLTAEKAAATSPKATMSPRILSSSGKPLST 480
DB 421 PPDAYQPYLSPTPTOLEFSAFGAFGKPSLSLTAEKAAATSPKATMSPRILSSSGKPLST 480
QY 421 PPDAYQPYLSPTPTOLEFSAFGAFGKPSLSLTAEKAAATSPKATMSPRILSSSGKPLST 480
DB 421 PPDAYQPYLSPTPTOLEFSAFGAFGKPSLSLTAEKAAATSPKATMSPRILSSSGKPLST 480
QY 481 KOEAKPRPGGCPQANRGVVRWMEYFRLRPLRFRAPDEPOQAVPHVGMGEVAGAPALRLQK 540
DB 481 KOEAKPRPGGCPQANRGVVRWMEYFRLRPLRFRAPDEPOQAVPHVGMGEVAGAPALRLQK 540
QY 481 KOEAKPRPGGCPQANRGVVRWMEYFRLRPLRFRAPDEPOQAVPHVGMGEVAGAPALRLQK 540
DB 481 KOEAKPRPGGCPQANRGVVRWMEYFRLRPLRFRAPDEPOQAVPHVGMGEVAGAPALRLQK 540
QY 541 SOSDLLERRERSVLRREQVVAERNNALFPEVFSPTPDENSQNSRSSQASGITGSYS 600
DB 541 SOSDLLERRERSVLRREQVVAERNNALFPEVFSPTPDENSQNSRSSQASGITGSYS 600
QY 541 SOSDLLERRERSVLRREQVVAERNNALFPEVFSPTPDENSQNSRSSQASGITGSYS 600
DB 541 SOSDLLERRERSVLRREQVVAERNNALFPEVFSPTPDENSQNSRSSQASGITGSYS 600
QY 601 VSESPPFSPIHLHSNVAMTWEDPVDSPAPGQKKEQWAGINPSDGINSEVLEAIRVTRH 660
DB 601 VSESPPFSPIHLHSNVAMTWEDPVDSPAPGQKKEQWAGINPSDGINSEVLEAIRVTRH 660
QY 601 VSESPPFSPIHLHSNVAMTWEDPVDSPAPGQKKEQWAGINPSDGINSEVLEAIRVTRH 660
DB 601 VSESPPFSPIHLHSNVAMTWEDPVDSPAPGQKKEQWAGINPSDGINSEVLEAIRVTRH 660
QY 661 KNAMAEWRMSRIYASEDD 679
DB 661 KNAMAEWRMSRIYASEDD 679
```

Db 661 KNMAERWESRIYASEDD 679

RESULT 4

ADN17172 standard; protein; 679 AA.

ADN17172;

17-JUN-2004 (first entry)

CS198 protein #1.

Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.

Unidentified.

US2004043406-A1.

04-MAR-2004.

22-AUG-2003; 2003US-00646873.

31-MAR-1997; 97US-00828855.

30-MAR-1998; 98US-00050516.

(BILL/) BILLINGEL P A.

(COHE/) COHEN M.

(COLP/) COLPITTS T L.

(FRIE/) FRIEDMAN P N.

(GORD/) GORDON J.

(GRAN/) GRANADOS E N.

(HAYD/) HAYDEN M A.

(HODG/) HODGES S C.

(KLAS/) KLAAS M R.

(KRAT/) KRATOCHVIL J D.

(ROBE/) ROBERTS-RAPP L.

(RUS/) RUSSELL J C.

(STRO/) STROUPE S D.

Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN, Hayden MA, Hodges SC, Klaas MR, Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD.

WPI; 2004-313754/29.

GENBANK; D87440.

Diagnosing diseases such as cancer of the gastrointestinal tract, by detecting aberrant expression or activity of the CS198 polypeptide, and associated treatment methods.

Claim 17; SEQ ID NO 42; 67pp; English.

The invention relates to reagents and methods for detecting diseases of the gastrointestinal (GI) tract. The method involves detecting the presence of target CS198 polynucleotide in the test sample. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the CS198 polypeptide, such as cancer of the gastrointestinal tract. These are also useful in gene therapy. The present sequence is a CS198 protein used to illustrate the method of the invention.

Sequence 679 AA;

Query Match 100.0%; Score 679; DB 8; Length 679;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRVTRVYILGIPQAHRTGVLDDDTSTYTHLVCMGSEASAGMGCDDEQPTWTHRAQOG 60

DB 1 MDRVTRVYILGIPQAHRTGVLDDDTSTYTHLVCMGSEASAGMGCDDEQPTWTHRAQOG 60

QY 61 VORQGVSYVHAAYTQSPRGLHSENREDEGMQVYRIGARDAYQGRPTMALRPEDGDXE 120

DB 61 VORQGVSYVHAAYTQSPRGLHSENREDEGMQVYRIGARDAYQGRPTMALRPEDGDXE 120

QY 121 MKTYRLDAGDADPRRLCDLREERWAVYQGOAVKSSVTALQSTPDHGDRTGPPSTP 180

DB 121 MKTYRLDAGDADPRRLCDLREERWAVYQGOAVKSSVTALQSTPDHGDRTGPPSTP 180

QY 181 LSENVVDREQIDFLAARQFLSLQANKGAPHSPPAGTTPGASQAPKAFNKPHLA 240

DB 181 LSENVVDREQIDFLAARQFLSLQANKGAPHSPPAGTTPGASQAPKAFNKPHLA 240

QY 241 NGHVVPKIPQVKGVBREKNRAVPTWASVQVDDPGSLASVSPGTPKETPIERIRLA 300

DB 241 NGHVVPKIPQVKGVBREKNRAVPTWASVQVDDPGSLASVSPGTPKETPIERIRLA 300

QY 301 QERADLREORGLRQATDHQELVEIPTRPLTLKSLITAPRRRGRPSLYVQRDIVQETQ 360

DB 301 QERADLREORGLRQATDHQELVEIPTRPLTLKSLITAPRRRGRPSLYVQRDIVQETQ 360

QY 361 REEDHREGLHVGRASTPDWVSEGPQGLRRLSDSILSPAPDARAADPAPEVRKYNRI 420

DB 361 REEDHREGLHVGRASTPDWVSEGPQGLRRLSDSILSPAPDARAADPAPEVRKYNRI 420

QY 421 PPDAVQPYLSPGTPOLEFSAFGAFGKSSLSTAEAKAATSPKATWSPRHLSESSGKPLST 480

DB 421 PPDAVQPYLSPGTPOLEFSAFGAFGKSSLSTAEAKAATSPKATWSPRHLSESSGKPLST 480

QY 481 KQKASKPPRCQPOANRGVVRWEYFRLRLPLFRAPDEQQAQVPHVGMWEVAGAPALRQK 540

DB 481 KQKASKPPRCQPOANRGVVRWEYFRLRLPLFRAPDEQQAQVPHVGMWEVAGAPALRQK 540

QY 541 SOSSDLERERESVLRQEAERERVALPPEYFSPTPDENSDONSSSQASGITSYS 600

DB 541 SOSSDLERERESVLRQEAERERVALPPEYFSPTPDENSDONSSSQASGITSYS 600

QY 601 VSESPFFSPILHLSNVAMTYEDPVDASAPGQKKEQWYAGINSPDGINSEVLRAIVTRH 660

DB 601 VSESPFFSPILHLSNVAMTYEDPVDASAPGQKKEQWYAGINSPDGINSEVLRAIVTRH 660

QY 661 KNMAERWESRIYASEDD 679

DB 661 KNMAERWESRIYASEDD 679

RESULT 5

ADX97562

ID ADX97562 standard; protein; 692 AA.

ADX97562;

21-APR-2005 (first entry)

Pancreatic cancer associated human protein, SEQ ID 110.

pancreas tumor; cytosolic.

Homo sapiens.

EP1471075-A2.

27-OCT-2004.

31-MAR-2004; 2004EP-00090124.

31-MAR-2003; 2003DE-01015834.

(HINZ/) HINZMANN B.

(ROSE/) ROSENTHAL A.

(PILA/) PILASKY C.

(DAHL/) DAHL E.

(SPEC/) SPECHT T.

(LICH/) LICHTNER R.

XX Rosenthal A, Pilarsky C, Dahl E, Specht T, Brummendorf T,
 FI Lichtner R, Staud E, Koepcke S, Li X;
 XX
 WP1, 2004-768082/76.
 DR N-P5DB, ADX97491.
 XX

CC The invention relates to a novel human nucleic acid sequence of the
CC pancreas and its encoded protein. The invention further comprises:
CC proteins and peptides, preferably isolated, that contain a sequence
CC encoded by the novel nucleic acid; and methods for diagnosis and
CC treatment of pancreatic cancer, using a substance that inhibits or binds
CC to the protein or its DNA, including: an antisense oligonucleotide, short
CC interfering RNA or ribozyme directed against the pancreatic protein, an
CC organic molecule, particularly having a molecular weight below 5000,
CC especially 500, that binds to the pancreatic DNA, an aptamer or
CC (monoclonal) antibody, preferably human or humanized, that binds to the
CC pancreatic DNA, or an anti-idiotypic antibody raised against the
CC monoclonal antibody, any of which may be derivatized with a reporter
CC group, cytotoxic compound, immunostimulant and/or radioisotope. The novel
CC human pancreatic proteins and their encoding DNA have cytostatic
CC activity. The novel sequences are useful for inhibiting transcription
CC and/or expression of genes and proteins associated with pancreatic
CC cancer. This sequence represents one of the novel human pancreatic
CC proteins of the invention. Note: This sequence is not shown in the
CC specification, it has been electronically downloaded from a DVD-ROM
CC provided with this specification by the European Patent Office.

SQ Sequence 692 AA;

Query Match	100.0%;	Score 679;	DB 8;	length 692;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 679; Conservative	0;	Mismatches	0;	Gaps 0

QY	1	MDRVTYRPLTGI:POAHRGGLVLDGOSTYTHYLVCXGPEASGCODEPOTWPFIDHAAOOG	60
Db	14	MDRVTYRPLTGI:POAHRGGLVLDGOSTYTHYLVCXGPEASGCODEPOTWPFIDHAAOOG	73
QY	61	VOROGVSVAHYATGQPSPEGLHSERBEDEGMQVYRLGARDAHQGRPTVALREDEDEGX	120
Db	74	VOROGVSVAHYATGQPSPEGLHSERBEDEGMQVYRLGARDAHQGRPTVALREDEDEGX	133
QY	121	MKTYRLDAGDADPRRLCDLEREMAVIOGQVAKSSTVATLQSTPHGDPRTGTGPPRSTP	180
Db	134	MKTYRLDAGDADPRRLCDLEREMAVIOGQVAKSSTVATLQSTPHGDPRTGTGPPRSTP	193
QY	181	LEENVVDREOIOIDPLARQOPLSLSEONKKAHPSSPARGPAGTIPGASQAPKAFNNPHLA	240
Db	194	LEENVVDREOIOIDPLARQOPLSLSEONKKAHPSSPARGPAGTIPGASQAPKAFNNPHLA	253
QY	241	NGHVVPKIQGVGVAAEENKVRNAVPTMASVOVDDDGSLASVSSPGTPEKTPIEREIRLA	300
Db	254	NGHVVPKIQGVGVAAEENKVRNAVPTMASVOVDDDGSLASVSSPGTPEKTPIEREIRLA	313
QY	301	QERADLREORGLQATDQELVEIFTRPLLYLUSLITABRRERGRPSLYORDIYOETO	360
Db	314	QERADLREORGLQATDQELVEIFTRPLLYLUSLITABRRERGRPSLYORDIYOETO	373
QY	361	REEDHRRREGLHGRASTPMWVSSGPOGCLPRAAISOSIISPADARADAPAEVRKNRI	420
Db	374	REEDHRRREGLHGRASTPMWVSSGPOGCLPRAAISOSIISPADARADAPAEVRKNRI	433
QY	421	PPDAYOPYLSPGTQOLEFSAFGAFGAPSSLSIAEAKAATSPKATMSPRHISESSGKPLST	480
Db	434	PPDAYOPYLSPGTQOLEFSAFGAFGAPSSLSIAEAKAATSPKATMSPRHISESSGKPLST	493
QY	481	KOEASKEPRGCGPANGVAVMEYFRLRLPRLFRAPDEBQOQOVPHVWGWAVAGAPALRLQK	540

Db	494	KQASBPBGCCPQANGVVRWVEFLRLARRAPADEPQQAQVPHVMGMEVAGAPALRLQK	553
Qy	541	SGSSDLLRRRESVTLRREQVVAEERRNALLPEVTVSPPTDENSDDNSSSSQASGITSYS	600
Db	554	SGSSDLLRRRESVTLRREQVVAEERRNALLPEVTVSPPTDENSDDNSSSSQASGITSYS	613
Qy	601	VSSSPFSPHLHSNVATVEDPVVSAPPQKKQOMYAGINSPDGINSEVLEAIRVTRH	660
Db	614	VSSSPFSPHLHSNVATVEDPVVSAPPQKKQOMYAGINSPDGINSEVLEAIRVTRH	673
Qy	661	KNMAERWESRIYASEEDD	679
Db	674	KNMAERWESRIYASEEDD	692

AAKT75574
ID AAKT75574 standard; protein; 672 AA.
XX
XX AAKT75574;
AC
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 3220.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00486914.
XX 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00650325.
PR 01-SEP-2000; 2000US-00654935.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HSE-) HSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao Qa, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
PI
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK52707.
XX
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
PT
XX
PS Claim 20; Page 288; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAK78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAK80020) are omitted as the relevant pages from the

CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 672 AA;

Query Match 92.0%; Score 625; DB 4; Length 672;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 17 RGTGLVLDGDTSYTHLVCMGPBAGSGMGDSPPQWPTPHRAQOQVORQGSYSVHAATGQ 76
Db 10 RGTGLVLDGDTSYTHLVCMGPBAGSGMGDSPPQWPTPHRAQOQVORQGSYSVHAATGQ 69
Oy 77 PSPRLSHSENDEDEGMQVYRLGADAHQGRPTWALRPEDGEDKEMKTYRLDAGDAPRL 136
Db 70 PSPRLSHSENDEDEGMQVYRLGADAHQGRPTWALRPEDGEDKEMKTYRLDAGDAPRL 129
Oy 137 CDLEBERRAVIQOQAVRKSSVTATIGTTPDHGDDPTTPPEPPSTPLEENVVDREQIDFLAA 196
Db 130 CDLEBERRAVIQOQAVRKSSVTATIGTTPDHGDDPTTPPEPPSTPLEENVVDREQIDFLAA 189
Oy 197 RQOFLSLSEQANKGAPHSSPARGTTPAGTTPGASQA PKAKNPKHLANGHVVPKIPQVKGVNR 256
Db 190 RQOFLSLSEQANKGAPHSSPARGTTPAGTTPGASQA PKAKNPKHLANGHVVPKIPQVKGVNR 249
Oy 257 EENKRAVPTWASVQVVDPPGSLASVESPGTPKETPIERERIRLAQEREADLREORGRLQA 316
Db 250 EENKRAVPTWASVQVVDPPGSLASVESPGTPKETPIERERIRLAQEREADLREORGRLQA 309
Oy 317 TDHQLVETPTPLITKLSLITTPARRERGRSLYQORDIVQETQREERHREGHLVGRAS 376
Db 310 TDHQLVETPTPLITKLSLITTPARRERGRSLYQORDIVQETQREERHREGHLVGRAS 369
Oy 377 TPDWVSESGPQGLRRALSSDSITLSPAPARADPAPEVRKVNRIIPDAYQPYLSPTGPOL 436
Db 370 TPDWVSESGPQGLRRALSSDSITLSPAPARADPAPEVRKVNRIIPDAYQPYLSPTGPOL 429
Oy 437 EFSAFAGFAPKSSSLSTAABAKATSPKATWSPRHLSESSGKPLSTKQEASKPCCPOANR 496
Db 430 EFSAFAGFAPKSSSLSTAABAKATSPKATWSPRHLSESSGKPLSTKQEASKPCCPOANR 489
Oy 497 GVNWMEYRLRPLRRARDEPQOAVPHVWMEVAGAPALRLQSSQSSDLERRERESTLR 556
Db 490 GVNWMEYRLRPLRRARDEPQOAVPHVWMEVAGAPALRLQSSQSSDLERRERESTLR 549
Oy 557 REQEAERERNAALPEVFSPTPDENSDDNSRSSQASGITTSYSVSESPFSPHLSNV 616
Db 550 REQEAERERNAALPEVFSPTPDENSDDNSRSSQASGITTSYSVSESPFSPHLSNV 609
Oy 617 AMTVEDPVDSAPPGQRKKEQWYAGI 641
Db 610 AMTVEDPVDSAPPGQRKKEQWYAGI 634

```

RESULT 7
 AAM78590
 ID AAM78590 standard; protein; 679 AA.

XX AC AAM78590;

XX DT 06-NOV-2001 (first entry)

XX DE Human protein SEQ ID NO 1252.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

XX OS Homo sapiens.

XX FN WO200157190-A2.

XX PD 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US04098.

XX 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.

XX (HYSB-) HYSBQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wehrman T, Goodrich R;

XX WPI; 2001-476283/51.

DR N-PSDB; AAK51723.

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.

PS Claim 20; Page 3512-3514; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK60302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoietic regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication

XX Sequence 679 AA;

Query Match 85.4%; Score 580; DB 4; Length 679;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 100 RDAHQGFPTALAPDEGEDKEMKTYRLDAGDADPRRLCDLEBERRAVIQOQAVRKSSVTA 159
Db 100 RDAHQGFPTALAPDEGEDKEMKTYRLDAGDADPRRLCDLEBERRAVIQOQAVRKSSVTA 159
Oy 160 TLOQTPDHGDPRTTPGPRSTPLEENVVDREQIDFLAAQOFLSLSEQANKGAPHSSPARGT 219
Db 160 TLOQTPDHGDPRTTPGPRSTPLEENVVDREQIDFLAAQOFLSLSEQANKGAPHSSPARGT 219
Oy 220 PACTTPGASQAPRAFNKPKHLANGHVPIKQVGVVREENKRAVPTWASVQVVDDBGSL 279
Db 220 PACTTPGASQAPRAFNKPKHLANGHVPIKQVGVVREENKRAVPTWASVQVVDDBGSL 279
Oy 280 ASVESPGTPKETPIERERIRLAQEREADLREORGRLQATDHOELVEIPTRLITLSTITA 339
Db 280 ASVESPGTPKETPIERERIRLAQEREADLREORGRLQATDHOELVEIPTRLITLSTITA 339
Oy 340 PRERGRPSLYVORDIVQETQREEDHREGHLVGRASTPMWSEGPQGLRRALSSDIL 399
Db 340 PRERGRPSLYVORDIVQETQREEDHREGHLVGRASTPMWSEGPQGLRRALSSDIL 399
Oy 400 SPAADAAADPAPEVRKVNRIIPDAYQPYLSPTGPOLSEFSAFGAFGRSSSLSTAABAAAT 459
Db 400 SPAADAAADPAPEVRKVNRIIPDAYQPYLSPTGPOLSEFSAFGAFGRSSSLSTAABAAAT 459
Oy 460 SPKATWSPRHLSSSGKPLSTKQEASKPCCPOANRGVVRWMEYRLRPLRRARDEPQO 519
Db 460 SPKATWSPRHLSSSGKPLSTKQEASKPCCPOANRGVVRWMEYRLRPLRRARDEPQO 519

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QY 520 ACPVHWGWEVAGAPALRLQKSSQSDLLERERESVLRREQVAAERRNALPPEVESPFPD 579
DB 520 ACPVHWGWEVAGAPALRLQKSSQSDLLERERESVLRREQVAAERRNALPPEVESPFPD 579
QY 580 ENSDONSRSQASGITSYSVSESPFPIHLHSNVAMTVEDPVDASAPGQKKEOMYA 639
DB 580 ENSDONSRSQASGITSYSVSESPFPIHLHSNVAMTVEDPVDASAPGQKKEOMYA 639
QY 640 GINPSDGINSEVLEAIRVTRHRNMAAERWESRIYASEEDD 679
DB 640 GINPSDGINSEVLEAIRVTRHRNMAAERWESRIYASEEDD 679

RESULT 8
ADG14341
ID ADG14341 standard; protein; 679 AA.

AC ADG14341;
DT 26-FEB-2004 (first entry)
DE Human NC2.
XX Human; NC1; NC2; NC3; PHH1; pancreas beta-cell; insulin; antidiabetic;
KW neuroprotective.
XX Homo sapiens.
XX WO2003078631-A1.
XX 25-SEP-2003.
XX 06-MAR-2003; 2003WO-JP002620.
XX 15-MAR-2002; 2002JP-00071592.
XX (KANP) KANEKA CORP.
XX Niwa H, Yamashita K;
XX WPI; 2003-767524/72.
XX N-PSDB; ADG14344.
DR Familial persistent hyperinsulinemic hypoglycemia of infancy (PHH1)
PT patient-expressed genes for detecting and screening e.g. proliferative
PT insulin-producing cells in treatment of PHH1.

PS Claim 1; SEQ ID NO 2; 34pp; Japanese.
XX The present invention relates to human NC1, NC2 and NC3 proteins and
XX coding sequences (ADG14340-ADG14345). The coding sequences are useful for
XX detecting and screening proliferative insulin-producing cells as well as
XX differentiation and proliferation of such cells and their precursors as
XX analogous cells in treatment of e.g. PHH1 and diseases due to
XX differentiation/proliferation abnormality, diseases of the nervous system
XX and pancreas. The coding sequences are also useful as spontaneous
XX NC3 proliferation models of pancreas beta-cells. The novel genes NC1, NC2 and
XX NC3 were isolated from the pancreas of PHH1 patients, which were used in
XX testing for the detection of proliferative insulin-producing cells or
XX pancreas beta-cells by Northern analysis.
XX Sequence 679 AA;

Query Match 38.9%; Score 264; DB 7; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.3e-259;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 HVGRASTPDWVSGPQGLRRALSSDSILSPAPDARAADPAPEVRKVNRIPPDAYOPYLS 430
DB 371 HVGRASTPDWVSGPQGLRRALSSDSILSPAPDARAADPAPEVRKVNRIPPDAYOPYLS 430
QY 431 PGTQPLEFSAGFGKPRSSLSLTAAKAATSPKATMSPRHLSSESGKPLSTQKQASKPPRG 490

DB 431 PGTQPLEFSAGFGKPRSSLSLTAAKAATSPKATMSPRHLSSESGKPLSTQKQASKPPRG 490
QY 491 CPQANRGVWWEYRRLAPLFRAPDEPQOAVPHVWGWEVAGAPALRLQKSSQSDLLERE 550
DB 491 CPQANRGVWWEYRRLAPLFRAPDEPQOAVPHVWGWEVAGAPALRLQKSSQSDLLERE 550
QY 551 RESVLRREQVAAERRNALPPEVESPFPDENSDONSRSQASGITSYSVSESPFPI 610
DB 551 RESVLRREQVAAERRNALPPEVESPFPDENSDONSRSQASGITSYSVSESPFPI 610
QY 611 HLHSNVAMTVEDPVDASAPGQKKE 634
DB 611 HLHSNVAMTVEDPVDASAPGQKKE 634

RESULT 9
AAW79681
ID AAW79681 standard; protein; 215 AA.

AC AAW79681;
DT 11-JAN-1999 (first entry)
DE Human CS198 protein C-terminal.
XX Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
KW human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
KW pancreatitis.

XX Homo sapiens.
XX WO9844159-A1.
XX 08-OCT-1998.
XX 30-MAR-1998; 98WO-US006251.
XX 31-MAR-1997; 97US-00828855.
XX (ABBO) ABBOTT LAB.
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX Pi Granados EN, Hayden M, Hodges SC, Klaas MR, Katsochvil JD;
XX Pi Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 1998-542714/46.

XX New gastrointestinal polynucleotides, CS198, and their detection - used
XX for developing products for the diagnosis and treatment of
XX gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
XX Claim 26; Page 103; 127pp; English.

XX This sequence represents the C-terminal of the human CS198 protein which
XX is used in a method to detect the presence of a target CS198
XX polynucleotide in a test sample. The CS198 gene is useful as a marker for
XX gastrointestinal (GI) tract disorders. The methods and products can be
XX used in detecting, diagnosing, staging, monitoring, prognosticating,
XX preventing or treating, or determining the predisposition to diseases and
XX conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
XX gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative
XX colitis, and pancreatitis
XX Sequence 215 AA;

Query Match 31.7%; Score 215; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.9e-210;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 MSPRHLSSESGKPLSTQKQASKPPRGCPQANRGVWWEYRRLAPLFRAPDEPQOAVPH 524

Db 1 MSPRLSSSGKPLSTKQESKPPGCPQANRGVVRWEYRLRLPRLFRAPDEPQOAVPH 60
 Qy 525 VMGWEVAGAPALRLQKSQSSDLLERERESVLRREQVEAERRNALPFEVFSPTDENSDQ 584
 Db 61 VMGWEVAGAPALRLQKSQSSDLLERERESVLRREQVEAERRNALPFEVFSPTDENSDQ 120
 Qy 585 NSRSSSQASGITGSYSVSESPFSPHLSNVAMTVEDPVDAPPGQRKKEQWYAGINPS 644
 Db 121 NSRSSSQASGITGSYSVSESPFSPHLSNVAMTVEDPVDAPPGQRKKEQWYAGINPS 180
 Qy 645 DGINSEVLEAIRVTRHKNAMAEWRMESRIYASEEDD 679
 Db 181 DGINSEVLEAIRVTRHKNAMAEWRMESRIYASEEDD 215

RESULT 10
 AA07324
 ID AA07324 standard; protein; 215 AA.
 XX
 AC AA07324;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human CS 198 protein C-terminal portion.
 XX
 KW CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
 KW gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
 KW Barrett's oesophagus; gene therapy; drug screening; human.
 KM
 XX Homo sapiens.
 OS
 XX US2001010904-A1.
 PN
 XX 02-AUG-2001.
 PD
 XX 30-MAR-1998; 98US-00050516.
 PF
 XX 31-MAR-1997; 97US-00828855.
 PR
 XX
 PA (BILL/) BILLINGEL P A.
 PA (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HAYD/) HAYDEN M.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUS/) RUSSELL J C.
 PA (STRO/) STROUDE S D.
 XX
 PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
 PI Granados EN, Hayden M, Hodges SC, KLAS MR, Kratochvil JD,
 PI Roberts-Rapp L, Russell JC, Stroude SD;
 XX
 XX WPI; 2001-496163/54.
 DR
 XX
 PT Detecting the presence of target CS 198 polynucleotide, useful for
 PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
 PT contacting test sample with at least one CS 198-specific polynucleotide.
 XX
 PS Claim 17; Page 52-53; 68pp; English.
 XX
 CC The invention relates to a method of detecting the presence of a target
 CC CS 198 polynucleotide comprising contacting the test sample with at least
 CC one CS 198-specific polynucleotide. The method is useful for detecting
 CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
 CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
 CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
 CC treating or determining predisposition to diseases and conditions of the
 CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,

CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
 CC polypeptides are useful as standards or reagents in diagnostic
 CC immunoassays, as components or as target sites for various therapies.
 CC Antibodies directed against at least one epitope contained within these
 CC polypeptides are useful for screening for conditions or diseases associated
 CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
 CC for the generation of chimeric antibodies for therapeutic use. The CS 198
 CC polynucleotide is also useful in gene therapy and drug screening. The
 CC method of the invention provides an alternative, non-surgical diagnostic
 CC method capable of detecting early stage GI tract disease such as cancer.
 CC The present sequence is C-terminal portion of human CS 198 polypeptide
 XX
 SO Sequence 215 AA;

Query Match 31.7%; Score 215; DB 4; Length 215;
 Best Local Similarity 100.0%; Pred. No. 6,9e-210; Indels 0; Gaps 0;
 Matches 215; Conservative 0; Mismatches 0;

Qy 465 MSPRLSSSGKPLSTKQESKPPGCPQANRGVVRWEYRLRLPRLFRAPDEPQOAVPH 524
 Db 1 MSPRLSSSGKPLSTKQESKPPGCPQANRGVVRWEYRLRLPRLFRAPDEPQOAVPH 60
 Qy 525 VMGWEVAGAPALRLQKSQSSDLLERERESVLRREQVEAERRNALPFEVFSPTDENSDQ 584
 Db 61 VMGWEVAGAPALRLQKSQSSDLLERERESVLRREQVEAERRNALPFEVFSPTDENSDQ 120
 Qy 585 NSRSSSQASGITGSYSVSESPFSPHLSNVAMTVEDPVDAPPGQRKKEQWYAGINPS 644
 Db 121 NSRSSSQASGITGSYSVSESPFSPHLSNVAMTVEDPVDAPPGQRKKEQWYAGINPS 180
 Qy 645 DGINSEVLEAIRVTRHKNAMAEWRMESRIYASEEDD 679
 Db 181 DGINSEVLEAIRVTRHKNAMAEWRMESRIYASEEDD 215

RESULT 11
 ADA26384
 ID ADA26384 standard; protein; 215 AA.
 XX
 AC ADA26384;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Synthetic peptide based on CS198 protein #5.
 XX
 KW CS198; cancer diagnosis; cancer staging; cancer monitoring;
 KW cancer prognosticating; cancer prevention; cancer;
 KW gastrointestinal tract disorder; gene therapy.
 KM
 XX Synthetic.
 OS
 XX US2003082619-A1.
 PN
 XX 01-MAY-2003.
 PD
 XX 23-OCT-2002; 2002US-00278547.
 PF
 XX 31-MAR-1997; 97US-00828855.
 PR 30-MAR-1998; 98US-00050516.
 PA (BILL/) BILLINGEL P A.
 PA (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HAYD/) HAYDEN M A.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUS/) RUSSELL J C.

PA (STROU) STROUPE S D.
 XX Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden MA, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 DR WPI; 2003-596961/56.
 XX Detecting the presence of a target CS198 polynucleotide in a test sample
 PT comprises contacting the sample with a CS198 specific polynucleotide and
 PT detecting the presence of the target CS198 polynucleotide in the test
 PT sample.
 XX Claim 52; Page 52; 67pp; English.
 XX The invention describes a method of detecting the presence of a target
 CC CS198 polynucleotide in a test sample. The method comprises contacting
 CC the test sample with at least one CS198 specific polynucleotide or its
 CC complement, and detecting the presence of the target CS198 polynucleotide
 CC in the test sample, where the CS198-specific polynucleotide has at least
 CC 50% identity to a polynucleotide having any of the 27 fully defined
 CC sequences of 34-2894 bp (SI-27) given in the specification, or their
 CC fragments or complements. The composition and methods are useful in
 CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
 CC or determining the predisposition of an individual to, diseases and
 CC conditions of the gastrointestinal tract, e.g. cancer and in gene
 CC therapy. This is the amino acid sequence of a synthetic peptide based on
 CC the predicted human CS198 protein sequence derived from the CS198
 CC consensus sequence shown in seq id 27.
 XX Sequence 215 AA;
 XX SQ
 Query Match 31.7%; Score 215; DB 6; Length 215;
 Best Local Similarity 100.0%; Pred. No. 6.9e-210; Indels 0; Gaps 0;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 465 MSPRLSSSGKPLSTKQKASKPRGCPQANRGVWMEYFRLRPLFRAPDEPQQAQVPH 524
 DB 1 MSPRLSSSGKPLSTKQKASKPRGCPQANRGVWMEYFRLRPLFRAPDEPQQAQVPH 60
 QY 525 VNGWEVAGAPALRLQKSSQSDLLERRESVLRREQVAERNNALPPEVFSPTPDNSDQ 584
 DB 61 VNGWEVAGAPALRLQKSSQSDLLERRESVLRREQVAERNNALPPEVFSPTPDNSDQ 120
 QY 585 NSRSSQASGIGTSVSVSPFSPHLSNVAMTVEDPVDSAPGQKCKEQMYAGINPS 644
 DB 121 NSRSSQASGIGTSVSVSPFSPHLSNVAMTVEDPVDSAPGQKCKEQMYAGINPS 180
 QY 645 DGINSEVLEAIRVTRHKNNMAERMSRIYASEED 679
 DB 181 DGINSEVLEAIRVTRHKNNMAERMSRIYASEED 215
 RESULT 12
 ADN17177
 ID ADN17177 standard; protein; 215 AA.
 XX ADN17177;
 XX 17-JUN-2004 (first entry)
 XX CS198 protein #2.
 DE CS198 protein #2.
 XX Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.
 XX Unidentified.
 OS US2004043406-A1.
 PN 04-MAR-2004.
 XX 22-AUG-2003; 2003US-00646873.
 XX

PR 31-MAR-1997; 97US-00828855.
 PR 30-MAR-1998; 98US-00050516.
 XX (BILL) BILLINGSEL P A.
 PA (COHE) COHEN M.
 PA (COLP) COLPITTS T L.
 PA (FRIE) FRIEDMAN P N.
 PA (GORD) GORDON J.
 PA (GRAN) GRANADOS E N.
 PA (HAYD) HAYDEN M A.
 PA (HODG) HODGES S C.
 PA (KLAS) KLAS M R.
 PA (KRAT) KRATOCHVIL J D.
 PA (ROBE) ROBERTS-RAPP L.
 PA (RUSSE) RUSSELL J C.
 PA (STRO) STROUPE S D.
 XX Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden MA, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 DR WPI; 2004-313754/29.
 XX Diagnosing diseases such as cancer of the gastrointestinal tract, by
 PT detecting aberrant expression or activity of the CS198 polypeptide, and
 PT associated treatment methods.
 XX Claim 17; SEQ ID NO 47; 67pp; English.
 XX The invention relates to reagents and methods for detecting diseases of
 CC the gastrointestinal (GI) tract. The method involves detecting the
 CC presence of target CS198 polynucleotide in the test sample. The methods
 CC and compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of diseases or conditions associated with
 CC aberrant expression or activity of the CS198 polypeptide, such as cancer
 CC of the gastrointestinal tract. These are also useful in gene therapy. The
 CC present sequence is a CS198 protein used to illustrate the method of the
 CC invention.
 XX Sequence 215 AA;
 XX SQ
 Query Match 31.7%; Score 215; DB 8; Length 215;
 Best Local Similarity 100.0%; Pred. No. 6.9e-210; Indels 0; Gaps 0;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 465 MSPRLSSSGKPLSTKQKASKPRGCPQANRGVWMEYFRLRPLFRAPDEPQQAQVPH 524
 DB 1 MSPRLSSSGKPLSTKQKASKPRGCPQANRGVWMEYFRLRPLFRAPDEPQQAQVPH 60
 QY 525 VNGWEVAGAPALRLQKSSQSDLLERRESVLRREQVAERNNALPPEVFSPTPDNSDQ 584
 DB 61 VNGWEVAGAPALRLQKSSQSDLLERRESVLRREQVAERNNALPPEVFSPTPDNSDQ 120
 QY 585 NSRSSQASGIGTSVSVSPFSPHLSNVAMTVEDPVDSAPGQKCKEQMYAGINPS 644
 DB 121 NSRSSQASGIGTSVSVSPFSPHLSNVAMTVEDPVDSAPGQKCKEQMYAGINPS 180
 QY 645 DGINSEVLEAIRVTRHKNNMAERMSRIYASEED 679
 DB 181 DGINSEVLEAIRVTRHKNNMAERMSRIYASEED 215
 RESULT 13
 AAG73987
 ID AAG73987 standard; protein; 172 AA.
 XX AAG73987;
 XX 03-SEP-2001 (first entry)
 XX Human colon cancer antigen protein SEQ ID NO:4751.
 DE Human; colon cancer; colon cancer antigen; diagnosis; detection;
 XX

KW colorectal carcinoma.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
PR 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Ruden SM, Barash SC, Birse CE, Rosen CA;
XX
XX WPI; 2001-235357/24.
DR N-PSDB; AAH33418.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.
XX
XX Claim 11; Page 6550-6551; 9803pp; English.
XX
XX AAH32943 to AAH37195 and AAG7788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patient's own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 172 AA;
Query Match 8.8%; Score 60; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 5,4e-52;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 563 EERRNALPEVPSPPDENSDONSSSSQASGITGSYSVSPFSPPIHLHSNVAMVTEED 622
DB 56 EERRNALPEVPSPPDENSDONSSSSQASGITGSYSVSPFSPPIHLHSNVAMVTEED 115

RESULT 14
ABO60042
ID ABO60042 standard; protein; 43 AA.
XX
AC ABO60042;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon protein #6276.
XX
KW Human; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
PN US2003194704-A1.
XX
PD 16-OCT-2003.

XX
XX 03-APR-2002; 2002US-00023386.
XX
PF 03-APR-2002; 2002US-00023386.
PR
XX
XX (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX
XX WPI; 2004-119264/12.
DR
XX
XX New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
XX Claim 45; SEQ ID NO 33676; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 688 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridizes under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subsequence, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterizing
CC alternative splicing events, in detecting and characterizing gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=20030194704
XX
XX Sequence 43 AA;
Query Match 6.3%; Score 43; DB 8; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 595 ITGSYSVSESPPFSPPIHLHSNVAMVTEEDPVDSAPGGRKEQW 637
DB 1 ITGSYSVSESPPFSPPIHLHSNVAMVTEEDPVDSAPGGRKEQW 43

RESULT 15
AAG75071
ID AAG75071 standard; protein; 57 AA.
XX
AC AAG75071;
XX

PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HAYD/) HAYDEN M.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUSS/) RUSSELL J C.
 PA (STRO/) STROUPE S D.
 PI Billings PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Kلاس MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX WPI, 2001-496163/54.

PT Detecting the presence of target CS 198 polynucleotide, useful for
 PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
 PT contacting test sample with at least one CS 198-specific polynucleotide.

XX Claim 17; Page 51; 68pp; English.

XX The invention relates to a method of detecting the presence of a target
 CC CS 198 polynucleotide comprising contacting the test sample with at least
 CC one CS 198-specific polynucleotide. The method is useful for detecting
 CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
 CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
 CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
 CC treating or determining predisposition to diseases and conditions of the
 CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
 CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
 CC polypeptides are useful as standards or reagents in diagnostic
 CC immunoassays, as components or as target sites for various therapies.
 CC Antibodies directed against at least one epitope contained within these
 CC polypeptides are useful as delivery agents for therapeutic agents, in
 CC diagnostic tests and for screening for conditions or diseases associated
 CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
 CC for the generation of chimeric antibodies for therapeutic use. The CS 198
 CC polynucleotide is also useful in gene therapy and drug screening. The
 CC method of the invention provides an alternative, non-surgical diagnostic
 CC method capable of detecting early stage GI tract disease such as cancer.
 CC The present sequence is a peptide derived from human CS 198 polypeptide
 CC consensus sequence

XX Sequence 36 AA;

Query Match 5.3%; Score 36; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.7e-28;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 465 MSPRHLSGGKPLSTKQKASKPRGCPQANRGVVR 500
 DB 1 MSPRHLSGGKPLSTKQKASKPRGCPQANRGVVR 36

RESULT 18
 ADA26380
 ID ADA26380 standard; protein; 36 AA.

XX ADA26380;

XX 20-NOV-2003 (first entry)

XX Synthetic peptide based on CS198 protein #1.

XX CS198; cancer diagnosis; cancer staging; cancer monitoring;

XX cancer prognosticating; cancer prevention; cancer;

XX gastrointestinal tract disorder; gene therapy.

XX Synthetic;

PN US2003082619-A1.
 XX 01-MAY-2003.
 XX 23-OCT-2002; 2002US-00278547.
 XX 31-MAR-1997; 97US-00828855.
 XX 30-MAR-1998; 98US-00050516.

PA (BILL/) BILLINGEL P A.
 PA (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HAYD/) HAYDEN M A.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUSS/) RUSSELL J C.
 PA (STRO/) STROUPE S D.

PI Billings PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX WPI, 2003-596961/56.

PT Detecting the presence of a target CS198 polynucleotide in a test sample
 PT comprises contacting the sample with a CS198 specific polynucleotide and
 PT detecting the presence of the target CS198 polynucleotide in the test
 PT sample.

XX Claim 17; Page 51; 67pp; English.

XX The invention describes a method of detecting the presence of a target
 CC CS198 polynucleotide in a test sample. The method comprises contacting
 CC the test sample with at least one CS198 specific polynucleotide or its
 CC complement, and detecting the presence of the target CS198 polynucleotide
 CC in the test sample, where the CS198-specific polynucleotide has at least
 CC 50% identity to a polynucleotide having any of the 27 fully defined
 CC sequences of 34-2894 bp (51-27) given in the specification, or their
 CC fragments or complements. The composition and methods are useful in
 CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
 CC or determining the predisposition of an individual to, diseases and
 CC conditions of the gastrointestinal tract, e.g. cancer and in gene
 CC therapy. This is the amino acid sequence of a synthetic peptide based on
 CC the predicted human CS198 protein sequence derived from the CS198
 CC consensus sequence shown in seq id 27.

XX Sequence 36 AA;

Query Match 5.3%; Score 36; DB 6; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.7e-28;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 465 MSPRHLSGGKPLSTKQKASKPRGCPQANRGVVR 500
 DB 1 MSPRHLSGGKPLSTKQKASKPRGCPQANRGVVR 36

RESULT 19
 ADN17173
 ID ADN17173 standard; peptide; 36 AA.

XX ADN17173;

XX 17-JUN-2004 (first entry)

XX CS198 peptide #1.

XX Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.

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XX OS Unidentified.
XX PN US2004043406-A1.
XX PD 04-MAR-2004.
XX PF 22-AUG-2003; 2003US-00646873.
XX PR 31-MAR-1997; 97US-00828855.
XX PR 30-MAR-1998; 98US-00050516.
XX PA (BILL/) BILLINGEL P A.
XX PA (COHE/) COHEN M.
XX PA (COLP/) COLPITTS T L.
XX PA (FRIE/) FRIEDMAN P N.
XX PA (GORD/) GORDON J.
XX PA (GRAN/) GRANADOS E N.
XX PA (HAYD/) HAYDEN M A.
XX PA (HODG/) HODGES S C.
XX PA (KLAS/) KLAS M R.
XX PA (KRAT/) KRATOCHVIL J D.
XX PA (ROBE/) ROBERTS-RAPP L.
XX PA (RUSS/) RUSSELL J C.
XX PA (STRO/) STROUPE S D.
XX PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
XX PI Granados EN, Hayden MA, Hodges SC, KLAS MR, Kratochvil JD;
XX PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX DR WPI; 2004-313754/29.
XX PR Diagnosing diseases such as cancer of the gastrointestinal tract, by
XX PR detecting aberrant expression or activity of the CS198 polypeptide, and
XX PR associated treatment methods.
XX PS Claim 17; SEQ ID NO 43; 67pp; English.
XX XX
XX CC The invention relates to reagents and methods for detecting diseases of
XX CC the gastrointestinal (GI) tract. The method involves detecting the
XX CC presence of target CS198 polynucleotide in the test sample. The methods
XX CC and compositions of the present invention are useful for the diagnosis,
XX CC prevention and/or treatment of diseases or conditions associated with
XX CC aberrant expression or activity of the CS198 polypeptide, such as cancer
XX CC of the gastrointestinal tract. These are also useful in gene therapy. The
XX CC present sequence is a CS198 peptide used to illustrate the method of the
XX CC invention.
XX CC
XX SQ Sequence 36 AA;
XX
XX Query Match 5.3%; Score 36; DB 8; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 3.7e-28;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 465 MSPRHLSSESGKPLSTKQKASKPPRCGCPQANRGVVR 500
XX DB 1 MSPRHLSSESGKPLSTKQKASKPPRCGCPQANRGVVR 36
XX
XX RESULT 20
XX ID AAW79679 standard; protein; 35 AA.
XX AC AAW79679;
XX XX
XX DT 11-JAN-1999 (first entry)
XX XX
XX DE Synthetic CS198 derived peptide #3.
XX KM Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
XX KM human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
XX KM gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
XX KM pancreatitis.

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XX OS Synthetic.
XX PN W09844159-A1.
XX XX
XX PD 08-OCT-1998.
XX PF 30-MAR-1998; 98MO-US006251.
XX PR 31-MAR-1997; 97US-00828855.
XX PA (ABBO ) ABBOTT LAB.
XX PI Billings-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX PI Granados EN, Hayden M, Hodges SC, KLAS MR, Kratochvil JD;
XX PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX DR WPI; 1998-542714/46.
XX PR New gastrointestinal polynucleotides, CS198, and their detection - used
XX PR for developing products for the diagnosis and treatment of
XX PR gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
XX PS Claim 26; Page 103; 127pp; English.
XX XX
XX CC AAW79677-W79680 are synthetic CS198 derived peptide fragments which are
XX CC used in a method to detect the presence of a target human CS198
XX CC polynucleotide in a test sample. The CS198 gene is useful as a marker for
XX CC gastrointestinal (GI) tract disorders. The methods and products can be
XX CC used in detecting, diagnosing, staging, monitoring, prognosticating,
XX CC preventing or treating, or determining the predisposition to diseases and
XX CC conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
XX CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative
XX CC colitis, and pancreatitis
XX CC
XX SQ Sequence 35 AA;
XX
XX Query Match 5.2%; Score 35; DB 2; Length 35;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-27;
XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 568 ALFPEVFSPTPDNSDQNSRSSQASGIRGSYSVS 602
XX DB 1 ALFPEVFSPTPDNSDQNSRSSQASGIRGSYSVS 35
XX
XX RESULT 21
XX ID AAE07322
XX AC AAE07322;
XX XX
XX DT 06-NOV-2001 (first entry)
XX XX
XX DE Human CS 198 peptide #3.
XX KM CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
XX KM gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
XX KM Barrett's oesophagus; gene therapy; drug screening; human.
XX XX
XX OS Homo sapiens.
XX XX
XX ID US2001010904-A1.
XX AC US2001010904-A1.
XX XX
XX PD 02-AUG-2001.
XX PF 30-MAR-1998; 98US-00050516.
XX PR 31-MAR-1997; 97US-00828855.
XX PA (BILL/) BILLINGEL P A.
XX PA (COHE/) COHEN M.
XX PA (COLP/) COLPITTS T L.

```

PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUS/) RUSSELL J C.
PA (STRO/) STROUPE S D.
XX Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden M, Hodges SC, Kلاس MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI: 2001-496163/54.
XX Detecting the presence of target CS 198 polynucleotide, useful for
PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
PT contacting test sample with at least one CS 198-specific polynucleotide.
XX Claim 17, Page 52; 68pp; English.
XX The invention relates to a method of detecting the presence of a target
CC CS 198 polynucleotide comprising contacting the test sample with at least
CC one CS 198-specific polynucleotide. The method is useful for detecting
CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
CC treating or determining predisposition to diseases and conditions of the
CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
CC polypeptides are useful as standards or reagents in diagnostic
CC immunoassays, as components or as target sites for various therapies.
CC Antibodies directed against at least one epitope contained within these
CC polypeptides are useful as delivery agents for therapeutic agents, in
CC diagnostic tests and for screening for conditions or diseases associated
CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
CC for the generation of chimeric antibodies for therapeutic use. The CS 198
CC polynucleotide is also useful in gene therapy and drug screening. The
CC method of the invention provides an alternative, non-surgical diagnostic
CC method capable of detecting early stage GI tract disease such as cancer.
CC The present sequence is a peptide derived from human CS 198 polypeptide
CC consensus sequence
XX
XX Sequence 35 AA;
SQ
Query Match 5.2%; Score 35; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.8e-27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 568 ALPPEVFSPTPDENSNDNSRSSSQASGITGSYSVS 602
DB 1 ALPPEVFSPTPDENSNDNSRSSSQASGITGSYSVS 35
RESULT 22
ADA26382
ID ADA26382 standard; protein; 35 AA.
XX
XX ADA26382;
XX
XX 20-NOV-2003 (first entry)
XX
XX Synthetic peptide based on CS198 protein #3.
XX
XX CS198; cancer diagnosis; cancer staging; cancer monitoring;
XX cancer prognosticating; cancer prevention; cancer;
XX gastrointestinal tract disorder; gene therapy.
XX
XX Synthetic;
XX
XX US2003082619-A1.
PN

XX
PD 01-MAY-2003.
XX
XX 23-OCT-2002; 2002US-00278547.
XX
XX 31-MAR-1997; 97US-00828855.
XX 30-MAR-1998; 98US-00050516.
XX
XX (BILL/) BILLINGSEL P A.
XX (COHE/) COHEN M.
XX (COLP/) COLPITTS T L.
XX (FRIE/) FRIEDMAN P N.
XX (GORD/) GORDON J.
XX (GRAN/) GRANADOS E N.
XX (HAYD/) HAYDEN M A.
XX (HODG/) HODGES S C.
XX (KLAS/) KLAS M R.
XX (KRAT/) KRATOCHVIL J D.
XX (ROBE/) ROBERTS-RAPP L.
XX (RUS/) RUSSELL J C.
XX (STRO/) STROUPE S D.
XX Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI: 2003-596961/56.
XX
XX Detecting the presence of a target CS198 polynucleotide in a test sample
PT comprises contacting the sample with a CS198 specific polynucleotide and
PT detecting the presence of the target CS198 polynucleotide in the test
PT sample.
XX
XX Claim 17, Page 51; 67pp; English.
XX
XX The invention describes a method of detecting the presence of a target
CC CS198 polynucleotide in a test sample. The method comprises contacting
CC the test sample with at least one CS198 specific polynucleotide or its
CC complement, and detecting the presence of the target CS198 polynucleotide
CC in the test sample, where the CS198-specific polynucleotide has at least
CC 50% identity to a polynucleotide having any of the 27 fully defined
CC sequences of 34-2894 bp (S1-27) given in the specification, or their
CC fragments or complements. The composition and methods are useful in
CC diagnosis, staging, monitoring, prognosticating, preventing or treating,
CC or determining the predisposition of an individual to, diseases and
CC therapy. This is the amino acid sequence of a synthetic peptide based on
CC the predicted human CS198 protein sequence derived from the CS198
CC consensus sequence shown in seq id 27.
XX
XX Sequence 35 AA;
SQ
Query Match 5.2%; Score 35; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.8e-27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 568 ALPPEVFSPTPDENSNDNSRSSSQASGITGSYSVS 602
DB 1 ALPPEVFSPTPDENSNDNSRSSSQASGITGSYSVS 35
RESULT 23
ADN17175
ID ADN17175 standard; peptide; 35 AA.
XX
XX ADN17175;
XX
XX 17-JUN-2004 (first entry)
XX
XX CS198 peptide #3.
XX
XX Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.
XX

OS Unidentified.
 XX US2004043406-A1.
 XX
 PD 04-MAR-2004.
 XX
 PF 22-AUG-2003; 2003US-00646873.
 XX
 PR 31-MAR-1997; 97US-00828855.
 PR 30-MAR-1998; 98US-00050516.
 XX
 PA (BILL/) BILLINGEL P A.
 PA (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HAYD/) HAYDEN M A.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUSS/) RUSSELL J C.
 PA (STRO/) STROUPE S D.
 XX
 PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden MA, Hodges SC, KLAS MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI; 2004-313754/29.
 XX
 PT Diagnosing diseases such as cancer of the gastrointestinal tract, by
 PT detecting aberrant expression or activity of the CS198 polypeptide, and
 PT associated treatment methods.
 XX
 SQ Claim 17; SEQ ID NO 45; 67bp; English.
 XX
 CC The invention relates to reagents and methods for detecting diseases of
 CC the gastrointestinal (GI) tract. The method involves detecting the
 CC presence of target CS198 polynucleotide in the test sample. The methods
 CC and compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of diseases or conditions associated with
 CC aberrant expression or activity of the CS198 polypeptide, such as cancer
 CC of the gastrointestinal tract. These are also useful in gene therapy. The
 CC present sequence is a CS198 peptide used to illustrate the method of the
 CC invention.
 XX
 SQ Sequence 35 AA;
 XX
 Query Match 5.2%; Score 35; DB 8; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.8e-27;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 568 ALPPEVFSPTPDNSQNSRSSQASGRTGSYSVS 602
 DB 1 ALPPEVFSPTPDNSQNSRSSQASGRTGSYSVS 35
 XX
 RESULT 24
 AAW79678
 ID AAW79678 standard; protein; 31 AA.
 XX
 AC AAW79678;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Synthetic CS198 derived peptide #2.
 XX
 KW Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
 KW human; predilection; treatment; Barrett's oesophagus; gastric ulcer;
 KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
 KW pancreatitis.
 XX

OS Synthetic.
 XX W09844159-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98WO-US006251.
 XX
 PR 31-MAR-1997; 97US-00828855.
 PR (ABBO) ABBOTT LAB.
 XX
 PI Billings-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, KLAS MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI; 1998-542714/46.
 XX
 PT New gastrointestinal polynucleotides, CS198, and their detection - used
 PT for developing products for the diagnosis and treatment of
 PT gastrointestinal disorders, e.g. cancer, gastric ulcer or gastritis.
 XX
 PS Claim 26; Page 102; 127bp; English.
 XX
 CC AAW79677-W79680 are synthetic CS198 derived peptide fragments which are
 CC used in a method to detect the presence of a target human CS198
 CC polynucleotide in a test sample. The CS198 gene is useful as a marker for
 CC gastrointestinal (GI) tract disorders. The methods and products can be
 CC used in detecting, diagnosing, staging, monitoring, prognosticating,
 CC preventing or treating, or determining the predisposition to diseases and
 CC conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
 CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative
 CC colitis, and pancreatitis
 XX
 SQ Sequence 31 AA;
 XX
 Query Match 4.6%; Score 31; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4e-23;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 537 RLKQSSDLERERESVLRQEVAAERRN 567
 DB 1 RLKQSSDLERERESVLRQEVAAERRN 31
 XX
 RESULT 25
 AAE07321
 ID AAE07321 standard; peptide; 31 AA.
 XX
 AC AAE07321;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human CS 198 peptide #2.
 XX
 KW CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
 KW gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
 KW Barrett's oesophagus; gene therapy; drug screening; human.
 XX
 OS Homo sapiens.
 XX
 PN US2001010904-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 30-MAR-1998; 98US-00050516.
 PF 31-MAR-1997; 97US-00828855.
 PR
 XX
 PA (BILL/) BILLINGEL P A.
 PA (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 XX


```

XX US2004043406-A1.
XX
XX PD 04-MAR-2004.
XX
XX 22-AUG-2003; 2003US-00646873.
XX
XX PP 31-MAR-1997; 97US-00828855.
XX PR 30-MAR-1998; 98US-00050516.
XX
PA (BIL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M A.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUSSE/) RUSSELL J C.
PA (STRO/) STROUPE S D.
XX
PI Billengel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden MA, Hodges SC, Klass MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
DR WPI; 2004-313754/29.
XX
PT Diagnosing diseases such as cancer of the gastrointestinal tract, by
PT detecting aberrant expression or activity of the CS198 polypeptide, and
PT associated treatment methods.
XX
PS Claim 17; SEQ ID NO 44; 67pp; English.
XX
CC The invention relates to reagents and methods for detecting diseases of
CC the gastrointestinal (GI) tract. The method involves detecting the
CC presence of target CS198 polynucleotide in the test sample. The methods
CC and compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the CS198 polypeptide, such as cancer
CC of the gastrointestinal tract. These are also useful in gene therapy. The
CC present sequence is a CS198 peptide used to illustrate the method of the
CC invention.
CC
SQ Sequence 31 AA;
Query Match 4.6%; Score 31; DB #: Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-23; Indels 0; Gaps 0
Matches 31; Conservative 0; Mismatches 0;
QY 537 RLKSGSSDDLRRERSVLRBOEVAAEEERN 567
| | | | | | | | | | | | | | | | | | | | |
Db 1 RLKSGSSDDLRRERSVLRBOEVAAEEERN 31
RESULT 28
AAW79680
ID AAW79680 standard; protein; 33 AA.
XX
XX AC AAW79680;
XX
XX DT 11-JAN-1999 (first entry)
XX
XX DE Synthetic CS198 derived peptide #4.
XX
XX KW Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
KW human; predisposition; treatment; Barrett's esophagus; gastric ulcer;
KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
KW pancreatitis.
XX
OS Synthetic.
```

XX		PN	WO9844159-A1.	
XX		PD	08-OCT-1998.	
XX		PF	30-MAR-1998;	98MO-US006251.
XX		PR	31-MAR-1997;	97US-00828855.
XX		PA	(ABBO) ABBOTT LAB.	
XX		P1	Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,	
XX		P1	Grenados EN, Hayden M, Hodges SC, Kloss MR, Kratochvil JD;	
XX		P1	Roberts-Rapp L, Russell JC, Stroupe SD;	
XX		DR	WPI; 1998-542714/46.	
XX		PT	New gastrointestinal polynucleotides, CS198, and their detection - used	
XX		PT	for developing products for the diagnosis and treatment of	
XX		PT	gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.	
XX		PS	Claim 26; Page 103; 127pp; English.	
XX		CC	AAW79677-W79680 are synthetic CS198 derived peptide fragments which are	
XX		CC	used in a method to detect the presence of a target human CS198	
XX		CC	polynucleotide in a test sample. The CS198 gene is useful as a marker for	
XX		CC	gastrointestinal (GI) tract disorders. The methods and products can be	
XX		CC	used in detecting, diagnosing, staging, monitoring, prognosticating,	
XX		CC	preventing or treating, or determining the predisposition to diseases and	
XX		CC	conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,	
XX		CC	gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative	
XX		CC	colitis, and pancreatitis	
XX		SQ	Sequence 33 AA;	
OY		Query Match	4.4%; Score 30; DB 2; Length 33;	
Dd		Best Local Similarity	100.0%; Pred. No. 4,4e-22;	
		Matches	30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
			624 VDSAPPGQRKKEOWYAGINPDSGINSEVLE 653 4 VDSAPPGQRKKEOWYAGINPDSGINSEVLE 33	
RESULT 29				
AAE07323		ID	AAE07323 standard; peptide; 33 AA.	
XX		AC	AAE07323;	
XX		DT	06-NOV-2001 (first entry)	
XX		DE	Human CS 198 peptide #4.	
XX		CS	CS 198: gastrointestinal tract disease; GI tract; cancer; gastric ulcer;	
KM		gastritis; Crohn's disease; ulcerative colitis; pancreatitis;		
XX		Barrett's oesophagus; gene therapy; drug screening; human.		
OS		Homo sapiens.		
XX		PN	US2001010904-A1.	
XX		PD	02-AUG-2001.	
XX		PF	30-MAR-1998;	98US-00050516.
XX		PR	31-MAR-1997;	97US-00828855.
XX		PA	(BILL/) BILLINGEL P A.	
XX		PA	(COHE/) COHEN M.	
XX		PA	(COLP/) COLPITTS T L.	
XX		PA	(FRIE/) FRIEDMAN P N.	
XX		PA	(GORD/) GORDON J.	

EN US2004043406-A1.
 XX
 PD 04-MAR-2004.
 XX
 PF 22-AUG-2003; 2003US-00646873.
 XX
 PR 31-MAR-1997; 97US-00828855.
 PR 30-MAR-1998; 98US-00050516.
 XX
 PA (BILL/) BILLINGEL P A.
 PA (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HAYD/) HAYDEN M A.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUSSE/) RUSSELL J C.
 PA (STRO/) STROUPE S D.
 XX
 PI Billengel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI; 2004-313754/29.
 XX
 PT Diagnosing diseases such as cancer of the gastrointestinal tract, by
 PT detecting aberrant expression or activity of the CS198 polypeptide, and
 PT associated treatment methods.
 XX
 PS Claim 17; SEQ ID NO 46; 67pp; English.
 XX
 CC The invention relates to reagents and methods for detecting diseases of
 CC the gastrointestinal (GI) tract. The method involves detecting the
 CC presence of target CS198 polynucleotide in the test sample. The methods
 CC and compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of diseases or conditions associated with
 CC aberrant expression or activity of the CS198 polypeptide, such as cancer
 CC of the gastrointestinal tract. These are also useful in gene therapy. The
 CC present sequence is a CS198 peptide used to illustrate the method of the
 CC invention.
 CC
 SQ Sequence 33 AA;
 Query Match 4.4%; Score 30; DB 8; Length 33;
 Best Local Similarity 100.0%; Pred. No. 4.4e-22;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 624 VDSAPGQRKKEQWYAGINPSDGINSEVLE 653
 DB 4 VDSAPGQRKKEQWYAGINPSDGINSEVLE 33

Search completed: March 3, 2006, 14:24:32
 Job time : 249.321 secs

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(order)

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OM protein - protein search, using sw model

Run on: March 3, 2006, 14:24:52 ; Search time 39.4944 Seconds
(without alignments)
1654.188 Million cell updates/sec

Title: US-10-646-873-42

Perfect score: 679
Sequence: 1 MDRVTRYPILGIPQAHRTG.....HKNAARWESRIYASEDD 679

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 283416 seqs, 9621673 residues

Word size: 20

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	679	100.0	679	2 T00636	hypothetical prote

ALIGNMENTS

RESULT 1
T00636
hypothetical protein F21856_2 - human
C/Species: Homo sapiens (man)
C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C/Accession: T00636
R/Lamerdin, J.E.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhardt-Schultz, K.; Grgescu, A.; Avila, J.; Liu, S.; Bruce, R.; Quan, G.; Montgomery, M.; Ow, D.; Nolan, M.; submitted to the EMBL Data Library, January 1998
A/Description: Sequence analysis of a 3.5 kb contig in 19p13.3 between CDC34 and D19S342
A/Reference number: Z14195
A/Accession: T00636
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-679 <LM>
A/Cross-references: UNIPROT:Q81VT2; UNIPARC:UP100000745CD; EMBL:AC004030; NID:g2804590;
C/Genetic:
A/Map position: 19p13.3
A/Intons: 594/1; 637/3; 650/3
A/Note: F21856_2

Query Match 100.0%; Score 679; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 0;

Matches	679; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	1 MDRVTRYPILGIPQAHRTGTVLVDGTSYTHVLCMGPEASGMQDPEQPTDHRAGQ				60
DB	1 MDRVTRYPILGIPQAHRTGTVLVDGTSYTHVLCMGPEASGMQDPEQPTDHRAGQ				60
QY	61 VORQGVSYVAHYVQSPRGLHSENEDEMGQVYRLGARDAHQGRPTWALRPDEGDK				120
DB	61 VORQGVSYVAHYVQSPRGLHSENEDEMGQVYRLGARDAHQGRPTWALRPDEGDK				120
QY	121 MKTYRLDAGDAPRLCDLEERNAVIQGAVRKSTVAITQCTPDHCDPTTPGPSTP				180
DB	121 MKTYRLDAGDAPRLCDLEERNAVIQGAVRKSTVAITQCTPDHCDPTTPGPSTP				180
QY	181 LEENVVDREQIDFLAARQOFLSLQANKAGHSSPARCTPGCTPGASQAKAFKPHLA				240
DB	181 LEENVVDREQIDFLAARQOFLSLQANKAGHSSPARCTPGCTPGASQAKAFKPHLA				240
QY	241 NGHVPIKPYKGVREENKRAVPTWASVQVDDPGSLASVESPGTPEPIEREIRLA				300
DB	241 NGHVPIKPYKGVREENKRAVPTWASVQVDDPGSLASVESPGTPEPIEREIRLA				300
QY	301 QERADLEORGLRQATDHQELVEIPIRPLITKSLITAPRRGRBELYQORDVQSTQ				360
DB	301 QERADLEORGLRQATDHQELVEIPIRPLITKSLITAPRRGRBELYQORDVQSTQ				360
QY	361 REEDRRRGLHVGRASTPDWSEGPQGLRRALSSTLSPADARADPAPEVKVRI				420
DB	361 REEDRRRGLHVGRASTPDWSEGPQGLRRALSSTLSPADARADPAPEVKVRI				420
QY	421 PPDAYQPLSPCTPQLEFSAFGAFKPSLSIAEKAATS PKATWSPHLSSESGKPLST				480
DB	421 PPDAYQPLSPCTPQLEFSAFGAFKPSLSIAEKAATS PKATWSPHLSSESGKPLST				480
QY	481 KOEASKPRGCGPOANGVVRMEYFLRLPRAPDEPOQAQVPHVWGEVACAPLRLQK				540
DB	481 KOEASKPRGCGPOANGVVRMEYFLRLPRAPDEPOQAQVPHVWGEVACAPLRLQK				540
QY	541 SOSDILLERERSVTRREQVNAERRNALFPVESPTDENSDONSRSOSAGITGSYS				600
DB	541 SOSDILLERERSVTRREQVNAERRNALFPVESPTDENSDONSRSOSAGITGSYS				600
QY	601 VESPEFSPFIHLSNVAVTDEPVDAPPGQKKEQWYAGINPSDGINSEVLEAIRVTH				660
DB	601 VESPEFSPFIHLSNVAVTDEPVDAPPGQKKEQWYAGINPSDGINSEVLEAIRVTH				660
QY	661 KNMAARWESRIYASEDD 679				
DB	661 KNMAARWESRIYASEDD 679				

Search completed: March 3, 2006, 14:30:52
Job time : 39.4944 secs

OY 601 VSESPFSPHSHNVATVEDPYDSAPPQGRKKQWYAGINPSDGINSEVLEAIRVTRH 660
 |||||
 DB 601 VSESPFSPHSHNVATVEDPYDSAPPQGRKKQWYAGINPSDGINSEVLEAIRVTRH 660
 |||||

OY 661 KNAMERWESRIYASEEDD 679
 |||||
 DB 661 KNAMERWESRIYASEEDD 679
 |||||

RESULT 2

CS021_PONPY STANDARD; PRT; 685 AA.
 ID CS021_PONPY
 AC OSRBH3;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Protein C19orf21 homolog.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Kidney;
 RG The German cDNA consortium;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.

CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----

CC -----
 CC EMBL; CR858675; CAH90887.1; -; mRNA.
 DR Coiled coil.
 KW COILED
 FT 551 575 Potential.
 SQ SEQUENCE 685 AA; 75892 MM; A3A99FA343396E81 CRC64;

Query Match 7.1%; Score 48; DB 1; Length 685;
 Best Local Similarity 100.0%; Pred. No. 1.Se-40;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 511 FRAPDEPQQAQVPHYWGWEVAGAPALRLQKSSQSDLERERESVLRRE 558
 |||||
 DB 517 FRAPDEPQQAQVPHYWGWEVAGAPALRLQKSSQSDLERERESVLRRE 564
 |||||

Search completed: March 3, 2006, 14:29:55
 Job time : 243.523 secs

GenCore version 5.1.7
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OW protein - protein search, using sw model

Run on: March 3, 2006, 14:30:17 ; Search time 50.1275 Seconds
(without alignments)
119.880 Million cell updates/sec

Title: US-10-646-873-42

Sequence: 1 MDRVTRYPILGIPQAHKGTG.....HKNAABERESRIYASEDD 679

Scoring table: Orligo
Gapop 60.0, Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size: 20

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database: Issued Patents, AA:*

1: /cgn2_6/ptodata/1/1aa/5-COMB.pep:.*
2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:.*
3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:.*
4: /cgn2_6/ptodata/1/1aa/BCTUS-COMB.pep:.*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:.*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	679	100.0	679	2	US-09-050-516-42
2	679	100.0	679	2	US-10-278-547-42
3	215	31.7	215	2	US-09-050-516-47
4	215	31.7	215	2	US-10-278-547-47
5	36	5.3	36	2	US-09-050-516-43
6	36	5.3	36	2	US-10-278-547-43
7	35	5.2	35	2	US-09-050-516-45
8	35	5.2	35	2	US-10-278-547-45
9	31	4.6	31	2	US-09-050-516-44
10	31	4.6	31	2	US-10-278-547-44
11	30	4.4	30	2	US-09-050-516-46
12	30	4.4	30	2	US-10-278-547-46

ALIGNMENTS

RESULT 1
US-09-050-516-42
; Sequence 42, Application US/09050516
; Patent No. 6627414
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN

QY	1	MDRVTRYPILGIPQAHKGTGVLDDGTSYTHLVCMGPASGMDPEPTWPTDHRACQG	60
DB	1	MDRVTRYPILGIPQAHKGTGVLDDGTSYTHLVCMGPASGMDPEPTWPTDHRACQG	60
QY	61	VOROGVSVAHYTQSPRGLHSNREDEGMQVTRLGARDAHQRPWALPDEGEXE	120
DB	61	VOROGVSVAHYTQSPRGLHSNREDEGMQVTRLGARDAHQRPWALPDEGEXE	120
QY	121	MKTIRLDAGDADPRRLCDLERRRMAVIOGAVERKSTVATLQGTDPHGPRTPGPRSTP	180
DB	121	MKTIRLDAGDADPRRLCDLERRRMAVIOGAVERKSTVATLQGTDPHGPRTPGPRSTP	180
QY	181	LEENVDREQIDFLAARQOFLSLQANKGAPHSPPAGTTPGASQAPRAFNKPHLA	240
DB	181	LEENVDREQIDFLAARQOFLSLQANKGAPHSPPAGTTPGASQAPRAFNKPHLA	240
QY	241	NGHVPIKQVGVVBEENKRAVPTWASVQVVDPGSLASVESPETPTETIEREIRLA	300
DB	241	NGHVPIKQVGVVBEENKRAVPTWASVQVVDPGSLASVESPETPTETIEREIRLA	300
QY	301	QERBARDREORGLRQATDHQELVEIPTRPLTKLSLITAPRERKRPSTLYVQRDVIQETQ	360

|||||
Db 301 QERADLRREGGLARQATDHQELVEIFRPLITTKLSLITAPRRERGRPSLYVQRDIYQETQ 360
|||
Qy 361 REEDHRRREGGLHVGASTPDWVSEGPQGLRRALSSDLSLSPADPARADPAPEVRKNRI 420
|||
Db 361 REEDHRRREGGLHVGASTPDWVSEGPQGLRRALSSDLSLSPADPARADPAPEVRKNRI 420
|||
Qy 421 PPDAVQPYLSPTGTPQLEFSARFAGKGSLSSTAARAKATSPKATWSPRHLSSESGKPLST 480
|||
Db 421 PPDAVQPYLSPTGTPQLEFSARFAGKGSLSSTAARAKATSPKATWSPRHLSSESGKPLST 480
|||
Qy 481 KOEASKEPRGCPQANRGVWMEYFRLRLPLRFAPDEPQQAQVPHVGMWEVAGAPALRLQK 540
|||
Db 481 KOEASKEPRGCPQANRGVWMEYFRLRLPLRFAPDEPQQAQVPHVGMWEVAGAPALRLQK 540
|||
Qy 541 SOSDDLLEERESVLRREQEVAERRNALPPEVSPPTPDNSDONSSSSQASGITGSYS 600
|||
Db 541 SOSDDLLEERESVLRREQEVAERRNALPPEVSPPTPDNSDONSSSSQASGITGSYS 600
|||
Qy 601 VSESPPFSPIHLHSNVAWTEVDVDSAPPGQRKKEQWYAGINPSDGINSEVLRAIRVTRH 660
|||
Db 601 VSESPPFSPIHLHSNVAWTEVDVDSAPPGQRKKEQWYAGINPSDGINSEVLRAIRVTRH 660
|||
Qy 661 KNMAERWESRIYASEED 679
|||
Db 661 KNMAERWESRIYASEED 679
|||

RESULT 2

US-10-278-547-42
; Sequence 42, Application US/10278547
; Patent No. 6660834

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITTS, TRACEY L.

FRIEDMAN, PAULA N.

GORDON, JULIAN

GRANDOS, EDWARD N.

HAYDEN, MARK

HODGES, STEVEN C.

KLASS, MICHAEL R.

KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547

FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065,US,PI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
; ;
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO: 6660834e
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-278-547-42

Query Match 100.0%; Score 679; DB 2; Length 679;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDRVTRYPILGIPQAHRTGLVLDGDTSYTHLVCKGPEASGWDPEQPTPTDRAQOG 60
|||
Db 1 MDRVTRYPILGIPQAHRTGLVLDGDTSYTHLVCKGPEASGWDPEQPTPTDRAQOG 60
|||
Qy 61 VQRQGVSYSHAYTQQSPRGLSENREDEGMQVYRLGADDAHQGRPTALRPDEGDKE 120
|||
Db 61 VQRQGVSYSHAYTQQSPRGLSENREDEGMQVYRLGADDAHQGRPTALRPDEGDKE 120
|||
Qy 121 MKTYRLDAGDADPRRLCDLERERNAVIOGOAVKSSVTATLOGTPPHGDPRTPGPRSTP 180
|||
Db 121 MKTYRLDAGDADPRRLCDLERERNAVIOGOAVKSSVTATLOGTPPHGDPRTPGPRSTP 180
|||
Qy 181 LLENVVDREQIDFLAARQOFLSLEQANKGAPHSSPARGTPTGASQAPKAFNKPHLA 240
|||
Db 181 LLENVVDREQIDFLAARQOFLSLEQANKGAPHSSPARGTPTGASQAPKAFNKPHLA 240
|||
Qy 241 NGHVVPKIPQVKGVARENKRAVPTWASVQVVDDEGSLASVESPGPKETPIEREIRLA 300
|||
Db 241 NGHVVPKIPQVKGVARENKRAVPTWASVQVVDDEGSLASVESPGPKETPIEREIRLA 300
|||
Qy 301 QERADLRREGGLARQATDHQELVEIFRPLITTKLSLITAPRRERGRPSLYVQRDIYQETQ 360
|||
Db 301 QERADLRREGGLARQATDHQELVEIFRPLITTKLSLITAPRRERGRPSLYVQRDIYQETQ 360
|||
Qy 361 REEDHRRREGGLHVGASTPDWVSEGPQGLRRALSSDLSLSPADPARADPAPEVRKNRI 420
|||
Db 361 REEDHRRREGGLHVGASTPDWVSEGPQGLRRALSSDLSLSPADPARADPAPEVRKNRI 420
|||
Qy 421 PPDAVQPYLSPTGTPQLEFSARFAGKGSLSSTAARAKATSPKATWSPRHLSSESGKPLST 480
|||
Db 421 PPDAVQPYLSPTGTPQLEFSARFAGKGSLSSTAARAKATSPKATWSPRHLSSESGKPLST 480
|||
Qy 481 KOEASKEPRGCPQANRGVWMEYFRLRLPLRFAPDEPQQAQVPHVGMWEVAGAPALRLQK 540
|||
Db 481 KOEASKEPRGCPQANRGVWMEYFRLRLPLRFAPDEPQQAQVPHVGMWEVAGAPALRLQK 540
|||
Qy 541 SOSDDLLEERESVLRREQEVAERRNALPPEVSPPTPDNSDONSSSSQASGITGSYS 600
|||
Db 541 SOSDDLLEERESVLRREQEVAERRNALPPEVSPPTPDNSDONSSSSQASGITGSYS 600
|||
Qy 601 VSESPPFSPIHLHSNVAWTEVDVDSAPPGQRKKEQWYAGINPSDGINSEVLRAIRVTRH 660
|||
Db 601 VSESPPFSPIHLHSNVAWTEVDVDSAPPGQRKKEQWYAGINPSDGINSEVLRAIRVTRH 660
|||
Qy 661 KNMAERWESRIYASEED 679
|||
Db 661 KNMAERWESRIYASEED 679
|||

RESULT 3

US-09-050-516-47

; Sequence 47, Application US/09050516

; Patent No. 6627414

; GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KATTOCHVIL, JON D.
APPLICANT: KRATOVICH, LISA
APPLICANT: ROBERTS-RAP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-47

Query Match 31.7%; Score 215; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 2e-204; Indels 0; Gaps 0;
Matches 215; Conservative 0; Mismatches 0;

QY 465 MSPRHLSESGKPLSTKQASKEPPRCQPOANRGVWMEYFRLPLFRAPDEPQOAVPH 524
DB 1 MSRRHLSESGKPLSTKQASKEPPRCQPOANRGVWMEYFRLPLFRAPDEPQOAVPH 60
QY 525 VMGWVAGAPALRLQKSSDILLERRESVLRREQVAEERRNALPPEVFSPTPDNSDQ 584
DB 61 VMGWVAGAPALRLQKSSDILLERRESVLRREQVAEERRNALPPEVFSPTPDNSDQ 120
QY 585 NSRSSQASGITGSYSVSESPFPIHLHSNVAMTVEDPVDASAPGQKKEQYAGINPS 644
DB 121 NSRSSQASGITGSYSVSESPFPIHLHSNVAMTVEDPVDASAPGQKKEQYAGINPS 180
QY 645 DGINSEVLEAIRVTRHKNAMAMERESRIYASEED 679
DB 181 DGINSEVLEAIRVTRHKNAMAMERESRIYASEED 215

RESULT 4

US-10-278-547-47
Sequence 47, Application US/10278547
Patent No. 660834
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOVICH, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-278-547-47

Query Match 31.7%; Score 215; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 2e-204; Indels 0; Gaps 0;
Matches 215; Conservative 0; Mismatches 0;

QY 465 MSPRHLSESGKPLSTKQASKEPPRCQPOANRGVWMEYFRLPLFRAPDEPQOAVPH 524
DB 1 MSRRHLSESGKPLSTKQASKEPPRCQPOANRGVWMEYFRLPLFRAPDEPQOAVPH 60
QY 525 VMGWVAGAPALRLQKSSDILLERRESVLRREQVAEERRNALPPEVFSPTPDNSDQ 584
DB 61 VMGWVAGAPALRLQKSSDILLERRESVLRREQVAEERRNALPPEVFSPTPDNSDQ 120
QY 585 NSRSSQASGITGSYSVSESPFPIHLHSNVAMTVEDPVDASAPGQKKEQYAGINPS 644
DB 121 NSRSSQASGITGSYSVSESPFPIHLHSNVAMTVEDPVDASAPGQKKEQYAGINPS 180

Oy 645 DGINSEVLEAIRVTRHKNAAMERMSRIYASEDD 679
Db 181 DGINSEVLEAIRVTRHKNAAMERMSRIYASEDD 215

RESULT 5

US-09-050-516-43
; Sequence 43, Application US/09050516
; Patent No. 6627414
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HAYDEN, MARK
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLAS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
; TITLE OF INVENTION: TRACT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/050.516
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,855
; FILING DATE: 31-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6065.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6627414e
; US-09-050-516-43

Query Match 5.3%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.8e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 465 MSPRLSSSGKPLSTKQZASKPRGCGPOANGVVR 500
Db 1 MSPRLSSSGKPLSTKQZASKPRGCGPOANGVVR 36

RESULT 6

US-10-278-547-43
; Sequence 43, Application US/10278547
; Patent No. 6660834
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HAYDEN, MARK
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLAS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
; TITLE OF INVENTION: TRACT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,547
; FILING DATE: 23-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/050.516
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/828,855
; FILING DATE: 31-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6065.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6660834e
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-278-547-43

Query Match 5.3%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.8e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 465 MSPRLSSSGKPLSTKQZASKPRGCGPOANGVVR 500
Db 1 MSPRLSSSGKPLSTKQZASKPRGCGPOANGVVR 36

RESULT 7

US-09-050-516-45
; Sequence 45, Application US/09050516
; Patent No. 6627414
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE

APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-45

Query Match 5.2%; Score 35; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.5e-27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 568 ALPPEVFSPTPDNSDNRSSSQASGITGSYSVS 602
DB 1 ALPPEVFSPTPDNSDNRSSSQASGITGSYSVS 35

RESULT 8
US-10-278-547-45
Sequence 45, Application US/10278547
Patent No. 6660834
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.

KLAAS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-278-547-45

Query Match 5.2%; Score 35; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.5e-27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 568 ALPPEVFSPTPDNSDNRSSSQASGITGSYSVS 602
DB 1 ALPPEVFSPTPDNSDNRSSSQASGITGSYSVS 35

RESULT 9
US-09-050-516-44
Sequence 44, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLAAS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-44

Query Match 4.6%; Score 31; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.3e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 537 RLOKQSSDLERERESVLRROEVAERRN 567
Db 1 RLOKQSSDLERERESVLRROEVAERRN 31

RESULT 10
US-10-278-547-44
Sequence 44, Application US/10278547
Patent No. 6660834
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLAAS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA

ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-OCT-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-278-547-44

Query Match 4.6%; Score 31; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.3e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 537 RLOKQSSDLERERESVLRROEVAERRN 567
Db 1 RLOKQSSDLERERESVLRROEVAERRN 31

RESULT 11
US-09-050-516-46
Sequence 46, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-46

Query Match      4.4% Score 30; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.5e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      624 VDSAPPGQRKKEQWYAGINPSDGINSEVLE 653
DB      4 VDSAPPGQRKKEQWYAGINPSDGINSEVLE 33

RESULT 12
US-10-278-547-46
Sequence 46, Application US/10278547
Patent No. 6660834
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KODGES, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516

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FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-278-547-46

Query Match      4.4% Score 30; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.5e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      624 VDSAPPGQRKKEQWYAGINPSDGINSEVLE 653
DB      4 VDSAPPGQRKKEQWYAGINPSDGINSEVLE 33

Search completed: March 3, 2006, 14:32:04
Job time : 50.1275 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 14:45:41 ; Search time 186.079 Seconds
(without alignments)
1524.651 Million cell updates/sec

Title: US-10-646-873-42

Sequence: 1 MDRVTRYPLIGIPQAHRTG.....HNMAERWESRIYASEDD 679

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size: 20

Total number of hits satisfying chosen parameters: 21

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database: Published Applications AA.Main:*

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- 2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep.*
- 6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	679	100.0	679	3	US-09-050-516-42 Sequence 42, Appl
2	679	100.0	679	4	US-10-278-547-42 Sequence 42, Appl
3	679	100.0	679	4	US-10-646-873-42 Sequence 42, Appl
4	215	31.7	215	3	US-09-050-516-47 Sequence 47, Appl
5	215	31.7	215	4	US-10-278-547-47 Sequence 47, Appl
6	215	31.7	215	4	US-10-646-873-47 Sequence 47, Appl
7	60	8.8	172	4	US-10-106-698-4761 Sequence 4761, Ap
8	43	6.3	43	4	US-10-029-386-33676 Sequence 33676, A
9	38	5.6	57	4	US-10-106-698-5845 Sequence 5845, Ap
10	36	5.3	36	3	US-09-050-516-43 Sequence 43, Appl
11	36	5.3	36	4	US-10-278-547-43 Sequence 43, Appl
12	36	5.3	36	4	US-10-646-873-43 Sequence 43, Appl
13	35	5.2	35	3	US-09-050-516-45 Sequence 45, Appl
14	35	5.2	35	4	US-10-278-547-45 Sequence 45, Appl
15	35	5.2	35	4	US-10-646-873-45 Sequence 45, Appl
16	31	4.6	31	3	US-09-050-516-44 Sequence 44, Appl
17	31	4.6	31	4	US-10-278-547-44 Sequence 44, Appl
18	31	4.6	31	4	US-10-646-873-44 Sequence 44, Appl
19	30	4.4	33	3	US-09-050-516-46 Sequence 46, Appl
20	30	4.4	33	4	US-10-278-547-46 Sequence 46, Appl
21	30	4.4	33	4	US-10-646-873-46 Sequence 46, Appl

ALIGNMENTS

RESULT 1

US-09-050-516-42	
Sequence 42, Application US/09050516	
Patent No. US20010010904A1	
GENERAL INFORMATION:	
APPLICANT: BILLING-MEDEL, PATRICIA	
APPLICANT: COHEN, MAURICE	
APPLICANT: COLPITTS, TRACEY L.	
APPLICANT: FRIEDMAN, PAULA N.	
APPLICANT: GORDON, JULIAN	
APPLICANT: GRANADOS, EDWARD N.	
APPLICANT: HAYDEN, MARK	
APPLICANT: HODGES, STEVEN C.	
APPLICANT: KLAS, MICHAEL R.	
APPLICANT: KRATOCHVIL, JON D.	
APPLICANT: ROBERTS-RAPP, LISA	
APPLICANT: RUSSELL, JOHN C.	
APPLICANT: STROUPE, STEPHEN D.	
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL	
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL	
TITLE OF INVENTION: TRACT	
NUMBER OF SEQUENCES: 49	
CORRESPONDENCE ADDRESS:	
ADDRESSEE: Abbott Laboratories	
STREET: 100 Abbott Park Road	
CITY: Abbott Park	
STATE: IL	
COUNTRY: USA	
ZIP: 60064-3500	
COMPUTER READABLE FORM:	
MEDIUM TYPE: Diskette	
COMPUTER: IBM Compatible	
OPERATING SYSTEM: DOS	
SOFTWARE: FASTSEQ for Windows Version 2.0	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/09/050,516	
FILING DATE:	
CLASSIFICATION:	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: 08/828,855	
FILING DATE: 31-MAR-1997	
ATTORNEY/AGENT INFORMATION:	
NAME: Becker, Cheryl L.	
REGISTRATION NUMBER: 35,441	
REFERENCE/DOCKET NUMBER: 6065.US.P1	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: 847/935-1729	
TELEFAX: 847/938-2623	
TELEX:	
INFORMATION FOR SEQ ID NO: 42:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 679 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: NO. US20010010904A1e	
US-09-050-516-42	
Query Match	
Best Local Similarity 100.0%; Score 679; DB 3; Length 679;	
Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MDRVTRYPLIGIPQAHRTGTLVDGTSYTHLVCKGPFASGQDEPQTPDHRQAQG 60
DB	1 MDRVTRYPLIGIPQAHRTGTLVDGTSYTHLVCKGPFASGQDEPQTPDHRQAQG 60
QY	61 VORQGVSYVHATGQSPRGHSENRDEGMQVRLGARDHOGSPYALRPEDQEDKE 120
DB	61 VORQGVSYVHATGQSPRGHSENRDEGMQVRLGARDHOGSPYALRPEDQEDKE 120
QY	121 MKTYRLADADPRLCDLERERWAVIQGAARKSSTVATLQGTDPHGDPRTPGPRSTP 180
DB	121 MKTYRLADADPRLCDLERERWAVIQGAARKSSTVATLQGTDPHGDPRTPGPRSTP 180

181 LEENVNDEQIDFLAARQOFLSLEQANKGAPHSPPAGTTPGASQAAPKAKPHLA 240
181 LEENVNDEQIDFLAARQOFLSLEQANKGAPHSPPAGTTPGASQAAPKAKPHLA 240
241 NGHVPIKPOYKGVREENVKRAVPTWASVOVDDPGSLASVESPGTPEKPIEREIRLA 300
241 NGHVPIKPOYKGVREENVKRAVPTWASVOVDDPGSLASVESPGTPEKPIEREIRLA 300
301 QERADLREORGLRQATDHQELVEIPTRPLITKLSLITAPRRERGRPSLYQORDIVQETO 360
301 QERADLREORGLRQATDHQELVEIPTRPLITKLSLITAPRRERGRPSLYQORDIVQETO 360
361 REEDHRRREGLVHGRASSTPDWVSEGPQGLRRALSSDSITLSPAPARADPAPEVKVNR 420
361 REEDHRRREGLVHGRASSTPDWVSEGPQGLRRALSSDSITLSPAPARADPAPEVKVNR 420
421 PPDAVQPYLSPTQPLEFSAFGAFGKPSLSLTAEKAAATSPKATWSPRHLSSESGKPLST 480
421 PPDAVQPYLSPTQPLEFSAFGAFGKPSLSLTAEKAAATSPKATWSPRHLSSESGKPLST 480
481 KOEASKPRGCGPOANRGVVRWEYFRLRLRPRADPEQQAQVPHVGMWVAGAPALRLQK 540
481 KOEASKPRGCGPOANRGVVRWEYFRLRLRPRADPEQQAQVPHVGMWVAGAPALRLQK 540
541 SOSDLERERESVLRREQVVAERRNALPPEVSPPTDENSDQNSRSSQASGITGSYS 600
541 SOSDLERERESVLRREQVVAERRNALPPEVSPPTDENSDQNSRSSQASGITGSYS 600
601 VSESPFSPILHLSNVATVEDPVDSAPPGQKKEQWYAGINPSDGINSEVLBAIRVTRH 660
601 VSESPFSPILHLSNVATVEDPVDSAPPGQKKEQWYAGINPSDGINSEVLBAIRVTRH 660
661 KNAAMERESRITYASEDD 679
661 KNAAMERESRITYASEDD 679

RESULT 2

US-10-278-547-42
Sequence 42, Application US/10278547
Publication No. US20030082619A1

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITTS, TRACEY L.

FRIEDMAN, PAULA N.

GORDON, JULIAN

GRANADOS, EDWARD N.

HAYDEN, MARK

HODGES, STEVEN C.

KLAAS, MICHAEL R.

KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSER: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ FOR Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547

FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065, US, P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-278-547-42

Query Match 100.0%; Score 679; DB 4; Length 679;

Best Local Similarly 100.0%; Pred. No. 0;

Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MDRVTRPIIGIPQAHKGTGLVDGRTSYTHYLCKMPBASGMQDDEPOTWTHRAQOG 60
61 VORQGVSYVHAATGQSPRGHLSENNEDGQVYRLGABDAHQGRPTWALRPEGDKE 120
61 VORQGVSYVHAATGQSPRGHLSENNEDGQVYRLGABDAHQGRPTWALRPEGDKE 120
121 MCTYRLDAGDADPRRLCDLREKRAVYIQQAIVKSSVTATLQCTPDGDDRTPGPPSTP 180
121 MCTYRLDAGDADPRRLCDLREKRAVYIQQAIVKSSVTATLQCTPDGDDRTPGPPSTP 180
181 LEENVNDEQIDFLAARQOFLSLEQANKGAPHSPPAGTTPGASQAAPKAKPHLA 240
181 LEENVNDEQIDFLAARQOFLSLEQANKGAPHSPPAGTTPGASQAAPKAKPHLA 240
241 NGHVPIKPOYKGVREENVKRAVPTWASVOVDDPGSLASVESPGTPEKPIEREIRLA 300
241 NGHVPIKPOYKGVREENVKRAVPTWASVOVDDPGSLASVESPGTPEKPIEREIRLA 300
301 QERADLREORGLRQATDHQELVEIPTRPLITKLSLITAPRRERGRPSLYQORDIVQETO 360
301 QERADLREORGLRQATDHQELVEIPTRPLITKLSLITAPRRERGRPSLYQORDIVQETO 360
361 REEDHRRREGLVHGRASSTPDWVSEGPQGLRRALSSDSITLSPAPARADPAPEVKVNR 420
361 REEDHRRREGLVHGRASSTPDWVSEGPQGLRRALSSDSITLSPAPARADPAPEVKVNR 420
421 PPDAVQPYLSPTQPLEFSAFGAFGKPSLSLTAEKAAATSPKATWSPRHLSSESGKPLST 480
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481 KOEASKPRGCGPOANRGVVRWEYFRLRLRPRADPEQQAQVPHVGMWVAGAPALRLQK 540
541 SOSDLERERESVLRREQVVAERRNALPPEVSPPTDENSDQNSRSSQASGITGSYS 600
541 SOSDLERERESVLRREQVVAERRNALPPEVSPPTDENSDQNSRSSQASGITGSYS 600
601 VSESPFSPILHLSNVATVEDPVDSAPPGQKKEQWYAGINPSDGINSEVLBAIRVTRH 660
601 VSESPFSPILHLSNVATVEDPVDSAPPGQKKEQWYAGINPSDGINSEVLBAIRVTRH 660
661 KNAAMERESRITYASEDD 679
661 KNAAMERESRITYASEDD 679

RESULT 3
US-10-646-873-42
Sequence 42, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-646-873-42
Query Match 100.0%; Score 679; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 MDRVTYPIIGIQAARGTGLVLDGPTSYTHLVCMGRPSSGSGDEPOTWPTDRAAQQG 60
DB 1 MDRVTYPIIGIQAARGTGLVLDGPTSYTHLVCMGRPSSGSGDEPOTWPTDRAAQQG 60
QY 61 VORQGVSYVHAYTGOESPRLGHSNREDEGMQVYRLGADAHQGRPTWALRDEDEDEDE 120
DB 61 VORQGVSYVHAYTGOESPRLGHSNREDEGMQVYRLGADAHQGRPTWALRDEDEDEDE 120
QY 121 MKTYRLDAGDADPRRLCDLERRERMAVYIQGAVRKSSTVATLQGTDPHGDRTPGPRSTP 180

DB 121 MKTYRLDAGDADPRRLCDLERRERMAVYIQGAVRKSSTVATLQGTDPHGDRTPGPRSTP 180
QY 181 LEENVVDREQIDFLAARQQLSLSEQANKGAPHSPPANGTTPGASQAPKANKPHLA 240
DB 181 LEENVVDREQIDFLAARQQLSLSEQANKGAPHSPPANGTTPGASQAPKANKPHLA 240
QY 241 NGHVVPFKPVQKGVVRENNKRAVPTVASVOVNDPSGLASVESPGTPKEPIREIRLA 300
DB 241 NGHVVPFKPVQKGVVRENNKRAVPTVASVOVNDPSGLASVESPGTPKEPIREIRLA 300
QY 301 QERADLREQRGLRQATDHQELVEIPTRPLTKLSLITAPRRERGRPSLYVQORDIYVETQ 360
DB 301 QERADLREQRGLRQATDHQELVEIPTRPLTKLSLITAPRRERGRPSLYVQORDIYVETQ 360
QY 361 REEDHRRRGLHVGASTPDWVSEGPQGLRALSSDSLSPAPDARAADPAPEVRKVRRI 420
DB 361 REEDHRRRGLHVGASTPDWVSEGPQGLRALSSDSLSPAPDARAADPAPEVRKVRRI 420
QY 421 PPDAVQPLSLSTGTOLEFSARFAGKPSLSLTAEXKATSPKATMSPPHLSSESGKPLST 480
DB 421 PPDAVQPLSLSTGTOLEFSARFAGKPSLSLTAEXKATSPKATMSPPHLSSESGKPLST 480
QY 481 KOEASKPRGCGPOANRGVVRWEYFRLRLFRAPDEPOQAQVPHVGMVEVAGAPALRLQK 540
DB 481 KOEASKPRGCGPOANRGVVRWEYFRLRLFRAPDEPOQAQVPHVGMVEVAGAPALRLQK 540
QY 541 SOSDDLREBRRESVLRREQVAAEERRNALPFEVSPPTDENSDONSRSSSQASGITGSYS 600
DB 541 SOSDDLREBRRESVLRREQVAAEERRNALPFEVSPPTDENSDONSRSSSQASGITGSYS 600
QY 601 VSESPFSPFIHLSHVATVDDPVDSAPPGQRKKEQWYAGINPSDGINSEVLEALRVTRH 660
DB 601 VSESPFSPFIHLSHVATVDDPVDSAPPGQRKKEQWYAGINPSDGINSEVLEALRVTRH 660
QY 661 KNAMERWESRIYASEEDD 679
DB 661 KNAMERWESRIYASEEDD 679

RESULT 4
US-09-050-516-47
Sequence 47, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSSELL, JOHN C.
STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065, US, P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-47

Query Match 31.7%; Score 215; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 9.8e-194;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 465 MSPRHLSSESGKPLSTQKASKEPRGCPQANRGVWMEYFRLPLRFRADEPQOAVPH 524
Db 1 MSPRHLSSESGKPLSTQKASKEPRGCPQANRGVWMEYFRLPLRFRADEPQOAVPH 60

Qy 525 VMGEVAGAPALRLQKSSDILLERERESVLRREQVAAERRNALLPFEVSPPTDENSQ 584
Db 61 VMGEVAGAPALRLQKSSDILLERERESVLRREQVAAERRNALLPFEVSPPTDENSQ 120

Qy 585 NSRSSQASGITGSYSSESPPFSPILHNSVAMTVEDPVDSAPPGQRKKEQWYAGINPS 644
Db 121 NSRSSQASGITGSYSSESPPFSPILHNSVAMTVEDPVDSAPPGQRKKEQWYAGINPS 180

Qy 645 DGINSEVLEAIRVTRHKNMAERWESRIYASEDD 679
Db 181 DGINSEVLEAIRVTRHKNMAERWESRIYASEDD 215

RESULT 5
US-10-278-547-47
Sequence 47, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065, US, P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-278-547-47

Query Match 31.7%; Score 215; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 9.8e-194;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 465 MSPRHLSSESGKPLSTQKASKEPRGCPQANRGVWMEYFRLPLRFRADEPQOAVPH 524
Db 1 MSPRHLSSESGKPLSTQKASKEPRGCPQANRGVWMEYFRLPLRFRADEPQOAVPH 60

Qy 525 VMGEVAGAPALRLQKSSDILLERERESVLRREQVAAERRNALLPFEVSPPTDENSQ 584
Db 61 VMGEVAGAPALRLQKSSDILLERERESVLRREQVAAERRNALLPFEVSPPTDENSQ 120

Qy 585 NSRSSQASGITGSYSSESPPFSPILHNSVAMTVEDPVDSAPPGQRKKEQWYAGINPS 644
Db 121 NSRSSQASGITGSYSSESPPFSPILHNSVAMTVEDPVDSAPPGQRKKEQWYAGINPS 180

Qy 645 DGINSEVLEAIRVTRHKNMAERWESRIYASEDD 679
Db 181 DGINSEVLEAIRVTRHKNMAERWESRIYASEDD 215

RESULT 6
US-10-646-873-47
Sequence 47, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories

STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASCSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-646-873-47
Query Match
Best Local Similarity 100.0%; Pred. No. 9.8e-194;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 465 MSPRLSSSGKPLSTKQKASKPRGCPQANNGVAVMEYFRPLRFRAPDEPQAAQVNH 524
DB 1 MSPRLSSSGKPLSTKQKASKPRGCPQANNGVAVMEYFRPLRFRAPDEPQAAQVNH 60
QY 525 VVGWEVAGAPALRLQKSSDDLREERESVLRDEQVAERNNALPEVFSPPTDENSQ 584
DB 61 VVGWEVAGAPALRLQKSSDDLREERESVLRDEQVAERNNALPEVFSPPTDENSQ 120
QY 585 NSRSSSQASGITGSYSVSESPFSPPIHLHSNVAMTVEDPVDASAPGQRKKEQMYAGINPS 644
DB 121 NSRSSSQASGITGSYSVSESPFSPPIHLHSNVAMTVEDPVDASAPGQRKKEQMYAGINPS 180
QY 645 DGINSEVLAIKRVTRHKNAERWESRIYASEED 679
DB 181 DGINSEVLAIKRVTRHKNAERWESRIYASEED 215
RESULT 7
US-10-106-698-4761
Sequence 4761, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 4761
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (55)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (116)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-4761
Query Match
Best Local Similarity 100.0%; Pred. No. 9.9e-48;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 563 EERRNALPEVFSPPTDENSQNSRSSQASGITGSYSVSESPFSPPIHLHSNVAMTVED 622
DB 56 EERRNALPEVFSPPTDENSQNSRSSQASGITGSYSVSESPFSPPIHLHSNVAMTVED 115
RESULT 8
US-10-029-386-33676
Sequence 33676, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
FILE REFERENCE: AEOICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33676
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004030.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.42
US-10-029-386-33676
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 595 TNGSYVSESPFSPPIHLHSNVAMTVEDPVDASAPGQRKKEQ 637
DB 1 TNGSYVSESPFSPPIHLHSNVAMTVEDPVDASAPGQRKKEQ 43
RESULT 9
US-10-106-698-5845
Sequence 5845, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 5845
LENGTH: 57
TYPE: PRT
ORGANISM: Homo sapiens
US-10-646-873-42

Query Match 5.6%; Score 38; DB 4; Length 57;
Best Local Similarity 100.0%; Pred. No. 26-27;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 305 ADLREGGLRQATDHOELVEIPTRLTKSLITAPRR 342
Db 1 ADLREGGLRQATDHOELVEIPTRLTKSLITAPRR 38

RESULT 10
US-09-050-516-43

Sequence 43, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

APPLICANT: COHEN, MAURICE

APPLICANT: COLPITTS, TRACEY L.

APPLICANT: FRIEDMAN, PAULA N.

APPLICANT: GORDON, JULIAN

APPLICANT: GRANADOS, EDWARD N.

APPLICANT: HAYDEN, MARK

APPLICANT: HODGES, STEVEN C.

APPLICANT: KLAS, MICHAEL R.

APPLICANT: KRATOCHVIL, JON D.

APPLICANT: ROBERTS-RAPP, LISA

APPLICANT: RUSSELL, JOHN C.

APPLICANT: STROUPE, STEPHEN D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TITLE OF INVENTION: TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065, US, P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-43

Query Match 5.3%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 465 MSPRLSSSGKPLSTKQKSKPPRCGCPQANRGVVR 500
Db 1 MSPRLSSSGKPLSTKQKSKPPRCGCPQANRGVVR 36

RESULT 11
US-10-278-547-43

Sequence 43, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

APPLICANT: COHEN, MAURICE

APPLICANT: COLPITTS, TRACEY L.

APPLICANT: FRIEDMAN, PAULA N.

APPLICANT: GORDON, JULIAN

APPLICANT: GRANADOS, EDWARD N.

APPLICANT: HAYDEN, MARK

APPLICANT: HODGES, STEVEN C.

APPLICANT: KLAS, MICHAEL R.

APPLICANT: KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TITLE OF INVENTION: TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547

FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065, US, P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: No. US20030082619A1e

SEQUENCE DESCRIPTION: SEQ ID NO: 43:

US-10-278-547-43

Query Match 5.3%; Score 36; DB 4; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-25;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 MSPRLSSSGKPLSTKQASKPPRCGCPQANRGVVR 500
DB 1 MSPRLSSSGKPLSTKQASKPPRCGCPQANRGVVR 36

RESULT 12
US-10-646-873-43
Sequence 43, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-646-873-43

Query Match 5.3%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 MSPRLSSSGKPLSTKQASKPPRCGCPQANRGVVR 500
DB 1 MSPRLSSSGKPLSTKQASKPPRCGCPQANRGVVR 36

RESULT 13
US-09-050-516-45
Sequence 45, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20010010904A1e
US-09-050-516-45

Query Match 5.2%; Score 35; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 8.8e-25;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 568 ALPEVFSPTPDNSDNRSSSQASGITGSYSVS 602
DB 1 ALPEVFSPTPDNSDNRSSSQASGITGSYSVS 35

RESULT 14
US-10-278-547-45
Sequence 45, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-278-547-45

Query Match 5.2%; Score 35; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 8.8e-25;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 568 ALPPEVFSPTDENSDONSRRSSSOASGITGSYSVS 602
Db 1 ALPPEVFSPTDENSDONSRRSSSOASGITGSYSVS 35

RESULT 15
US-10-646-873-45
Sequence 45, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK

HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-646-873-45

Query Match 5.2%; Score 35; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 8.8e-25;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 568 ALPPEVFSPTDENSDONSRRSSSOASGITGSYSVS 602
Db 1 ALPPEVFSPTDENSDONSRRSSSOASGITGSYSVS 35

RESULT 16
US-09-050-516-44
Sequence 44, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAFF, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUP, STEPHEN D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20010010904A1e
US-09-050-516-44

Query Match 4.6%; Score 31; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.7e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 RLOKSQSSDLERERESVLRREQEVAERRN 567
DB 1 RLOKSQSSDLERERESVLRREQEVAERRN 31

RESULT 17
US-10-278-547-44
Sequence 44, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL

COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-278-547-44

Query Match 4.6%; Score 31; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.7e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 RLOKSQSSDLERERESVLRREQEVAERRN 567
DB 1 RLOKSQSSDLERERESVLRREQEVAERRN 31

RESULT 18
US-10-646-873-44
Sequence 44, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-646-873-44

Query Match 4.6%; Score 31; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 4,7e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 RLOKSQSSDLRRESEVLRREOFVAEERRN 567
DB 1 RLOKSQSSDLRRESEVLRREOFVAEERRN 31

RESULT 19
US-09-050-516-46
Sequence 46, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-46

Query Match 4.4%; Score 30; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 4,3e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 624 VDSAPGQRKKEQWYAGINPSDGINSEVLE 653
DB 4 VDSAPGQRKKEQWYAGINPSDGINSEVLE 33

RESULT 20
US-10-278-547-46
Sequence 46, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-278-547-46

Query Match 4.4%; Score 30; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 624 VDSAPPGQRKKEQWYAGINPSDGINSEVLE 653
Db 4 VDSAPPGQRKKEQWYAGINPSDGINSEVLE 33

RESULT 21

US-10-646-873-46
Sequence 46, Application US/10646873
Publication No. US20040043406A1

GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL

COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998

APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-646-873-46

Query Match 4.4%; Score 30; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 624 VDSAPPGQRKKEQWYAGINPSDGINSEVLE 653
Db 4 VDSAPPGQRKKEQWYAGINPSDGINSEVLE 33

Search completed: March 3, 2006, 14:50:28
Job time: 187.079 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using SW model

Run on: March 3, 2006, 14:46:31 ; Search time 18.9877 Seconds
(without alignments)
715.215 Million cell updates/sec

Title: US-10-646-873-42

Perfect score: 679
Sequence: 1 MDRVTRYPIIGIPQAHKGTG.....HKMAAEKESRIVASEDD 679

Scoring-table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 135346 seqs, 20000420 residues

Word-size: 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 500 summaries

Database :

- Published Applications AA_New:*
- 1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: March 3, 2006, 14:50:59
Job time : 18.9877 secs

Page Black (uspo)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: March 3, 2006, 13:19:17 ; Search time 19.242 Seconds

(without alignments)
822.038 Million cell updates/sec

Title: US-10-646-873-43

Perfect score: 189
Sequence: 1 MSPRLSSSGKPISTKQKASKPPRCFQANRGVVR 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0
Maximum Match 100%

Listing filter 45 summaries

Database :

A_Geneseq.21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189	100.0	36	2	AAW79677
2	189	100.0	36	4	AAE07320
3	189	100.0	36	6	ADA26380
4	189	100.0	36	8	ADN17173
5	189	100.0	215	2	AAW79681
6	189	100.0	215	4	AAE07324
7	189	100.0	215	6	ADA26384
8	189	100.0	215	8	ADN17177
9	189	100.0	672	4	AAW79574
10	189	100.0	679	2	AAW79676
11	189	100.0	679	4	AAE07319
12	189	100.0	679	6	AAW78590
13	189	100.0	679	8	ADA26379
14	189	100.0	679	7	ADG14341
15	189	100.0	679	8	ADN17172
16	189	100.0	679	8	ADN17172
17	189	100.0	679	8	ADN17172
18	189	100.0	679	8	ADN17172
19	189	100.0	679	8	ADN17172
20	189	100.0	679	8	ADN17172
21	189	100.0	679	8	ADN17172
22	189	100.0	679	8	ADN17172
23	189	100.0	679	8	ADN17172
24	189	100.0	679	8	ADN17172

25	57	30.2	488	7	ADG73027	Adg73027 Pseudomon
26	57	30.2	488	7	ADL12082	Adl12082 Pseudomon
27	56	29.6	1416	4	ABE6066	ABE6066 Drosophila
28	56	29.6	1520	6	ABE30107	ABE30107 Drosophila
29	56	29.6	1543	9	ABE53773	ABE53773 Drosophila
30	55.5	29.4	111	5	ABP64335	ABP64335 Human ORF
31	55.5	29.4	1036	9	ABM95019	ABM95019 M. xanthu
32	55	29.1	112	4	AAE95016	AAE95016 Human pro
33	55	29.1	115	3	AAE45467	AAE45467 Arabidops
34	55	29.1	268	3	AAE49854	AAE49854 Arabidops
35	55	29.1	294	4	ABG15476	ABG15476 Novel hum
36	55	29.1	319	3	AAE19454	AAE19454 Arabidops
37	55	29.1	322	3	AAE49849	AAE49849 Arabidops
38	55	29.1	333	3	AAE49853	AAE49853 Arabidops
39	55	29.1	369	6	ADN15601	ADN15601 A. thalia
40	55	29.1	369	7	ADD31039	ADD31039 Plant yie
41	55	29.1	369	8	AD143795	AD143795 Plant tra
42	55	29.1	369	8	AD001717	AD001717 Thalecres
43	55	29.1	374	8	ADT60504	ADT60504 Plant pol
44	55	29.1	384	3	AAE19453	AAE19453 Arabidops
45	55	29.1	387	3	AAE49848	AAE49848 Arabidops

ALIGNMENTS

RESULT 1
AAW79677 standard; protein; 36 AA.
ID AAW79677

AAW79677;

11-JAN-1999 (first entry)

Synthetic CS198 derived peptide #1.

Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
pancreatitis.

Synthetic.

WO9844159-A1.

08-OCT-1998.

30-MAR-1998; 98WO-US006251.

31-MAR-1997; 97US-00828855.

(ABBO) ABBOTT LAB.

Billing-Medell PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
Granados EN, Hayden M, Hodges SC, Klaus MR, Kratochvil JD;
Roberts-Rapp L, Russell JC, Stroupe SD;

WPI; 1998-542714/46.

New gastrointestinal polynucleotides, CS198, and their detection - used
for developing products for the diagnosis and treatment of
gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.

Claim 26; Page 102; 127pp; English.

AAW79677-W79680 are synthetic CS198 derived peptide fragments which are
used in a method to detect the presence of a target human CS198
polynucleotide in a test sample. The CS198 gene is useful as a marker for
gastrointestinal (GI) tract disorders. The methods and products can be
used in detecting, diagnosing, staging, monitoring, prognosticating,
preventing or treating, or determining the predisposition to diseases and
conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative

CC colitis, and pancreatitis
XX
SQ Sequence 36 AA;
Query Match 100.0%; Score 189; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.1e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSPRHLSSESGKPLSTKQKASKPPRGCPQANRGVVR 36
Db 1 MSPRHLSSESGKPLSTKQKASKPPRGCPQANRGVVR 36
RESULT 2
AAE07320
ID AAE07320 standard; peptide; 36 AA.
XX
AC AAE07320;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human CS 198 peptide #1.
XX
CS CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
KM gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
KM Barrett's oesophagus; gene therapy; drug screening; human.
XX
OS Homo sapiens.
XX
PN US2001010904-A1.
XX
PD 02-AUG-2001.
XX
PF 30-MAR-1998; 98US-00050516.
XX
PR 31-MAR-1997; 97US-00828855.
XX
PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUS/) RUSSELL J C.
PA (STRO/) STROUPE S D.
PI Billinge P A, Cohen M, Colpitta TL, Friedman PN, Gordon J;
PI Granados EN, Hayden M, Hodges SC, Klaas MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 2001-496163/54.
XX
DR Detecting the presence of target CS 198 polynucleotide, useful for
PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
PT contacting test sample with at least one CS 198-specific polynucleotide.
XX
PS Claim 17; Page 51; 68pp; English.
XX
CC The invention relates to a method of detecting the presence of a target
CC CS 198 polynucleotide comprising contacting the test sample with at least
CC one CS 198-specific polynucleotide. The method is useful for detecting
CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
CC treating or determining predisposition to diseases and conditions of the
CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
CC polypeptides are useful as standards or reagents in diagnostic

CC immunoassay, as components or as target sites for various therapies.
CC Antibodies directed against at least one epitope contained within these
CC polypeptides are useful as delivery agents for therapeutic agents, in
CC diagnostic tests and for screening for conditions or diseases associated
CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
CC for the generation of chimeric antibodies for therapeutic use. The CS 198
CC polynucleotide is also useful in gene therapy and drug screening. The
CC method of the invention provides an alternative, non-surgical diagnostic
CC method capable of detecting early stage GI tract disease such as cancer.
CC The present sequence is a peptide derived from human CS 198 polypeptide
CC consensus sequence
XX
SQ Sequence 36 AA;
Query Match 100.0%; Score 189; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.1e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSPRHLSSESGKPLSTKQKASKPPRGCPQANRGVVR 36
Db 1 MSPRHLSSESGKPLSTKQKASKPPRGCPQANRGVVR 36
RESULT 3
ADA26380
ID ADA26380 standard; protein; 36 AA.
XX
AC ADA26380;
XX
DT 20-NOV-2003 (first entry)
XX
DE Synthetic peptide based on CS198 protein #1.
XX
CS CS198; cancer diagnosis; cancer staging; cancer monitoring;
KM cancer prognosticating; cancer prevention; cancer;
KM gastrointestinal tract disorder; gene therapy.
XX
OS Synthetic;
XX
PN US2003082619-A1.
XX
PD 01-MAY-2003.
XX
PF 23-OCT-2002; 2002US-00278547.
XX
PR 31-MAR-1997; 97US-00828855.
XX
PR 30-MAR-1998; 98US-00050516.
XX
PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M A.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUS/) RUSSELL J C.
PA (STRO/) STROUPE S D.
PI Billinge P A, Cohen M, Colpitta TL, Friedman PN, Gordon J;
PI Granados EN, Hayden MA, Hodges SC, Klaas MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 2003-536961/56.
XX
DR Detecting the presence of a target CS198 polynucleotide in a test sample
PT comprises contacting the sample with a CS198 specific polynucleotide and
PT detecting the presence of the target CS198 polynucleotide in the test
PT sample.
XX

PS Claim 17, Page 51, 67pp; English.

XX
 CC The invention describes a method of detecting the presence of a target
 CC CS198 polynucleotide in a test sample. The method comprises contacting
 CC the test sample with at least one CS198 specific polynucleotide or its
 CC complement, and detecting the presence of the target CS198 polynucleotide
 CC in the test sample, where the CS198-specific polynucleotide has at least
 CC 50% identity to a polynucleotide having any of the 27 fully defined
 CC sequences of 34-2894 bp (SI-27) given in the specification, or their
 CC fragments or complements. The composition and methods are useful in
 CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
 CC or determining the predisposition of an individual to, diseases and
 CC conditions of the gastrointestinal tract, e.g. cancer and in gene
 CC therapy. This is the amino acid sequence of a synthetic peptide based on
 CC the predicted human CS198 protein sequence derived from the CS198
 CC consensus sequence shown in seq id 27.

XX
 SQ Sequence 36 AA;

Query Match 100.0%; Score 189; DB 6; Length 36;
 Best Local Similarity 100.0%; Pred. No. 6,1e-18;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQKASKPRGCPQANRGVVR 36
 Db 1 MSPRLSSSGKPLSTKQKASKPRGCPQANRGVVR 36

RESULT 4
 ADN17173
 ID ADN17173 standard; peptide; 36 AA.

XX
 AC ADN17173;
 DT 17-JUN-2004 (first entry)
 DE CS198 peptide #1.
 XX
 DE CS198 peptide #1.
 KW Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.
 XX
 OS Unidentified.
 OS
 XX
 PN US2004043406-A1.
 XX
 PD 04-MAR-2004.
 XX
 PF 22-AUG-2003; 2003US-00646873.
 XX
 PR 31-MAR-1997; 97US-00828855.
 PR 30-MAR-1997; 98US-00050516.
 XX
 PA (BILL/) BILLINGEL P A.
 PA (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HAYD/) HAYDEN M A.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUSSE/) RUSSELL J C.
 PA (STROU/) STROUPE S D.
 XX
 PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
 PI Grandos EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI; 2004-313754/29.
 XX
 PT Diagnosing diseases such as cancer of the gastrointestinal tract, by
 PT detecting aberrant expression or activity of the CS198 polypeptide, and

PT associated treatment methods.

XX
 PS Claim 17, SEQ ID NO 43, 67pp; English.

XX
 CC The invention relates to reagents and methods for detecting diseases of
 CC the gastrointestinal (GI) tract. The method involves detecting the
 CC presence of target CS198 polynucleotide in the test sample. The methods
 CC and compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of diseases or conditions associated with
 CC aberrant expression or activity of the CS198 polypeptide, such as cancer
 CC of the gastrointestinal tract. These are also useful in gene therapy. The
 CC present sequence is a CS198 peptide used to illustrate the method of the
 CC invention.

XX
 SQ Sequence 36 AA;

Query Match 100.0%; Score 189; DB 8; Length 36;
 Best Local Similarity 100.0%; Pred. No. 6,1e-18;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQKASKPRGCPQANRGVVR 36
 Db 1 MSPRLSSSGKPLSTKQKASKPRGCPQANRGVVR 36

RESULT 5
 AAW79681
 ID AAW79681 standard; protein; 215 AA.

XX
 AC AAW79681;
 DT 11-JAN-1999 (first entry)
 DE Human CS198 protein C-terminal.
 XX
 DE Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
 KW human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
 KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
 KW pancreatitis.
 XX
 OS Homo sapiens.
 OS
 XX
 PN WO9844159-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98WO-US006251.
 XX
 PR 31-MAR-1997; 97US-00828855.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billings-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
 PI Grandos EN, Hayden M, Hodges SC, Kلاس MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI; 1998-542714/46.
 XX
 PT New gastrointestinal polynucleotides, CS198, and their detection - used
 PT for developing products for the diagnosis and treatment of
 PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
 XX
 Claim 26; Page 103; 127pp; English.

XX
 CC This sequence represents the C-terminal of the human CS198 protein which
 CC is used in a method to detect the presence of a target CS198
 CC polynucleotide in a test sample. The CS198 gene is useful as a marker for
 CC gastrointestinal (GI) tract disorders. The methods and products can be
 CC used in detecting, diagnosing, staging, monitoring, prognosticating,
 CC preventing or treating, or determining the predisposition to diseases and
 CC conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
 CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative
 CC colitis, and pancreatitis

XX Sequence 215 AA;
SQ Query Match 100.0%; Score 189, DB 2, Length 215;
Best Local Similarity 100.0%; Pred. No. 4,4e-17;
Matches 36, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
Oy 1 MSPRHLSSESGKPLSTKQKASKPPRGCPQANRGVVR 36
Db 1 MSPRHLSSESGKPLSTKQKASKPPRGCPQANRGVVR 36

RESULT 6
AAE07324 ID AAE07324 standard; protein: 215 AA.
XX AAE07324;
AC AAE07324;
XX 06-NOV-2001 (first entry)
DT 06-NOV-2001 (first entry)
XX Human CS 198 protein C-terminal portion.
DE Human CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
XX gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
KW Barrett's oesophagus; gene therapy; drug screening; human.
XX
XX Homo sapiens.
XX US2001010904-A1.
XX 02-AUG-2001.
PD 02-AUG-2001.
XX 30-MAR-1998; 98US-00050516.
PF 30-MAR-1998; 98US-00050516.
XX 31-MAR-1997; 97US-00828855.
PR 31-MAR-1997; 97US-00828855.
XX (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M.
PA (HODG/) HODGES S C.
PA (KLAAS/) KLAAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUSSE/) RUSSELL J C.
PA (STRO/) STROUPE S D.
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden M, Hodges SC, Klaas MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
DR WPI, 2001-496163/54.
XX Detecting the presence of target CS 198 polynucleotide, useful for
PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
PT contacting test sample with at least one CS 198-specific polynucleotide.
XX
PS Claim 17; Page 52-53; 68pp; English.
XX
CC The invention relates to a method of detecting the presence of a target
CC CS 198 polynucleotide comprising contacting the test sample with at least
CC one CS 198-specific polynucleotide. The method is useful for detecting
CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
CC treating or determining predisposition to diseases and conditions of the
CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
CC polypeptides are useful as standards or reagents in diagnostic
CC immunoassays, as components or as target sites for various therapies.

CC Antibodies directed against at least one epitope contained within these
CC polypeptides are useful as delivery agents for therapeutic agents, in
CC diagnostic tests and for screening for conditions or diseases associated
CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
CC for the generation of chimeric antibodies for therapeutic use. The CS 198
CC polynucleotide is also useful in gene therapy and drug screening. The
CC method of the invention provides an alternative, non-surgical diagnostic
CC method capable of detecting early stage GI tract disease such as cancer.
CC The present sequence is C-terminal portion of human CS 198 polypeptide
XX
SQ Sequence 215 AA;
Oy Query Match 100.0%; Score 189, DB 4, Length 215;
Best Local Similarity 100.0%; Pred. No. 4,4e-17;
Matches 36, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
Db 1 MSPRHLSSESGKPLSTKQKASKPPRGCPQANRGVVR 36
Oy 1 MSPRHLSSESGKPLSTKQKASKPPRGCPQANRGVVR 36
Db 1 MSPRHLSSESGKPLSTKQKASKPPRGCPQANRGVVR 36

RESULT 7
ADA26384 ID ADA26384 standard; protein: 215 AA.
XX ADA26384;
AC ADA26384;
XX 20-NOV-2003 (first entry)
DT 20-NOV-2003 (first entry)
XX Synthetic peptide based on CS198 protein #5.
DE Synthetic peptide based on CS198 protein #5.
XX CS198; cancer diagnosis; cancer staging; cancer monitoring;
XX cancer prognosticating; cancer prevention; cancer;
KW gastrointestinal tract disorder; gene therapy.
XX
XX Synthetic.
XX US2003082619-A1.
XX 01-MAY-2003.
PD 01-MAY-2003.
XX 23-OCT-2002; 2002US-00278547.
PF 23-OCT-2002; 2002US-00278547.
XX 31-MAR-1997; 97US-00828855.
PR 30-MAR-1998; 98US-00050516.
XX (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M A.
PA (HODG/) HODGES S C.
PA (KLAAS/) KLAAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUSSE/) RUSSELL J C.
PA (STRO/) STROUPE S D.
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden MA, Hodges SC, Klaas MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
DR WPI, 2003-596961/56.
XX
XX Detecting the presence of a target CS198 polynucleotide in a test sample
PT comprises contacting the sample with a CS198 specific polynucleotide and
PT detecting the presence of the target CS198 polynucleotide in the test
PT sample.
XX Claim 52; Page 52; 67pp; English.
XX

CC The invention describes a method of detecting the presence of a target
 CC CS198 polynucleotide in a test sample. The method comprises contacting
 CC the test sample with at least one CS198 specific polynucleotide or its
 CC complement, and detecting the presence of the target CS198 polynucleotide
 CC in the test sample, where the CS198-specific polynucleotide has at least
 CC 50% identity to a polynucleotide having any of the 27 fully defined
 CC sequences of 34-2894 bp (SI-27) given in the specification, or their
 CC fragments or complements. The composition and methods are useful in
 CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
 CC or determining the predisposition of an individual to, diseases and
 CC conditions of the gastrointestinal tract, e.g. cancer and in gene
 CC therapy. This is the amino acid sequence of a synthetic peptide based on
 CC the predicted human CS198 protein sequence derived from the CS198
 CC consensus sequence shown in seq id 27.

CC Sequence 215 AA;

Query Match 100.0%; Score 189; DB 6; Length 215;
 Best Local Similarity 100.0%; Pred. No. 4,4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MSPRLSSSGKPLSTKQKSKPPRGCPQANRGVVR 36
 Db 1 MSPRLSSSGKPLSTKQKSKPPRGCPQANRGVVR 36

RESULT 8

ID ADN17177 standard; protein; 215 AA.

AC ADN17177;

DT 17-JUN-2004 (first entry)

DE CS198 protein #2.

KW Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.

OS Unidentified.

PN US2004043406-A1.

PD 04-MAR-2004.

PF 22-AUG-2003; 2003US-00646872.

PR 31-MAR-1997; 97US-00828855.

PR 30-MAR-1998; 98US-00050516.

PA (BILL/) BILLINGEL P A.

PA (COHE/) COHEN M.

PA (CORP/) CORPITTS T L.

PA (FRIE/) FRIEDMAN P N.

PA (GORD/) GORDON J.

PA (GRAN/) GRANADOS E N.

PA (HAYD/) HAYDEN M A.

PA (HODG/) HODGES S C.

PA (KLAS/) KLAS M R.

PA (KRAT/) KRATOCHVIL J D.

PA (ROBE/) ROBERTS-RAEP L.

PA (RUSSE/) RUSSELL J C.

PA (STRO/) STROUPE S D.

XX

PS Claim 17; SEQ ID NO 47; 67bp; English.

XX The invention relates to reagents and methods for detecting diseases of
 CC the gastrointestinal (GI) tract. The method involves detecting the
 CC presence of target CS198 polynucleotide in the test sample. The methods
 CC and compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of diseases or conditions associated with
 CC aberrant expression or activity of the CS198 polypeptide, such as cancer
 CC of the gastrointestinal tract. These are also useful in gene therapy. The
 CC present sequence is a CS198 protein used to illustrate the method of the
 CC invention.

XX Sequence 215 AA;

Query Match 100.0%; Score 189; DB 6; Length 215;
 Best Local Similarity 100.0%; Pred. No. 4,4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MSPRLSSSGKPLSTKQKSKPPRGCPQANRGVVR 36
 Db 1 MSPRLSSSGKPLSTKQKSKPPRGCPQANRGVVR 36

RESULT 9

ID AAM79574 standard; protein; 672 AA.

AC AAM79574;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 3220.

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

PN WO200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US004098.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00649336.

PR 15-SEP-2000; 2000US-00663561.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

PA (HYSB-) HYSB INC.

PI Tang YR, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Gao Y;

PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

DR WPI; 2001-476283/51.

DR N-PSDB; AAK52707.

XX

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 in diagnosis and gene therapy.

PS Claim 20; Page 288; 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoietic regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 210 (AAK52581), 211
 CC (AAK52582) and 366 (AAW80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication

XX Sequence 672 AA;

Query Match 100.0%; Score 189; DB 4; Length 672;

Best Local Similarity 100.0%; Pred. No. 1.5e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRHSSSGKPLSTQKASKPPRGCPQANRGVVR 36
 Db 458 MSPRHSSSGKPLSTQKASKPPRGCPQANRGVVR 493

RESULT 10
 AAW79676 ID AAW79676 standard; protein; 679 AA.
 XX AAW79676;

XX 11-JAN-1999 (first entry)

XX Human CS198 protein.

XX Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
 KW human predisposition; treatment; Barrett's oesophagus; gastric ulcer;
 KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
 KW pancreatitis.

XX Homo sapiens.

XX W09844159-A1.

XX 08-OCT-1998.

XX 30-MAR-1998; 98WO-US006251.

XX 31-MAR-1997; 97US-00828855.

XX (ABBO) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI; 1998-542714/46.

XX New gastrointestinal polynucleotides, CS198, and their detection - used
 PT for developing products for the diagnosis and treatment of
 PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.

XX Claim 26; Page 100-102; 127pp; English.

XX This sequence represents the human CS198 protein which is used in a
 CC method to detect the presence of a target CS198 polynucleotide in a test
 CC sample. The CS198 gene is useful as a marker for gastrointestinal (GI)
 CC tract disorders. The methods and products can be used in detecting,
 CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
 CC or determining the predisposition to diseases and conditions of the GI
 CC tract, such as GI tract cancer, Barrett's oesophagus, gastric ulcer,
 CC gastritis, leiomyoma, polyps, Crohn's disease, ulcerative colitis, and
 CC pancreatitis

XX Sequence 679 AA;

XX Query Match

XX 100.0%; Score 189; DB 2; Length 679;

Best Local Similarity 100.0%; Pred. No. 1.6e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRHSSSGKPLSTQKASKPPRGCPQANRGVVR 36
 Db 465 MSPRHSSSGKPLSTQKASKPPRGCPQANRGVVR 500

RESULT 11

AAE07319 ID AAE07319 standard; protein; 679 AA.

XX AAE07319;

XX 06-NOV-2001 (first entry)

XX Human CS 198 protein.

XX CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
 KW gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
 KW Barrett's oesophagus; gene therapy; drug screening; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 353 /note= "Encoded by CGSN"

XX US2001010904-A1.

XX 02-AUG-2001.

XX 30-MAR-1998; 98US-00050516.

XX 31-MAR-1997; 97US-00828855.

XX (BILL/) BILLINGEL P A.

XX (COHE/) COHEN M.

XX (COLP/) COLPITTS T L.

XX (FRIE/) FRIEDMAN P N.

XX (GORD/) GORDON J.

XX (GRAN/) GRANADOS E N.

XX (HAYD/) HAYDEN M.

XX (HODG/) HODGES S C.

XX (KLAS/) KLAS M R.

XX (KRAT/) KRATOCHVIL J D.

XX (ROBE/) ROBERTS-RAPP L.

XX (RUSSE/) RUSSELL J C.

XX (STRO/) STROUPE S D.

XX Billingel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI; 2001-496163/54.

XX N-PSDB; AAD13637.

XX Detecting the presence of target CS 198 polynucleotide, useful for
 PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
 PT contacting test sample with at least one CS 198-specific polynucleotide.

XX Claim 17; Page 49-51; 68pp; English.

XX The invention relates to a method of detecting the presence of a target
 CC CS 198 polynucleotide comprising contacting the test sample with at least
 CC one CS 198-specific polynucleotide. The method is useful for detecting
 CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
 CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
 CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
 CC treating or determining predisposition to diseases and conditions of the
 CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
 CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
 CC polypeptides are useful as standards or reagents in diagnostic

CC immunosays, as components or as target sites for various therapies.
CC Antibodies directed against at least one epitope contained within these
CC polypeptides are useful as delivery agents for therapeutic agents, in
CC diagnostic tests and for screening for conditions or diseases associated
CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
CC for the generation of chimeric antibodies for therapeutic use. The CS 198
CC polynucleotide is also useful in gene therapy and drug screening. The
CC method of the invention provides an alternative, non-surgical diagnostic
CC method capable of detecting early stage GI tract disease such as cancer.
CC The present sequence is human CS 198 polypeptide
XX
SQ Sequence 679 AA;

Query Match 100.0%; Score 189; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSPRLSSSGKPLSTKQASKPPRGCPQANRGVVR 36
DB 465 MSPRLSSSGKPLSTKQASKPPRGCPQANRGVVR 500

RESULT 12

AAM78590 AAM78590 standard; protein; 679 AA.

AC AAM78590;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1252.

KM Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM tissue growth factor; immunomodulatory; cancer; leukaemia;
KM nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

PN WO200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US004098.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663561.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

PA (HYSE-) HYSEQ INC.

PA Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX WPI; 2001-476283/51.
XX N-PSDB; AAK51723.

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.

PS Claim 20; Page 3512-3514; 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78523-AAK80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 679 AA;

Query Match 100.0%; Score 189; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSPRLSSSGKPLSTKQASKPPRGCPQANRGVVR 36
DB 465 MSPRLSSSGKPLSTKQASKPPRGCPQANRGVVR 500

RESULT 13

ADA26379 ADA26379 standard; protein; 679 AA.

AC ADA26379;

DT 20-NOV-2003 (first entry)

DE Predicted amino acid sequence of the CS198 protein.

KM CS198; cancer diagnosis; cancer staging; cancer monitoring;
KM cancer prognosticating; cancer prevention; cancer;
KM gastrointestinal tract disorder; gene therapy.

XX Synthetic;

OS US2003082619-A1.

PN 01-MAY-2003.

PD 23-OCT-2002; 2002US-00278547.

PF 31-MAR-1997; 97US-00828855.

PR 30-MAR-1996; 96US-00050516.

PA (BILL/) BILLINGEL P A.

PA (COH/) COHEN M.

PA (COLP/) COLPITTS T L.

PA (FRIE/) FRIEDMAN P N.

PA (GORD/) GORDON J.

PA (GRAN/) GRANADOS E N.

PA (HAYD/) HAYDEN M A.

PA (HODG/) HODGES S C.

PA (KLAS/) KLAS M R.

PA (KRAT/) KRATOCHVIL J D.

PA (ROBE/) ROBERTS-RAPP L.

PA (RUSSE/) RUSSELL J C.

PA (STRO/) STROUPE S D.

PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden MA, Hodges SC, KLAS MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 2003-596961/56.

CC Detecting the presence of a target CS198 polynucleotide in a test sample
CC comprises contacting the sample with a CS198 specific polynucleotide and
CC detecting the presence of the target CS198 polynucleotide in the test
CC sample.
PS Claim 17; Page 49-50; 67pp; English.
XX The invention describes a method of detecting the presence of a target

CC CS198 polynucleotide in a test sample. The method comprises contacting
CC the test sample with at least one CS198 specific polynucleotide or its
CC complement, and detecting the presence of the target CS198 polynucleotide
CC in the test sample, where the CS198-specific polynucleotide has at least
CC 50% identity to a polynucleotide having any of the 27 fully defined
CC sequences of 34-2894 bp (S1-27) given in the specification, or their
CC fragments or complements. The composition and methods are useful in
CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
CC or determining the predisposition of an individual to, diseases and
CC conditions of the gastrointestinal tract, e.g. cancer and in gene
CC therapy. This is the predicted amino acid sequence of the human CS198
CC protein derived from the CS198 consensus sequence shown in seq id 27.

XX Sequence 679 AA;

Query Match 100.0%; Score 189; DB 6; Length 679;

Best Local Similarity 100.0%; Pred. No. 1.6e-16; Mismatches 0; Gaps 0;

Matches 36; Conservative 0; Indels 0; Gaps 0;

Qy 1 MSPRHSSSGKPLSTKQKSKPPRCGCPQANRGVVR 36
Db 465 MSPRHSSSGKPLSTKQKSKPPRCGCPQANRGVVR 500

RESULT 14
ADG14341
ID ADG14341 standard; protein: 679 AA.

XX ADG14341;

XX 26-FEB-2004 (first entry)

XX Human NC2.

XX Human; NC1; NC2; NC3; PHH1; pancreas beta-cell; insulin; antidiabetic;
XX neuroprotective.

XX Homo sapiens.

XX WO2003078631-A1.

XX 25-SEP-2003.

XX 06-MAR-2003; 2003WO-JP002620.

XX 15-MAR-2002; 2002JP-00071592.

XX (KANF) KANEXA CORP.

XX Niwa H, Yamashita K;

XX WPI; 2003-767524/72.

XX N-PSDB; ADG14344.

PT Familial persistent hyperinsulinemic hypoglycemia of infancy (PHH1)
PT patient-expressed genes for detecting and screening e.g. proliferative
PT insulin-producing cells in treatment of PHH1.

XX Claim 1; SEQ ID NO 2; 34pp; Japanese.

XX The present invention relates to human NC1, NC2 and NC3 proteins and
XX coding sequences (ADG14340-ADG14345). The coding sequences are useful for
XX detecting and screening proliferative insulin-producing cells as well as
XX differentiation and proliferation of such cells and their precursors as
XX analogous cells in treatment of e.g. PHH1 and diseases due to
XX differentiation/proliferation abnormality, diseases of the nervous system
XX and pancreas. The coding sequences are also useful as spontaneous
XX proliferation models of pancreas beta-cells. The novel genes NC1, NC2 and
XX NC3 were isolated from the pancreas of PHH1 patients, which were used in
XX testing for the detection of proliferative insulin-producing cells or
XX pancreas beta-cells by Northern analysis.

XX Sequence 679 AA;

Query Match 100.0%; Score 189; DB 7; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.6e-16; Mismatches 0; Gaps 0;
Matches 36; Conservative 0; Indels 0; Gaps 0;

Qy 1 MSPRHSSSGKPLSTKQKSKPPRCGCPQANRGVVR 36
Db 465 MSPRHSSSGKPLSTKQKSKPPRCGCPQANRGVVR 500

RESULT 15
ADN17172
ID ADN17172 standard; protein: 679 AA.

XX ADN17172;

XX 17-JUN-2004 (first entry)

XX CS198 protein #1.

XX Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.

XX Unidentified.

XX US2004043406-A1.

XX 04-MAR-2004.

XX 22-AUG-2003; 2003US-00646873.

XX 31-MAR-1997; 97US-00828855.

XX 30-MAR-1998; 98US-00050516.

XX (BILL/) BILLINGEL P A.
XX (COHE/) COHEN M.
XX (COLP/) COLPITTS T L.
XX (FRIE/) FRIEDMAN P N.
XX (GORD/) GORDON J.
XX (GRAN/) GRANADOS E N.
XX (HAYD/) HAYDEN M A.
XX (HODG/) HODGES S C.
XX (KLAS/) KLAS M R.
XX (KRAT/) KRATOCHVIL J D.
XX (ROBE/) ROBERTS-RAPP L.
XX (RUS/) RUSSELL J C.
XX (STRO/) STROUPE S D.

XX Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX Granados EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;
XX Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI; 2004-313754/29.

XX GENBANK; D87440.

XX Diagnosing diseases such as cancer of the gastrointestinal tract, by

XX detecting aberrant expression or activity of the CS198 polypeptide, and

XX associated treatment methods.

XX Claim 17; SEQ ID NO 42; 67pp; English.

XX The invention relates to reagents and methods for detecting diseases of
XX the gastrointestinal (GI) tract. The method involves detecting the
XX presence of target CS198 polynucleotide in the test sample. The methods
XX and compositions of the present invention are useful for the diagnosis,
XX prevention and/or treatment of diseases or conditions associated with
XX aberrant expression or activity of the CS198 polypeptide, such as cancer
XX of the gastrointestinal tract. These are also useful in gene therapy. The
XX present sequence is a CS198 protein used to illustrate the method of the
XX invention.

XX Sequence 679 AA;

Query Match 100.0%; Score 189; DB 8; Length 679;

Best Local Similarity 100.0%; Pred. No. 1.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSPRLSSSGKPLSTKQKASKPPRGCPQANRGVVR 36
Db 465 MSPRLSSSGKPLSTKQKASKPPRGCPQANRGVVR 500

Search completed: March 3, 2006, 13:35:20
Job time : 21.242 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 13:26:31 ; Search time 2.27405 Seconds
(without alignments)
1523.185 Million cell updates/sec

Title: US-10-646-873-43

Perfect score: 189

Sequence: 1 MSPRHLSSSGKPLSTKQKASKPPRCGPQANRGVVR 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	189	100.0	679	2 T00636	hypothetical prote
2	55	29.1	218	2 T51887	hypothetical prote
3	54.5	28.8	518	2 B84514	probable cytochrom
4	54	28.6	315	2 T37273	highly charged pro
5	54	28.6	823	2 D86165	protein P15K9.3 (l
6	53.5	28.3	360	2 T33124	hypothetical prote
7	53.5	28.3	453	2 S39866	outer membrane pro
8	53	28.0	268	2 T27242	hypothetical prote
9	53	28.0	308	2 H96827	protein P20H17.12
10	53	28.0	748	2 A60202	cholesterol O-acetyl
11	53	28.0	1108	2 T16353	protein P97 - Myco
12	53	28.0	1126	2 T20801	hypothetical prote
13	52.5	27.8	292	2 T02377	probable ubiquitin
14	52	27.5	197	2 T36584	hypothetical prote
15	52	27.5	226	1 S51660	histone H1-5 (vali
16	52	27.5	324	1 S51660	radar protein - Sul
17	52	27.5	324	1 S51660	DNA repair protein
18	52	27.5	324	1 S51660	hypothetical prote
19	52	27.5	324	1 S51660	chloride channel C
20	52	27.5	852	2 G87304	hypothetical prote
21	52	27.5	878	2 H87315	hypothetical prote
22	52	27.5	1829	2 T14280	RMI protein - mous
23	51.5	27.2	760	2 F86387	probable Pco kinase
24	51	27.0	104	1 GMDG	gasterin precursor
25	51	27.0	338	1 PC4365	calcium-binding pr
26	51	27.0	391	2 S27850	surface antigen Ic
27	51	27.0	425	2 JEO086	SH3-domain binding
28	51	27.0	1099	2 T18357	mbp1 protein - Myc
29	50.5	26.7	227	2 T21298	hypothetical prote

30	50.5	26.7	274	2 S47791	hypothetical prote
31	50.5	26.7	442	2 JC4978	oxidative stress p
32	50	26.5	90	2 T31980	hypothetical prote
33	50	26.5	351	2 H84847	probable protein k
34	50	26.5	351	2 S50754	hypothetical prote
35	50	26.5	383	2 JC5775	aspartate transami
36	50	26.5	686	2 A45483	chloride channel,
37	50	26.5	998	2 T23427	hypothetical prote
38	50	26.5	2176	2 T13806	locus gene protei
39	50	26.5	2825	2 T14271	Doc4 protein, stre
40	49.5	26.2	274	2 A10979	probable exported
41	49.5	26.2	641	2 A39961	cholesterol O-acetyl
42	49.5	26.2	654	2 T39785	hypothetical prote
43	49.5	26.2	3938	2 T42761	Basoon protein -
44	49	25.9	58	2 AG3127	hypothetical prote
45	49	25.9	69	2 B98160	hypothetical prote

ALIGNMENTS

RESULT 1
T00636
hypothetical protein P21856_2 - human
C.Species: Homo sapiens (man)
C.Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C.Accession: T00636
R.Lamerdin, J.E.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhart-Schultz, K.; C
regescu, A.; Avila, J.; Liu, S.; Bruce, R.; Quan, G.; Montgomery, M.; Ow, D.; Nolan, M.;
submitted to the EMBL Data Library, January 1998
A.Description: Sequence analysis of a 3.5 Mb contig in 19p13.3 between CDC34 and D19S342
A.Reference number: Z14195
A.Accession: T00636
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-679 <LMA>
A.Cross-references: UNIPROT:Q81VT2; UNIPARC:UPI00000745CD; EMBL:AC004030; NID:G2804590;
C.Genetics:
A.Map position: 19p13.3
A.Introns: 594/1; 637/3; 650/3
A.Note: P21856_2

Query Match 100.0%; Score 189; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MSPRHLSSSGKPLSTKQKASKPPRCGPQANRGVVR 36
DB 465 MSPRHLSSSGKPLSTKQKASKPPRCGPQANRGVVR 500

RESULT 2
T51887
hypothetical protein DKFZP762K222.1 - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C.Accession: T51887
R.Koehrer, K.; Beyer, A.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, July 2000
A.Reference number: Z25855
A.Accession: T51887
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-218 <AAA>
A.Cross-references: UNIPROT:Q9NPS8; UNIPARC:UPI000006E97D; EMBL:AL390216
A.Experimental source: adult melanoma (Mewo cell line); clone DKFZP762K222
C.Genetics:
A.Note: DKFZP762K222.1

Query Match 29.1%; Score 55; DB 2; Length 218;
Best Local Similarity 46.2%; Pred. No. 16;
Matches 12; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Oy 9 SSGKPLSTKQASKPPRCGPQANRGV 34
 Db 1 SSRPVGKESPPKPGCGPAAAGCV 26

RESULT 3

probable cytochrome P450 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C/Accession: B84514
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Umayam, L.; Tallon, L.;
 euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A/Reference number: A84420; MUID:20083487; PMID:10617197
 A/Accession: B84514
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-518 <STO>
 A/Cross-references: UNIPROT:Q9S149; UNIPARC:UPI00000A96C6; GB:AE002093; NID:94587680; P1
 C/Genetics:
 A/Gene: At2g14100
 A/Map position: 2
 C/Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C/Keywords: heme; iron; metalloprotein
 F/43/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 28.8%; Score 54.5; DB 2; Length 518;
 Best Local Similarity 37.8%; Pred. No. 41;
 Matches 14; Conservative 3; Mismatches 15; Indels 5; Gaps 1;

Oy 4 RHLSSESGKPLSTKQASKPPRCGPQANRGV 35
 Db 425 RFLASSRGRKEBERQELKTYIFGSGRRCGPVNLGYI 461

RESULT 4

highly charged protein - human
 C/Species: Homo sapiens (man)
 C/Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
 C/Accession: J17273; S19884
 R/Wilton, A.N.; Zehavi-Refeman, T.; Fleming, J.; Baker, E.; Chen, L.Z.; Cooper, D.W.
 Cytogenet. Cell Genet. 58, 1985, 1991
 A/Title: A unique intronless gene or gene segment on chromosome 13 specifying a highly c
 A/Reference number: J17273
 A/Accession: J17273
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-315 <RES>
 A/Cross-references: UNIPROT:Q14109; UNIPARC:UPI0000179D14; EMBL:X59131; NID:930387; PID:
 A/Notes: submitted to the EMBL Data Library, April 1991
 C/Genetics:
 A/Map position: 13
 A/Introns: #status absent

Query Match 28.6%; Score 54; DB 2; Length 315;
 Best Local Similarity 40.7%; Pred. No. 30;
 Matches 11; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Oy 5 HLSSSGKPLSTKQASKPPRCGPQAN 31
 Db 179 HVSKKARKASAKPPISKPPAGPSSN 205

RESULT 5

protein F15K9.3 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: D86165

R/Theologie, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marzalli,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: D86165
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-823 <STO>
 A/Cross-references: UNIPROT:Q9ZV78; UNIPARC:UPI000009BCD9; GB:AE005172; NID:93850566; P1
 C/Genetics:
 A/Gene: F15K9.3
 A/Map position: 1
 C/Superfamily: Arabidopsis thaliana probable apoptosis inhibitor T419.12

Query Match 28.6%; Score 54; DB 2; Length 823;
 Best Local Similarity 40.7%; Pred. No. 73;
 Matches 11; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Oy 6 LSSESGKPLSTKQASKPPRCGPQANR 32
 Db 232 LGAESNPKSSDPDNPKPQSDPSNR 258

RESULT 6

hypothetical protein B0511.1 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T33124
 R/Tin-Mollam, A.; Sutterer, C.; Ozeraky, P.
 submitted to the EMBL Data Library, May 1998
 A/Description: The sequence of C. elegans cosmid B0511.
 A/Reference number: Z21285
 A/Accession: T33124
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-360 <TIN>
 A/Cross-references: UNIPROT:O61826; UNIPARC:UPI000017B6F8; EMBL:AF067608; PIDN:AACT1657.3
 A/Experimental source: strain Bristol N2, clone B0511
 C/Genetics:
 A/Gene: CESP.B0511.1
 A/Map position: 1
 A/Introns: 57/1; 118/3; 143/3; 176/3; 279/2; 336/3
 F/135-181/Domain: BMBP-type peptidylprolyl isomerase homology <PPI>

Query Match 28.3%; Score 53.5; DB 2; Length 360;
 Best Local Similarity 48.1%; Pred. No. 39;
 Matches 13; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

Oy 4 RHLSSESGKPLSTKQASKPPRCGPQ 29
 Db 104 RHLSSEMDGSLDKTKTVPKCPQ 130

RESULT 7

outer membrane protein CD precursor - Moraxella catarrhalis
 C/Species: Moraxella catarrhalis
 C/Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
 C/Accession: S39866
 R/Murphy, T.F.; Kirkham, C.; Lesse, A.J.
 Mol. Microbiol. 10, 87-97, 1993
 A/Title: The major heat-modifiable outer membrane protein CD is highly conserved among s
 A/Reference number: S39866; MUID:95058186; PMID:7968522
 A/Accession: S39866
 A/Molecule type: DNA

A:Residues: 1-453 <MUR>
 A:Cross-references: UNIPROT:Q08657; UNIPARC:UPI00000BB8DE; EMBL:LI0755; NID:g149756; PID
 C:Keywords: membrane protein
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-453/Product: outer membrane protein CD #status predicted <MAT>

Query Match 28.3%; Score 53.5; DB 2; Length 453;
 Best Local Similarity 43.3%; Pred. No. 48;
 Matches 13; Conservative 3; Mismatches 9; Indels 5; Gaps 2;
 Db 3 PRHLESGSKPLSTQKASKEPRGCP-QAN 31
 294 PDHLCACPEPTVIVD---PRGCEVQVN 319

RESULT 8
 T27242
 Hypothetical protein Y57G11C.32 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
 C:Accession: T27242
 R:McMurray, A.
 Submitted to the EMBL Data Library, September 1997
 A:Reference number: Z20330
 A:Accession: T27242
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-266 <WIL>
 A:Cross-references: UNIPROT:Q9U205; UNIPARC:UPI0000082309; EMBL:Z99281; PIDN:CAB54455.1;
 A:Experimental source: clone Y57G11C
 C:Genetic8:
 A:Gene: CRSP:Y57G11C.32
 A:Map position: 4
 A:Introns: 70/3; 118/3

Query Match 28.0%; Score 53; DB 2; Length 268;
 Best Local Similarity 50.0%; Pred. No. 34;
 Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 2 SPRHLESGSKPLSTQKASKEPRGCP 23
 Db 127 TPTPISENGSKSLSTQKSFENP 148

RESULT 9
 H96827
 Protein F20B17.12 [Imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
 C:Accession: H96827
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chinn, N.R.; Chung, M.K.; Com, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
 Aeneas, C.R.; Hughes, B.; Huizart, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luroso, J.S.; Maltli, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sekano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H96827
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-308 <STO>
 A:Cross-references: UNIPROT:Q9NA06; UNIPARC:UPI000009FF2E; GB:AE005173; NID:g7715603; PI
 C:Genetic8:
 A:Gene: F20B17.12
 A:Map position: 1
 C:Superfamily: floral homeotic protein / AP2 domain transcription factor
 Query Match 28.0%; Score 53; DB 2; Length 308;
 Best Local Similarity 38.2%; Pred. No. 39;

Matches 13; Conservative 5; Mismatches 12; Indels 4; Gaps 1;
 Qy 7 SESSGSKPLSTQKASKEPRGCP-----QANRCVVR 36
 Db 25 SESASIALTSRKRRKSPRNAPLQSSPEYRQVTR 58

RESULT 10
 A60202
 choline O-acetyltransferase (EC 2.3.1.6) - human
 N:Alternate names: choline acetylase
 C:Species: Homo sapiens (man)
 C>Date: 10-Nov-1992 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: I52631; A60202; S24416; S14483; PH1571; T01786; PC4342; PC4344; PC4343
 R:Oda, Y.; Nakashima, I.; Deguchi, T.
 Brain Res. Mol. Brain Res. 16, 287-294, 1992
 A:Title: A complementary DNA for human choline acetyltransferase induces two forms of en
 A:Reference number: I52631; MUID:93180642; PMID:1337937
 A:Accession: I52631
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-748 <RES>
 A:Cross-references: UNIPROT:P28329; UNIPARC:UPI0000161BC7; GB:S56138; NID:g301095; PID:g
 J:Herzh, L.B.; Takane, K.; Gylis, K.; Moosaw, C.; Staughter, C.
 J:Neurochem. 51, 1843-1845, 1988
 A:Title: Conservation of amino acid sequences between human and porcine choline acetyltr
 A:Reference number: A60202; MUID:89036242; PMID:3183663
 A:Accession: A60202
 A:Molecule type: protein
 A:Residues: 'XX', 153-182, 271-295, 340-352, 376-382, 404-415, 550-559, 572-583, 620-632, 644-648
 A:Cross-references: UNIPARC:UPI0000175363; UNIPARC:UPI0000175364; UNIPARC:UPI0000175365;
 364; UNIPARC:UPI0000175366; UNIPARC:UPI0000175367; UNIPARC:UPI0000175368; UNIPARC:UPI0000175369;
 R:Toussaint, J.L.; Geofroy, V.; Schmitt, M.; Werner, A.; Garnier, J.M.; Simon, P.; Ker
 Genomics 12, 412-416, 1992
 A:Title: Human choline acetyltransferase (CHAT): partial gene sequence and potential cor
 A:Reference number: S24416; MUID:92155737; PMID:1339386
 A:Accession: S24416
 A:Molecule type: DNA
 A:Residues: 109-150, 'Q', 152-232 <TOU>
 A:Cross-references: UNIPARC:UPI000016A6CA; EMBL:X56879; NID:g29940; PID:g29941
 R:Herzh, L.B.; Kong, C.P.; Sampson, C.; Mues, G.; Li, Y.P.; Fisher, A.; Hill, D.; Baetge
 J. Neurochem. 61, 306-314, 1993
 A:Title: Comparison of the promoter region of the human and porcine choline acetyltransf
 A:Reference number: PH1571; MUID:93294599; PMID:8515278
 A:Accession: PH1571
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-95 <HEZ>
 A:Cross-references: UNIPARC:UPI00000004CA
 A:Experimental source: GB:S13337
 A:Note: Genbank sequence 950535 (accession L33837) is missing one nucleotide C at posi.
 R:Lorenzi, M.V.; Trinidad, A.C.; Zhang, R.; Straus, W.L.
 DNA Cell Biol. 11, 593-603, 1992
 A:Title: Two mRNAs are transcribed from the human gene for choline acetyltransferase.
 A:Reference number: Z14429; MUID:93000480; PMID:1388731
 A:Accession: T01786
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 111-119, 'T', 121-260, 'GQ', 263-331, 'A', 393-395, 'L', 397-433, 'G', 435-528, 'S', 531
 A:Cross-references: UNIPARC:UPI000016B393; EMBL:S45018; NID:g257109; PIDN:AA23557.2; PI
 R:Masawa, H.; Matsunaga, J.; Oda, Y.; Takahashi, R.; Deguchi, T.
 Mol. Brain Res. 44, 323-333, 1997
 A:Title: Human choline acetyltransferase mRNAs with different 5'-region produce a 69-kD.
 A:Reference number: PC4342; MUID:97225904; PMID:9073174
 A:Accession: PC4342

A:Molecule type: mRNA
 A:Residues: 119-167 'E', 169-256 <MTS>
 A:Cross-references: UNIPARC:UPI000017536E; DDBJ:D82340
 A:Experimental source: Brain
 A:Accession: PC4344
 A:Molecule type: mRNA
 A:Residues: 119-152 <MT3>
 A:Cross-references: UNIPARC:UPI000000373; DDBJ:D82341; NID:g1906787; PIDN:BA18945.1; F
 A:Experimental source: Brain
 A:Accession: PC4343
 A:Molecule type: mRNA
 A:Residues: 119-152 <MT2>
 A:Cross-references: UNIPARC:UPI000000373; DDBJ:D82342; NID:g1906789; PIDN:BA18946.1; F
 A:Experimental source: Brain
 C:Comment: This enzyme is responsible for the biosynthesis of the neurotransmitter acetylcholine
 C:Comment: This enzyme is involved in the synthesis of the neurotransmitter acetylcholine
 C:Comment: This enzyme is involved in the synthesis of the neurotransmitter acetylcholine
 C:Comment: This enzyme is involved in the synthesis of the neurotransmitter acetylcholine
 C:Keywords: acetyltransferase, coenzyme A
 A:Gene: GDB:CHAT
 A:Cross-references: GDB:119775; OMIM:118490
 A:Map position: 10q11.2-10q11.2
 A:Introns: 129/3; 193/3
 C:Superfamily: carnitine O-acetyltransferase
 C:Keywords: acyltransferase, coenzyme A

Query 6 LSESSGKPLSTKQKASKPPRCPOANG 26
 Db 725 LPPTESKPLATKKAATRSQGS 745

RESULT 11
 T18353
 protein P97 - Mycoplasma hyopneumoniae
 C:Species: Mycoplasma hyopneumoniae
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T18353; T03805
 R:Hu, T.; Artushin, S.; Minlon, F.C.
 J. Bacteriol. 179, 1317-1323, 1997
 A:Title: Cloning and functional analysis of the P97 swine ciliium adhesin gene of Mycoplasma
 A:Reference number: Z18886; MUID:97175562; PMID:9023217
 A:Accession: T18353
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1108 <HSU>
 A:Cross-references: UNIPROT:Q49542; UNIPARC:UPI00000A9388; EMBL:U50901; NID:g1399524; F
 R:Hu, T.; Minlon, F.C.
 Gene 214, 13-23, 1998
 A:Title: Molecular analysis of the P97 ciliium adhesin operon of Mycoplasma hyopneumoniae
 A:Reference number: Z15097; MUID:98391007; PMID:9729120
 A:Accession: T03805
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1089-1108 <HS2>
 A:Cross-references: UNIPARC:UPI0000161AD; EMBL:AF012905; NID:g2654768; PIDN:AAC32526.1;
 A:Experimental source: Strain 232A
 C:Genetics:
 A:Genetic code: SGC3
 A>Note: P97

Query Match 28.0%; Score 53; DB 2; Length 1108;
 Best Local Similarity 34.4%; Pred. No. 1.3e+02;
 Matches 11; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 3 PRHLSGSKPLSTKQKASKPPRCPOANGV 34
 Db 837 PEAAKPEAKPVAAKPEAKPVAAKPEAKPV 868

RESULT 12

T20801
 hypothetical protein F12F6.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T20801
 R:Kernaw, J.
 submitted to the EMBL Data Library, May 1996
 A:Reference number: Z19326
 A:Accession: T20801
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1126 <MTL>
 A:Cross-references: UNIPROT:Q19371; UNIPARC:UPI00000778EA; EMBL:Z73425; PIDN:CAA97788.1;
 A:Experimental source: clone F12F6
 C:Genetics:
 A:Gene: CESP:F12F6.6
 A:Map position: 4
 A:Introns: 34/1; 90/1; 126/1; 441/3; 526/3; 604/1; 757/3; 1051/3

Query Match 28.0%; Score 53; DB 2; Length 1126;
 Best Local Similarity 40.7%; Pred. No. 1.3e+02;
 Matches 11; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 7 SSSGKPLSTKQKASKPPRCPOANG 33
 Db 128 SATPAGPLQAMQAPATPTPTPTPTSG 154

RESULT 13
 T02737
 probable ubiquitin fusion-degradation protein At2g29070 [Imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C:Accession: T02737; B84692
 R:Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Roun
 submitted to the EMBL Data Library, August 1998
 A:Description: Arabidopsis thaliana chromosome II BAC T914 genomic sequence.
 A:Reference number: Z14710
 A:Accession: T02737
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-292 <STO>
 A:Cross-references: UNIPROT:O81075; UNIPARC:UPI00000A4C4F; EMBL:AC005315; NID:g3461834; F
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentio, M.T.; Town, C.D.; Fujii, C.Y.; R
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: B84692
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-292 <STO>
 A:Cross-references: UNIPARC:UPI00000A4C4F; GB:AE002093; NID:g3461847; PIDN:AAC33233.1; GS
 C:Genetics:
 A:Gene: At2g29070; T914.15
 A:Map position: 2
 A:Introns: 11/1; 22/1; 62/3; 106/2; 181/1; 260/3
 C:Superfamily: Caenorhabditis elegans hypothetical protein F19B6.2b

Query Match 27.8%; Score 52.5; DB 2; Length 292;
 Best Local Similarity 38.2%; Pred. No. 43;
 Matches 13; Conservative 6; Mismatches 12; Indels 3; Gaps 1;

Qy 3 PRHLSGSKPLSTKQKASKPPRCPOANG 33
 Db 168 POKLTPEKRPLOVKEEBPAKVPKPTPTSG 201

RESULT 14
 T36584
 hypothetical protein SCH24.19c - Streptomyces coelicolor

C/Species: Streptomyces coelicolor
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: J36584
 R/Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Randleman, M.A.
 submitted to the EMBL Data Library, May 1999
 A/Reference number: J21575
 A/Accession: J36584
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-197 <OLI>
 A/Cross-references: UNIPROT:Q9X8R3; UNIPARC:UPI00000DB068; EMBL:AL049826; PIDN:CAB42725.
 A/Experimental source: strain AJ12
 C/Genetics:
 A/Gene: SCOEDB:SCM24.19C

Query Match 27.5%; Score 52; DB 2; Length 197;
 Best Local Similarity 42.9%; Pred. No. 34;
 Matches 12; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 3 PRHLSSGKPLSTKQKSKPPGCPQA 30
 DB 15 PRHAPISGPPVTTQ---PPQGMPFA 38

RESULT 15

SS1660
 histone H1-5 [validated] - human
 N/Alternate names: histone H1.5; histone H1a
 C/Species: Homo sapiens (man)
 C/Date: 03-Mar-2000 #sequence_revision 03-Mar-2000 #text_change 03-Jul-2004
 C/Accession: SS1660; JX0087; I59499
 R/Albig, W.; Doenecke, D.
 submitted to the EMBL Data Library, December 1994
 A/Description: A human histone gene cluster containing a complete set of histone genes.
 A/Reference number: SS1660
 A/Accession: SS1660
 A/Molecule type: DNA
 A/Residues: 1-226 <ALB>
 A/Cross-references: UNIPROT:P16401; UNIPARC:UPI000001BDA; EMBL:X83509; NID:G603550; PID
 R/Ohe, Y.; Hayashi, H.; Iwai, K.
 J. Biochem. 106, 844-857, 1989
 A/Title: Human spleen histone H1; isolation and amino acid sequences of three minor vari
 A/Reference number: JX0080; WUID:90130391; PMID:2613692
 A/Accession: JX0087
 A/Molecule type: protein
 A/Residues: 2-214, 218-226 <OHE>
 A/Cross-references: UNIPARC:UPI000014DACF
 R/Ciarozzi, N.; Marash, F.; Plumb, M.; Zimmerman, S.; Zimmerman, A.; Coles, L.S.; Wells,
 Science 224, 1115-1117, 1984
 A/Title: Clustering of human H1 and core histone genes.
 A/Reference number: I59499; WUID:84196423; PMID:6719136
 A/Accession: I59499
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-36, 'I', 38, 'A', 40-51, 'P', 53-58, 'A' <CAR>
 A/Cross-references: UNIPARC:UPI000006CF66; GB:X02570; NID:G183746; PIDN:AAA35943.1; PID:
 C/Genetics:
 A/Gene: GDB:H1F5
 A/Cross-references: GDB:6261922; OMIM:142711
 A/Map position: 6p22.2-6p21.1
 C/Superfamily: histone H1
 C/Keywords: acetylated amino end; chromosomal protein; DNA binding; nucleosome; nucleus
 F/2-226/Product: histone H1-5 #status experimental <MAT>
 F/2-37/Domain: amino-terminal <ATD>
 F/38-112/Domain: globular <GLB>
 F/113-226/Domain: carboxyl-terminal <CTD>
 F/2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 27.5%; Score 52; DB 1; Length 226;
 Best Local Similarity 35.7%; Pred. No. 39;
 Matches 10; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 3 PRHLSSGKPLSTKQKSKPPGCPQA 30

DB 183 PKKATKSPAKKAVKPPKAKKAKPKA 210
 Search completed: March 3, 2006, 13:36:31
 Job time : 4.27405 secs

11. Sign and
Stamp (date)

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 13:19:17 ; Search time 13.7493 Seconds
(without alignments)
1847.299 Million cell updates/sec

Title: US-10-646-873-43

Perfect score: 189
Sequence: 1 MSPRLSESSGKPISTKQKASPPRCPOANRGVVR 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189	100.0	679	1 CS021 HUMAN	081v2 homo sapien
2	155	82.0	685	1 CS021 PONY	051d3 pongo pygma
3	100	52.9	648	1 CS021 MOUSE	09d779 mus musculi
4	73	38.6	389	2 099XR0 MOUSE	099x70 mus musculi
5	73	38.6	319	2 08C911 MOUSE	08C911 mus musculi
6	73	38.6	553	2 08B117 MOUSE	08B117 mus musculi
7	73	38.6	554	2 08VE06 MOUSE	08VE06 mus musculi
8	73	38.6	554	2 09DB11 MOUSE	09DB11 mus musculi
9	65	34.4	553	2 06P747 RAT	06P747 rattus norv
10	64.5	34.1	403	2 04P7A4 USITMA	04P7A4 usitlago na
11	63	33.3	688	2 04NSH5 9DELT	04NSH5 anemomyxob
12	63	33.3	926	2 09SK63 MACRA	09SK63 macaca fasc
13	63	33.3	950	2 09P2F5 HUMAN	09P2F5 homo sapien
14	62	32.8	732	2 0611M2 CAEBR	0611M2 caenorhabdi
15	62	32.8	930	2 060KX3 CAEBR	060KX3 caenorhabdi
16	61	32.3	801	2 08CD11 MOUSE	08CD11 mus musculi
17	61	32.3	876	2 06ZP63 MOUSE	06ZP63 mus musculi
18	60.5	32.0	140	2 091086 9EMTO	091086 human echov
19	60.5	32.0	141	2 09WRM4 9EMTO	09WRM4 human echov
20	60.5	32.0	141	2 09WRM5 9EMTO	09WRM5 human echov
21	60.5	32.0	143	2 09JA74 9EMTO	09JA74 human echov
22	60.5	32.0	143	2 09JA76 9EMTO	09JA76 human echov
23	60.5	32.0	143	2 09JA89 9EMTO	09JA89 human echov
24	60.5	32.0	312	2 080617 9EMTO	080617 human echov
25	60.5	32.0	420	2 080616 9EMTO	080616 human echov
26	58.5	31.0	639	2 06UDM4 9HERP	06UDM4 psittacid n
27	58	30.7	278	2 04SC62 TETNG	04SC62 tetraodon h
28	58	30.7	368	2 07SLD0 ORYSA	07SLD0 oryza sativ
29	58	30.7	368	2 06BK82 DEBHA	06BK82 debrayomyce
30	58	30.7	453	2 08N0M6 CTEPE	08N0M6 ctenocephal
31	58	30.7	1219	2 09X209 DROME	09X209 drosophila

ALIGNMENTS

RESULT 1	CS021_HUMAN	STANDARD	PRT	679 AA.
AC	081v2			
DT	13-SEP-2005 (Rel. 48, Created)			
DT	13-SEP-2005 (Rel. 48, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DN	Protein C19orf21.			
GN	Name=C19orf21;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OC	Homo			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	Tissue=Brain, and Colon;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Datchenko L., Murusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,			
RA	Brownstein W.J., Usdin T.B., Tashy S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Pahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,			
RT	Scherer A., Schein J.E., Jones S.J.M., Marra M.A.,			
RT	Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
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CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	EMBL; BC042125; AAH42125.1; -; mRNA.			
CC	EMBL; BC052235; AAH52235.1; -; mRNA.			
DR	PIR; T00636; T00636.			
DR	Ensembl; ENSG0000009812; Homo sapiens.			
DR	HGNC; HGNC:27000; C19orf21.			
KW	Coiled coil.			
FT	COILED 545 569 Potential.			
SQ	SEQUENCE 679 AA; 75357 MW; D2881CF5087B61F8 CRC64;			

Query Match 100.0%; Score 189; DB 1; Length 679;
 Best Local Similarity 100.0%; Pred. No. 4,5e-15;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQASKPPGCGQANRGVVR 36
 |||||
 Db 465 MSPRLSSSGKPLSTKQASKPPGCGQANRGVVR 500

RESULT 2
 CS021_MOUSE STANDARD; PRT; 685 AA.
 ID CS021_MOUSE
 AC QSRB3;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Protein C19orf21 homolog.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Pongo.
 NCBI_TaxID=9600;

CC
 CC NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Kidney;
 RG The German cDNA consortium;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 CC EMBL; CR858675; CAH90887.1; -; mRNA.
 DR Colled coll.
 FT COILED 551 575 Potential.
 SQ SEQUENCE 685 AA; 75892 MW; A3M9P4343396E81 CRC64;

Qy 1 MSPRLSSSGKPLSTKQASKPPGCGQANRGVVR 36
 |||||
 Db 471 MSPRLSSSGKPLSTKQASKPPGCGQANRGVVR 506

Query Match 82.0%; Score 155; DB 1; Length 665;
 Best Local Similarity 86.1%; Pred. No. 8.6e-11;
 Matches 31; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQASKPPGCGQANRGVVR 36
 |||||
 Db 471 MSPRLSSSGKPLSTKQASKPPGCGQANRGVVR 506

RESULT 3
 CS021_MOUSE STANDARD; PRT; 648 AA.
 ID CS021_MOUSE
 AC Q9D279;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Protein C19orf21 homolog.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

CC
 CC NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nakai T., Ohtsuka N., Saito R., Suzuki H., Yamashita I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balderas R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schmitt L.M., Kanapin A., Matsumoto H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad T., Brusic V., Chochia J., Corbett L.E., Cousins S.,
 RA Dalia E., Dregani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guerninich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kogiya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagasaka T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takekida Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wohlschuetz C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski B., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai K., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Saeki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).

[2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marishta K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bata S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.D., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schneringer A., Schein J.E., Jones S.J.M., Meira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AK020266; BAB32049.1; -; mRNA.
 DR EMBL; BC013508; AAH13508.1; -; mRNA.
 DR EMBL; ENSMUSG0000035852; Mus musculus.
 DR MGI; MGI:1926156; 9130017N09R1k.
 KW Colled coll.

FT COILED 511 534 Potential.
 SQ SEQUENCE 648 AA; 72281 MW; 1B395B7063B3D1F CRC64;

Query Match 52.9%; Score 100; DB 1; Length 648;
 Best Local Similarity 65.7%; Pred. No. 0.00066;
 Matches 23; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 2 SPRLSSSGKPLSTKQASKPPGCGQANRGVVR 36
 |||||
 Db 434 SPRLSSSGKPLSTKQASKPPGCGQANRGVVR 466

RESULT 4
 Q99KRO_MOUSE PRELIMINARY; PRT; 389 AA.
 ID Q99KRO_MOUSE
 AC Q99KRO;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TReMBLrel. 17, last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, last annotation update)
 DE Hspbp3 protein (Fragment).
 DE Name=Hspbp3;
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Mix FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
 RX MEDLINE=22388257; PubMed=1477932; DOI=10.1073/pnae.242603899;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rosh S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bask S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield J.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Mix FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
 RL Strusberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, RC004053, RAH04053.1, -, mRNA.
 DR HSP, P02259, IHS1.
 DR MG1, MG1:109369, Hspbp3.
 DR GO, GO:0005694, C:chromosome; IEA.
 DR GO, GO:0000786, C:nucleosome; IEA.
 DR GO, GO:0005634, C:nucleus; IEA.
 DR GO, GO:0003677, F:DNA binding; IEA.
 DR GO, GO:0005334, P:nucleosome assembly; IEA.
 DR InterPro, IPR005819, Histone H1/H5.
 DR InterPro, IPR011991, Wing hlx DNA_bd.
 DR Pfam, PF00638, Linker histone 3.
 DR PRINTS, PR00624, HISTONEHS.
 DR SMART, SM00526; H1S, 3.
 DR Chromosomal protein.
 FT NON TER 1 1
 SO SEQUENCE 389 AA; 42815 MW; 95BF67EDF113D95C CRC64;

DT 01-MAR-2004 (TReMBLrel. 26, last annotation update)
 DE Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
 DE enriched library, clone:A730077D13 product:heeterochromatin protein 2,
 DE binding protein 3, full insert sequence.
 DE Name=Hspbp3;
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RT Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
 RA Kawaji T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Caesteiro U., Nikaudo I., Pesole G., Quackenbush J.,
 RA Kuehl J., Lewis S., Maturo Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldairelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombarts P.,
 RA Nordone P., Ring B., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyrhew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RT Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RA The FANTOM Consortium;
 RA the RIKEN genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RT Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RT Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Katsuna T., Taahito H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara S., Wachihi M.,
 RA Tameda Y., Ishikawa Y., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RT Genome Res. 10:1757-1771(2000).
 RN [6]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).
DR EMBL; AK043260; BAC1507.1; -; mRNA.
DR HSSP; P02259; IHST.
DR Ensemble; ENSMUSG00000028759; Mus musculus.
DR MGI; MGI:109369; Hplbp3.
DR GO; GO:0005694; C:chromosome; IEA.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006334; P:nucleosome assembly; IEA.
DR InterPro; IPR005818; Histone H1/H5.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00538; Linker_histone; 3.
DR PRINTS; PR00624; HISTONEH5.
DR SMART; SM00526; H15; 3.
KM Chromosomal protein; Nuclear protein.
SQ SEQUENCE 516 AA; 56841 MW; 95FCF9348F26688B CRC64;

Query Match 38.6%; Score 73; DB 2; Length 516;
Best Local Similarity 53.3%; Pred. No. 1.3;
Matches 16; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

Cy 7 SESSGKPLSTKQBAKPPRGCPQNRGVVR 36
Db 426 AKSGKRTSMKRGSKPARKVPAAKRGKVR 455

RESULT 6
Q8BT17 MOUSE PRELIMINARY; PRT; 553 AA.
ID Q8BT17;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE cDNA library, clone:2610024J01 product:heterochromatin protein 2,
DE binding protein 3, full insert sequence.
GN Name=Hplbp3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

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RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochua H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L. M., Staudt F., Suzuki R., Tomita M., Wagner L., Weng L.,
RA Saito K., Orito T., Furuno M., Kono H., Baldarelli R., Barch G.,
RA Blake J., Bonfield D., Bojunga M., Carninci P., de Bonaldo M. F.,
RA Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guncionstein S., Hill D., Hofmann M., Hume D. A., Kamiya M., Lee N. H.,
RA Lyons P., Marchionni L., Mashima T., Mazzei J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K. H., Wetz C., Whitaker C., Wilming L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The PANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).
DR EMBL; AK028181; BAC25794.1; -; mRNA.
DR HSSP; P02259; IHST.
DR Ensemble; ENSMUSG00000028759; Mus musculus.
DR MGI; MGI:109369; Hplbp3.
DR GO; GO:0005694; C:chromosome; IEA.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006334; P:nucleosome assembly; IEA.
DR InterPro; IPR005818; Histone H1/H5.

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DR InterPro; IPR005819; Histone_H5.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00538; Linker histone_3.
DR SMART; SM00526; H15; 3.
DR Chromosomal protein; Nuclear protein.
KM SEQUENCE 553 AA; 60738 MW; BA903BF37792223A CRC64;
SQ SEQUENCE 553 AA; 60738 MW; BA903BF37792223A CRC64;
Query Match 38.6%; Score 73; DB 2; Length 553;
Best Local Similarity 53.3%; Pred. No. 1.4;
Matches 16; Conservative 2; Mismatches 12; Indels 0; Gaps 0;
Qy 7 SESSGKPLSTKQKASKEPPGCPQANRGVVR 36
Db 463 AKSGKTAASKMGKRGSKPARKVPAARQKVR 492
RESULT 7
Q8VE06 MOUSE PRELIMINARY; PRT; 554 AA.
AC Q8VE06;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heterochromatin protein 1, binding protein 3.
GN Name=Hplbp3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=2238657; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Schenker C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasle F.,
RA Ditchenko L., Marusheva K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleon M., Soares M.B., Bonaldi M.P., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange G.D.,
RA Rana S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherhorn A., Schain J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Director MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; BC020024; AAH20024.1; -; mRNA.
DR HSRP; P02259; 1HST.
DR Ensembl; ENSMUSG00000028759; Mus musculus.
DR MGI; MGI:109369; Hplbp3.
DR GO; GO:0005694; C:chromosome; IEA.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0006777; F:DNA binding; IEA.
DR GO; GO:0006334; P:nucleosome assembly; IEA.
DR InterPro; IPR005818; Histone_H1/H5.
DR InterPro; IPR005819; Histone_H5.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.

DR Pfam; PF00538; Linker histone_3.
DR PRINTS; PR00624; HISTONHS.
DR SMART; SM00526; H15; 3.
DR Chromosomal protein; Nuclear protein.
KM SEQUENCE 554 AA; 60856 MW; BD77604FF7AE3259 CRC64;
SQ SEQUENCE 554 AA; 60856 MW; BD77604FF7AE3259 CRC64;
Query Match 38.6%; Score 73; DB 2; Length 554;
Best Local Similarity 53.3%; Pred. No. 1.4;
Matches 16; Conservative 2; Mismatches 12; Indels 0; Gaps 0;
Qy 7 SESSGKPLSTKQKASKEPPGCPQANRGVVR 36
Db 464 AKSGKTAASKMGKRGSKPARKVPAARQKVR 493
RESULT 8
Q9DB11 MOUSE PRELIMINARY; PRT; 554 AA.
AC Q9DB11;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male liver cDNA, RIKEN full-length enriched
DE library, clone:130008A17 product:heterochromatin protein 2, binding
DE protein 3, full insert sequence.
GN Name=Hplbp3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukumishi Y., Kono H., Adachi U., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kanakawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuwari P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schmitt L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarini R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kanliya M., Lee N.H.,
RA Lyons P., Marchionni L., Washima U., Mazzarelli J., Mombere P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohntani S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA The PANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Liver;

RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.",
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagata S., Sasaki N., Carninci P.,
RA Kono H., Akiyama Y., Nishi K., Kitamura T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto S., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Iizawa M., Ohara E., Matsuki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "Riken integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Aizawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hasegaki T., Hara A., Hayatsu N., Hiramoto K., Hirakawa T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Iizawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numataki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AK004938; BAB2683.1; -, mRNA.
DR HSSBL; P02259; IHST.
DR Ensembl; ENSMUSG00000028759; Mus musculus.
DR MGI; MGI:109369; Hsp1b3.
DR GO; GO:0005634; C:chromosome; IEA.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0006377; F:DNA binding; IEA.
DR GO; GO:0006334; P:nucleosome assembly; IEA.
DR InterPro; IPR005818; Histone_H1/H5.
DR InterPro; IPR005819; Histone_H5.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00538; Linker_histone; 3.
DR PRINTS; PR00624; HISTONEH5.
DR SMART; SM00526; H15; 3.
KW Chromosomal protein; Nuclear protein.
SQ SEQUENCE 554 AA; 60868 MW; 7BC6CA49F2F02F70 CRC64;
QY
Query Match 38.6%; Score 73; DB 2; Length 554;
Best Local Similarity 53.3%; Pred. No. 1.4;
Matches 16; Conservative 2; Mismatches 12; Indels 0; Gaps 0;
Db 464 AKSQKTRASKMKRGSKPARKVPAARGKVR 493
QY 7 SESSGKPLSTKQKASKEPPRGCPQANRGVVR 36
:::|||||:::|||||
Db 464 AKSQKTRASKMKRGSKPARKVPAARGKVR 493
RESULT 9
ID Q6P747_RAT PRELIMINARY; PRT; 553 AA.
AC Q6P747;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC72624.
GN Name=MGC72624;
OS Rattus norvegicus (Rat).
RN

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Eumarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Kraemer R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang U., Heien F.,
RA Diatchenko L., Matulis A., Farmer A.A., Rubin G.M., Hong L.,
RA Scapellato M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedon T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX Strassberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; BC061837; AA61837.1; -, mRNA.
DR Ensembl; ENSRNOG00000014445; Rattus norvegicus.
DR RGD; 735099; MGC72624.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006334; P:nucleosome assembly; IEA.
DR InterPro; IPR005818; Histone_H1/H5.
DR InterPro; IPR005819; Histone_H5.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00538; Linker_histone; 3.
DR PRINTS; PR00624; HISTONEH5.
DR SMART; SM00526; H15; 3.
KW Chromosomal protein; Hypothetical protein; Nuclear protein.
SQ SEQUENCE 553 AA; 60807 MW; 1647A5B69ABEFEB CRC64;
QY
Query Match 34.4%; Score 65; DB 2; Length 553;
Best Local Similarity 46.7%; Pred. No. 14;
Matches 14; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
Db 462 AKPQKTRASKMKRGSKPARKVPAARGKVR 491
QY 7 SESSGKPLSTKQKASKEPPRGCPQANRGVVR 36
:::|||||:::|||||
Db 462 AKPQKTRASKMKRGSKPARKVPAARGKVR 491
RESULT 10
ID Q4P7A4_USTWA
AC Q4P7A4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=UM04009.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN-521;
 RA Birren B., Nuebaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Archel H., Armbruster J., Bachantang P., Baldwin J., Barry A.,
 RA Bayrol T., Bilscheyn B., Bloom T., Blye J., Boguslavsky L.,
 RA Botwary M., Boukhalter B., Brumache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Chesnang Y., Clitren M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawe T., Degray S., Dodge S., Dooley K., Dorje R.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Fato S., Ferreira P., Fischer H., Gnerre S.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearn G., Gnerre S.,
 RA Gitzke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hatz N.,
 RA Hagopian D., Hages B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Hornan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamel M., Kamat A., Kamysseles M., Karlsson E.,
 RA Kellis C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokysang T., Lokysang Y., Lueten O.,
 RA Lui A., Ma L., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marabelli R., Maru K., Matthews C., Maucelli B.,
 RA McArthur M., McDonough S., Mcghee T., Meldrum J., Mensus L.,
 RA Meztov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunhang P., Pignat B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Rector R., Richardson S., Rhee C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutan M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnuez C.,
 RA Spencer B., Stalker J., Stange-chomann N., Stavropoulos S.,
 RA Steenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchunga P.,
 RA Tenzing P., Teffaye S., Theodore J., Thoultsang Y., Topham K.,
 RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of *Ustilago maydis*."
 RC Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AAC0100140; EMBL5106.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 403 AA; 43814 MW; 4C40A6BEBBC2B8E7 CRC64;

Query Match 34.1%; Score 64.5; DB 2; Length 403;
 Best local similarity 56.0%; Pred. No. 12;
 Matches 14; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 3 PRLHSSSGKPLSTKQKASKPPRG 26
 DB 303 PTHLAIRSKPISTASBAATKPARG 327

RESULT 11
 QANSH5_9DELTA PRELIMINARY; PRT; 688 AA.
 AC QANSH5;
 DT 13-SEP-2005 (T-EMBLrel. 31, Created)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=adeHRAFT_1840;
 OS Anaeromyxobacter dehalogenans 2CP-C.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
 OC Cytophactereae; Myxococcaceae; Anaeromyxobacter.
 OK NCBI_TaxID=290397;
 RN
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN-2CP-C;
 RG US DOE Joint Genome Institute (JGI-DOE);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
 RA Hammon N., Ibrani S., Pittuck S., Richardson P.,
 RT "Sequencing of the draft genome assembly of *Anaeromyxobacter*
 RT *dehalogenans* 2CP-C."
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN-2CP-C;
 RG US DOE Joint Genome Institute (JGI-DOE);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of *Anaeromyxobacter*
 RT *dehalogenans* 2CP-C."
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AA00100022; EAL78484.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 688 AA; 75748 MW; 251BA3B9B77E0C82 CRC64;

Query Match 33.3%; Score 63; DB 2; Length 688;
 Best local similarity 48.4%; Pred. No. 33;
 Matches 15; Conservative 6; Mismatches 8; Indels 2; Gaps 2;

QY 3 PRLHSSSGKPLSTKQKASKPPRGCPQANRG 33
 DB 114 PRR-SRSSGAPWTCSTRTATPARG-PRSSRG 142

RESULT 12
 Q9SK63_MACPA PRELIMINARY; PRT; 926 AA.
 ID Q9SK63 MACPA
 AC Q9SK63;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Macaca fascicularis (Craab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 OK NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Medulla oblongata;
 RA Oseada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB065526; BAB62204.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 926 AA; 102534 MW; 8F0A496C4CA1A00C CRC64;

Query Match 33.3%; Score 63; DB 2; Length 926;
 Best local similarity 42.4%; Pred. No. 45;
 Matches 14; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 2 SPRHSSSGKPLSTKQKASKPPRGCPQANRGV 34
 DB 639 SDRVPHSSRPVGHKESPKPGGGPAAAGV 671

RESULT 13
 Q9P2P5_HUMAN PRELIMINARY; PRT; 950 AA.
 ID Q9P2P5 HUMAN
 AC Q9P2P5;
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
 DE KIAA1392 protein (Fragment).

```

GN Name=K1AA1392;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=20181126; PubMed=10718198;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVI.
RT The complete sequences of 150 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:65-73(2000).
DR EMBL; AB037813; BAA92630.1; -; mRNA.
DR Ensembl; ENSG00000173320; Homo sapiens.
FT NON TER
SQ SEQUENCE 950 AA; 105132 MW; 83D23F5081770689 CRC64;

Query Match 33.3%; Score 63; DB 2; Length 950;
Best Local Similarity 42.4%; Pred. No. 46;
Matches 14; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Oy 2 SPRHSSSGKPLSTKQASKPPRCGPQANR 34
Db 663 SDRVPHSSRPVGHKESPKGPGGPAASGV 695

RESULT 14
O611M2_CABBR PRELIMINARY; PRT; 732 AA.
AC O611M2_2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein CBG17014.
GN Name=CBG17014;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC01000080; CAB70437.1; -; Genomic DNA.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001841; Znf_RING.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Nuclear protein; Zinc;
KW Zinc-finger.
SQ SEQUENCE 732 AA; 84426 MW; F62612AB8A1BABA9 CRC64;

Query Match 32.8%; Score 62; DB 2; Length 732;
Best Local Similarity 44.8%; Pred. No. 46;
Matches 13; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Oy 4 RHLSSESGKPLSTKQASKPPRCGPQANR 32
Db 383 RSTSESSSPSEMPSSKESQSPKCSR 411

RESULT 15
O60KX3_CABBR PRELIMINARY; PRT; 930 AA.

```

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AC O60KX3;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein CBG23864.
GN Name=CBG23864;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC01000197; CAB56229.1; -; Genomic DNA.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001841; Znf_RING.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Nuclear protein; Zinc;
KW Zinc-finger.
SQ SEQUENCE 930 AA; 106885 MW; A557783EF3BA15EB CRC64;

Query Match 32.8%; Score 62; DB 2; Length 930;
Best Local Similarity 44.8%; Pred. No. 60;
Matches 13; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Oy 4 RHLSSESGKPLSTKQASKPPRCGPQANR 32
Db 582 RSTSESSSPSEMPSSKESQSPKCSR 610

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Search completed: March 3, 2006, 13:26:06
 Job time : 15.7493 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleleration Ltd.

OM protein - protein search, using 6w model

Run on: March 3, 2006, 13:35:46 ; Search time 4.82799 Seconds
(without alignments)
616.473 Million cell updates/sec

Title: US-10-646-873-43

Perfect score: 189
Sequence: 1 MSPHLLSSSSKPKPLSTKQKASKPRGCPQANRQVVR 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5-COMB.pep: *
2: /cgn2_6/prodata/1/1aa/6-COMB.pep: *
3: /cgn2_6/prodata/1/1aa/H-COMB.pep: *
4: /cgn2_6/prodata/1/1aa/PCTUS-COMB.pep: *
5: /cgn2_6/prodata/1/1aa/RE-COMB.pep: *
6: /cgn2_6/prodata/1/1aa/backfillset1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189	100.0	36	2	US-09-050-516-43
2	189	100.0	36	2	US-10-278-547-43
3	189	100.0	215	2	US-09-050-516-47
4	189	100.0	215	2	US-10-278-547-47
5	189	100.0	679	2	US-09-050-516-42
6	189	100.0	679	2	US-10-278-547-42
7	58	30.7	108	2	US-09-270-767-57993
8	58	30.7	374	2	US-09-270-767-42674
9	58	30.7	453	2	US-09-686-5838-12
10	55.5	29.4	1036	2	US-09-302-540-14218
11	54.5	28.8	305	2	US-09-248-796A-17640
12	54.5	28.8	424	2	US-09-149-476-555
13	53.5	28.3	726	2	US-09-252-991A-32256
14	53	28.0	116	2	US-09-270-767-59667
15	53	28.0	248	2	US-09-270-767-44243
16	53	28.0	454	2	US-09-252-991A-22080
17	53	28.0	630	2	US-09-657-252-4
18	52.5	27.8	84	2	US-09-461-325-455
19	52.5	27.8	84	2	US-10-012-542-455
20	52.5	27.8	84	2	US-10-115-123-455
21	52.5	27.8	84	2	US-09-252-991A-28970
22	52	27.5	55	2	US-09-041-889-41
23	52	27.5	55	2	US-09-417-264-41
24	52	27.5	132	2	US-09-252-991A-20779
25	52	27.5	158	2	US-09-041-889-40
26	52	27.5	158	2	US-09-417-264-40
27	52	27.5	222	2	US-09-041-889-3

28	52	27.5	222	2	US-08-837-058-3	Sequence 3, Appl
29	52	27.5	222	2	US-09-417-264-3	Sequence 3, Appl
30	52	27.5	226	2	US-09-041-889-32	Sequence 32, Appl
31	52	27.5	226	2	US-09-417-264-12	Sequence 32, Appl
32	52	27.5	416	2	US-09-902-540-10136	Sequence 10136, A
33	51.5	27.2	713	2	US-09-335-409-11	Sequence 11, Appl
34	51.5	27.2	713	2	US-09-567-969-11	Sequence 11, Appl
35	51.5	27.2	713	2	US-09-567-969-11	Sequence 11, Appl
36	51.5	27.2	713	2	US-09-568-480-11	Sequence 11, Appl
37	51.5	27.2	713	2	US-09-568-486-11	Sequence 11, Appl
38	51.5	27.2	713	2	US-09-568-472-11	Sequence 11, Appl
39	51.5	27.2	713	2	US-09-567-899-11	Sequence 11, Appl
40	51.5	27.2	713	2	US-10-014-717-11	Sequence 11, Appl
41	51	27.0	254	2	US-09-252-991A-26135	Sequence 26135, A
42	51	27.0	279	2	US-09-252-991A-18863	Sequence 18863, A
43	51	27.0	399	2	US-10-023-180-64	Sequence 64, Appl
44	51	27.0	474	2	US-08-729-416C-11	Sequence 11, Appl
45	51	27.0	474	2	US-09-433-353-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-050-516-43
Sequence 43, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPE, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/938-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPR: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-43

Query Match 100.0%; Score 189; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.6e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRHSSSGKPLSTKQASKPPRCGCPQANRGVVR 36
Db 1 MSPRHSSSGKPLSTKQASKPPRCGCPQANRGVVR 36

RESULT 2
US-10-278-547-43

Sequence 43, Application US/10278547
Patent No. 6660834
GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPR: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:

US-10-278-547-43

Query Match 100.0%; Score 189; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.6e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRHSSSGKPLSTKQASKPPRCGCPQANRGVVR 36
Db 1 MSPRHSSSGKPLSTKQASKPPRCGCPQANRGVVR 36

RESULT 3
US-09-050-516-47

Sequence 47, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAP, LISA
RUSSELL, JOHN C.

APPLICANT: STROUPE, STEPHEN D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPR: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-47

Query Match 100.0%; Score 189; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 7.3e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRHLSSSGKPLSTKQASKPPRCGPQANRGVVR 36
DB 1 MSPRHLSSSGKPLSTKQASKPPRCGPQANRGVVR 36

RESULT 4

US-10-278-547-47
Sequence 47, Application US/10278547
Patent No. 6660834

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547

FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065.US.PI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6660834e

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-10-278-547-47

Query Match 100.0%; Score 189; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 7.3e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRHLSSSGKPLSTKQASKPPRCGPQANRGVVR 36
DB 1 MSPRHLSSSGKPLSTKQASKPPRCGPQANRGVVR 36

RESULT 5

US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. 6627414

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITTS, TRACEY L.

FRIEDMAN, PAULA N.

GORDON, JULIAN

GRANADOS, EDWARD N.

HAYDEN, MARK

HODGES, STEVEN C.

KLASS, MICHAEL R.

KRATOCHVIL, JON D.

ROBERTS-RAPP, LISA

RUSSELL, JOHN C.

STROUPE, STEPHEN D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065.US.PI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 679 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6627414e

US-09-050-516-42

Query Match 100.0%; Score 189; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRHLSSSGKPLSTKQASKPPRCGPQANRGVVR 36
DB 465 MSPRHLSSSGKPLSTKQASKPPRCGPQANRGVVR 500

RESULT 6

US-10-278-547-42

Sequence 42, Application US/10278547

Patent No. 6660834

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-278-547-42

Query Match 100.0%; Score 189; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQKASKPPRCGPQANGVVR 36
Db 465 MSPRLSSSGKPLSTKQKASKPPRCGPQANGVVR 500

RESULT 7
US-09-270-767-57993
Sequence 57993, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57993

LENGTH: 108
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-57993

Query Match 30.7%; Score 58; DB 2; Length 108;
Best Local Similarity 48.3%; Pred. No. 1.1;
Matches 14; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

Qy 2 SPRLSSSGKPLSTKQKASKPPRCGPQ 30
Db 47 APTALSVSAGQPLATQATG--PGGQPQ 73

RESULT 8
US-09-270-767-42674
Sequence 42674, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42674
LENGTH: 374
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42674

Query Match 30.7%; Score 58; DB 2; Length 374;
Best Local Similarity 48.3%; Pred. No. 5;
Matches 14; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

Qy 2 SPRLSSSGKPLSTKQKASKPPRCGPQ 30
Db 313 APTALSVSAGQPLATQATG--PGGQPQ 339

RESULT 9
US-09-686-583B-12
Sequence 12, Application US/09686583B
Patent No. 6576750
GENERAL INFORMATION:
APPLICANT: Heska Corporation
APPLICANT: Gaines, Patrick J.
APPLICANT: Mienski, Nancy
TITLE OF INVENTION: FLUA PERITOPHIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
FILE REFERENCE: FC-6-C2
CURRENT APPLICATION NUMBER: US/09/686,583B
CURRENT FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: 09/543,668
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,704
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 453
TYPE: PRT
ORGANISM: Ctenocephalides felis
US-09-686-583B-12

Query Match 30.7%; Score 58; DB 2; Length 453;
Best Local Similarity 44.4%; Pred. No. 6.3;
Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 7 SSSGKPLSTKQKASKPPRCGPQANG 33
Db 3 SSSGKPLSTKQKASKPPRCGPQANG 33

Db 318 TBPSTKPTSTPTATKPPQEIFCKQGS 344

RESULT 10

US-09-902-540-14218
 / Sequence 14218, Application US/09902540
 / Patent No. 6833447
 / GENERAL INFORMATION:
 / APPLICANT: Goldman, Barry S.
 / APPLICANT: Hinkle, Gregory J.
 / APPLICANT: Slater, Steven C.
 / APPLICANT: Wiegand, Roger C.
 / TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 / FILE REFERENCE: 38-10(15849)B
 / CURRENT APPLICATION NUMBER: US/09/902,540
 / PRIOR FILING DATE: 2001-07-10
 / PRIOR APPLICATION NUMBER: 60/217,883
 / PRIOR FILING DATE: 2000-07-10
 / NUMBER OF SEQ ID NOS: 16825
 / SEQ ID NO 14218
 / LENGTH: 1036
 / TYPE: PRT
 / ORGANISM: Myxococcus xanthus
 / US-09-902-540-14218

Query Match 29.4%; Score 55.5; DB 2; Length 1036;
 Best Local Similarity 48.1%; Pred. No. 38;

Matches 13; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

Qy 2 SPRHLSGSGKPLSTKQKSKPPRCGP 28

Db 581 APGHGAPLGGP-STSDASPPGAP 606

RESULT 11

US-09-248-796A-17640
 / Sequence 17640, Application US/09248796A
 / Patent No. 6747137
 / GENERAL INFORMATION:
 / APPLICANT: Kelch Weinstock et al
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 / FILE REFERENCE: 107196.132
 / CURRENT APPLICATION NUMBER: US/09/248,796A
 / PRIOR FILING DATE: 1999-02-12
 / PRIOR APPLICATION NUMBER: US 60/074,725
 / PRIOR FILING DATE: 1998-02-13
 / PRIOR APPLICATION NUMBER: US 60/096,409
 / PRIOR FILING DATE: 1998-08-13
 / NUMBER OF SEQ ID NOS: 28208
 / SEQ ID NO 17640
 / LENGTH: 305
 / TYPE: PRT
 / ORGANISM: Candida albicans
 / US-09-248-796A-17640

Query Match 28.8%; Score 54.5; DB 2; Length 305;
 Best Local Similarity 43.8%; Pred. No. 12;

Matches 14; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

Qy 4 RHLSSGKPLSTKQKSKPPRCGPQANRGV 35

Db 144 RLSSGSKVPSRLRTVSKTYR-----EGIV 170

RESULT 12

US-09-149-476-555
 / Sequence 555, Application US/09149476
 / Patent No. 6420526
 / GENERAL INFORMATION:
 / APPLICANT: Rosen et al.
 / TITLE OF INVENTION: 186 Human Secreted proteins
 / FILE REFERENCE: P2002PI

CURRENT APPLICATION NUMBER: US/09/149,476
 / CURRENT FILING DATE: 1998-09-08
 / EARLIER APPLICATION NUMBER: PCT/US98/04493
 / EARLIER FILING DATE: 1998-03-06
 / EARLIER APPLICATION NUMBER: 60/040,162
 / EARLIER FILING DATE: 1997-03-07
 / EARLIER APPLICATION NUMBER: 60/040,333
 / EARLIER FILING DATE: 1997-03-07
 / EARLIER APPLICATION NUMBER: 60/038,621
 / EARLIER FILING DATE: 1997-03-07
 / EARLIER APPLICATION NUMBER: 60/040,626
 / EARLIER FILING DATE: 1997-03-07
 / EARLIER APPLICATION NUMBER: 60/040,334
 / EARLIER FILING DATE: 1997-03-07
 / EARLIER APPLICATION NUMBER: 60/040,336
 / EARLIER FILING DATE: 1997-03-07
 / EARLIER APPLICATION NUMBER: 60/040,163
 / EARLIER FILING DATE: 1997-03-07
 / EARLIER APPLICATION NUMBER: 60/047,600
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,615
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,597
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,583
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,617
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,618
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,503
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,592
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,581
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,584
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,500
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,587
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,492
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,598
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,613
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,582
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,596
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/047,612
 / EARLIER FILING DATE: 1997-05-23
 / EARLIER APPLICATION NUMBER: 60/043,580
 / EARLIER FILING DATE: 1997-04-11
 / EARLIER APPLICATION NUMBER: 60/043,568
 / EARLIER FILING DATE: 1997-04-11
 / EARLIER APPLICATION NUMBER: 60/043,314
 / EARLIER FILING DATE: 1997-04-11
 / EARLIER APPLICATION NUMBER: 60/043,569
 / EARLIER FILING DATE: 1997-04-11
 / EARLIER APPLICATION NUMBER: 60/043,311
 / EARLIER FILING DATE: 1997-04-11
 / EARLIER APPLICATION NUMBER: 60/043,671

EARLIER FILING DATE: 1997-04-11
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EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/043, 315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048, 974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056, 886
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 662
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047, 590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 589
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 614
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047, 501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043, 670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056, 632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 876
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057, 650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056, 884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057, 669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049, 610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061, 060
EARLIER FILING DATE: 1997-10-02

Query Match 28.8%; Score 54.5; DB 2; Length 424;
Best Local Similarity 42.9%; Pred. No. 18;
Matches 11; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Cy 2 SPRHSSGKPLSTKQASKPPRCQ 29
Db 359 APRHYXSSGEVGV-QEGDPPSQGXQ 385

RESULT 13
US-09-252-991A-32256
Sequence 32256, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OR INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074, 788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094, 190
PRIOR FILING DATE: 1998-07-27

Job time : 5.99466 secs

NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 32256
 LENGTH: 736
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-32256

Query Match 28.3%; Score 53.5; DB 2; Length 736;
 Best Local Similarity 31.1%; Pred. No. 49;
 Matches 14; Conservative 6; Mismatches 12; Indels 13; Gaps 1;

QY 2 SPRHSESSGK-----LSTKQKASKPPGCPQANRG 33
 DB 76 SPTVSEDPQPRQAGRTPEITDDRSVATHQKAAHROGCPQRYPG 120

RESULT 14
 US-09-270-767-59667
 Sequence 59667, Application US/09270767
 Patent No. 6703491
 GENERAL INFORMATION:
 APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 FILE REFERENCE: File Reference: 7326-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 CURRENT FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 59667
 LENGTH: 116.
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 US-09-270-767-59667

Query Match 28.0%; Score 53; DB 2; Length 116;
 Best Local Similarity 34.0%; Pred. No. 63;
 Matches 16; Conservative 6; Mismatches 11; Indels 14; Gaps 2;

QY 4 RHLSESSGK-----PLSTKQKASKPPR-----GCPQANRGVVR 36
 DB 45 RHRAKAYKCDICSMPLATKQDLSLHMRHHKNDRRYKCDKCNKGVR 91

RESULT 15
 US-09-270-767-44243
 Sequence 44243, Application US/09270767
 Patent No. 6703491
 GENERAL INFORMATION:
 APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 FILE REFERENCE: File Reference: 7326-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 CURRENT FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 44243
 LENGTH: 248
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 FEATURE:
 OTHER INFORMATION: Xaa means any amino acid
 US-09-270-767-44243

Query Match 28.0%; Score 53; DB 2; Length 248;
 Best Local Similarity 34.0%; Pred. No. 16;
 Matches 16; Conservative 6; Mismatches 11; Indels 14; Gaps 2;

QY 4 RHLSESSGK-----PLSTKQKASKPPR-----GCPQANRGVVR 36
 DB 45 RHRAKAYKCDICSMPLATKQDLSLHMRHHKNDRRYKCDKCNKGVR 91

Search completed: March 3, 2006, 13:38:52

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OM protein - protein search, using sw model

Run on: March 3, 2006, 14:09:14 ; Search time 15.8134 Seconds
(without alignments)
951.209 Million cell updates/sec

Title: US-10-646-873-43

Perfect score: 189
Sequence: 1 MSPRHLSSSGKPISTKQKASPRGCPQANRGVVR 36

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA Main:*

- 1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep.*
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- 6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189	100.0	36	3 US-09-050-516-43	Sequence 43, Appl
2	189	100.0	36	4 US-10-278-547-43	Sequence 43, Appl
3	189	100.0	36	4 US-10-646-873-43	Sequence 43, Appl
4	189	100.0	215	3 US-09-050-516-47	Sequence 47, Appl
5	189	100.0	215	4 US-10-278-547-47	Sequence 47, Appl
6	189	100.0	215	4 US-10-646-873-47	Sequence 47, Appl
7	189	100.0	679	3 US-09-050-516-42	Sequence 42, Appl
8	189	100.0	679	4 US-10-278-547-42	Sequence 42, Appl
9	189	100.0	679	4 US-10-646-873-42	Sequence 42, Appl
10	65	34.4	88	4 US-10-425-115-311348	Sequence 311348, Ap
11	63	33.3	950	5 US-10-756-149-5275	Sequence 308283, Ap
12	60	31.7	484	4 US-10-425-115-308283	Sequence 308283, Ap
13	59.5	31.5	112	4 US-10-425-115-238611	Sequence 113926, Ap
14	59	31.2	344	4 US-10-437-963-113926	Sequence 113926, Ap
15	58	30.7	118	4 US-10-425-115-270466	Sequence 270466, Ap
16	58	30.7	162	4 US-10-425-115-48907	Sequence 48907, A
17	58	30.7	453	3 US-09-991-936-1883	Sequence 1883, Ap
18	58	30.7	453	4 US-10-401-324-12	Sequence 12, Appl
19	58	30.7	453	5 US-10-978-245-1883	Sequence 1883, Ap
20	58	30.7	453	4 US-10-437-963-179332	Sequence 179332, Ap
21	58	30.7	1219	6 US-11-097-143-22956	Sequence 22956, A
22	57	30.2	107	4 US-10-029-386-28838	Sequence 28838, A
23	57	30.2	116	4 US-10-425-115-284578	Sequence 284578, A
24	57	30.2	435	4 US-10-425-115-240156	Sequence 240156, A
25	57	30.2	488	4 US-10-385-742-20	Sequence 20, Appl
26	57	30.2	620	4 US-10-767-701-45482	Sequence 45482, A
27	57	30.2	737	4 US-10-437-963-161203	Sequence 161203, A

ALIGNMENTS

28	56.5	29.9	71	4 US-10-437-963-122399	Sequence 122399, A
29	56.5	29.9	231	4 US-10-767-701-38778	Sequence 38778, A
30	56	29.6	70	4 US-10-425-115-315597	Sequence 315597, A
31	56	29.6	127	4 US-10-425-115-344980	Sequence 344980, A
32	56	29.6	157	4 US-10-437-963-198615	Sequence 198615, A
33	56	29.6	179	4 US-10-425-115-335339	Sequence 335339, A
34	56	29.6	446	4 US-10-437-963-179677	Sequence 179677, A
35	56	29.6	449	4 US-10-425-115-304540	Sequence 304540, A
36	56	29.6	1104	4 US-10-437-963-114194	Sequence 114194, A
37	56	29.6	1416	6 US-11-097-143-24990	Sequence 24990, A
38	56	29.6	1520	5 US-10-467-555-14	Sequence 14, Appl
39	55.5	29.4	111	3 US-09-867-550-1410	Sequence 1410, Ap
40	55.5	29.4	120	4 US-10-425-115-314833	Sequence 314833, A
41	55.5	29.4	123	4 US-10-425-115-239201	Sequence 239201, A
42	55.5	29.4	132	4 US-10-425-115-222414	Sequence 222414, A
43	55.5	29.4	150	4 US-10-425-115-214955	Sequence 214955, A
44	55	29.1	110	4 US-10-437-963-113542	Sequence 113542, A
45	55	29.1	151	4 US-10-424-599-253081	Sequence 253081, A

RESULT 1
US-09-050-516-43
Sequence 43, Application US/09050516
Patent No. US20100109041
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-PAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/938-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-43

Query Match 100.0%; Score 189; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRHSSSGKPLSTKQASKPPRGCPQANRGVVR 36
Db 1 MSPRHSSSGKPLSTKQASKPPRGCPQANRGVVR 36

RESULT 2
US-10-278-547-43
Sequence 43, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:

US-10-278-547-43

Query Match 100.0%; Score 189; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRHSSSGKPLSTKQASKPPRGCPQANRGVVR 36
Db 1 MSPRHSSSGKPLSTKQASKPPRGCPQANRGVVR 36

RESULT 3
US-10-646-873-43
Sequence 43, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-646-873-43

Query Match 100.0%; Score 189; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRHLSSSGKPLSTKQASKPPRCPOANGVVR 36
DB 1 MSPRHLSSSGKPLSTKQASKPPRCPOANGVVR 36

RESULT 4

US-09-050-516-47
Sequence 47, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-47

Query Match 100.0%; Score 189; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.8e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRHLSSSGKPLSTKQASKPPRCPOANGVVR 36
DB 1 MSPRHLSSSGKPLSTKQASKPPRCPOANGVVR 36

RESULT 5.

US-10-278-547-47
Sequence 47, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-278-547-47

Query Match 100.0%; Score 189; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.8e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRHLSSSGKPLSTKQASKPPRCPOANGVVR 36
DB 1 MSPRHLSSSGKPLSTKQASKPPRCPOANGVVR 36

RESULT 6

US-10-646-873-47
Sequence 47, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE

COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040643406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-646-873-47
Query Match 100.0%; Score 189; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.8e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 MSPRHSSSGKPLSTKQASKPPRGCPQANRGVVR 36
Db 1 MSPRHSSSGKPLSTKQASKPPRGCPQANRGVVR 36
RESULT 7
US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANDOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.

APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-42
Query Match 100.0%; Score 189; DB 3; Length 679;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 MSPRHSSSGKPLSTKQASKPPRGCPQANRGVVR 36
Db 465 MSPRHSSSGKPLSTKQASKPPRGCPQANRGVVR 500
RESULT 8
US-10-278-547-42
Sequence 42, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANDOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-278-547-42

Query Match
Best Local Similarity 100.0%; Score 189; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRHSSESGKPLSTKQASKEPRGCPQANRGVVR 36
|||||
DB 465 MSPRHSSESGKPLSTKQASKEPRGCPQANRGVVR 500

RESULT 9
US-10-646-873-42
; Sequence 42, Application US/10646873
; Publication No. US20040043406A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; COHEN, MAURICE
; COLPITS, TRACEY L.
; FRIEDMAN, PAULA N.
; GORDON, JULIAN
; GRANADOS, EDWARD N.
; HAYDEN, MARK
; HODGES, STEVEN C.
; KLAS, MICHAEL R.
; KRATOCHVIL, JON D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE GASTROINTESTINAL
; TRACT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-646-873-42

Query Match
Best Local Similarity 100.0%; Score 189; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRHSSESGKPLSTKQASKEPRGCPQANRGVVR 36
|||||
DB 465 MSPRHSSESGKPLSTKQASKEPRGCPQANRGVVR 500

RESULT 10
US-10-425-115-311348
; Sequence 311348, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 311348
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(88)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_47002C.1.pep
; US-10-425-115-311348

Query Match
Best Local Similarity 34.4%; Score 65; DB 4; Length 88;
Best Local Similarity 47.8%; Pred. No. 1.7;
Matches 11; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Oy 11 GKPLSTKQASKPPRGCPQANRG 33
Db 3 GRPKGCPGCGKPPGCGCPQMRG 25

RESULT 11

US-10-756-149-5275
; Sequence 5275, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5275
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5275

Query Match 33.3%; Score 63; DB 5; Length 950;
Best Local Similarity 42.4%; Pred. No. 42;
Matches 14; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Oy 2 SPRHLSSESGKPLSTKQASKPPRGCPQANRGV 34
Db 663 SDRQVPHSRPVPVGHKESPPKGGCPAASGV 695

RESULT 12

US-10-425-115-308283
; Sequence 308283, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 308283
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(494)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_44220C.1.pcp
US-10-425-115-308283

Query Match 31.7%; Score 60; DB 4; Length 494;
Best Local Similarity 45.2%; Pred. No. 49;
Matches 14; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

Oy 2 SPRHLSSESGKPLSTKQASKPPRGCPQANR 32
Db 8 SPRHLSFSPTRAPSTPRPASPPSPNAPSSKR 38

RESULT 13

US-10-425-115-238611
; Sequence 238611, Application US/10425115

; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 238611
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_17668C.1.pcp
US-10-425-115-238611

Query Match 31.5%; Score 59.5; DB 4; Length 112;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 13; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

Oy 3 PRHLSSESGKPLSTKQASKPPRGCP 27
Db 44 PRSSSSRRAPLGTBRPALKPSRSC 69

RESULT 14

US-10-437-963-113926
; Sequence 113926, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 113926
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(344)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_17668C.1.pcp
US-10-437-963-113926

Query Match 31.2%; Score 59; DB 4; Length 344;
Best Local Similarity 36.7%; Pred. No. 44;
Matches 11; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Oy 3 PRHLSSESGKPLSTKQASKPPRGCPQANR 32
Db 135 PRHGEAPXGAPLRRRTSPAPRPPSPXSTR 164

RESULT 15

US-10-425-115-270466
; Sequence 270466, Application US/10425115
; Publication No. US20040214272A1

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; GENERAL INFORMATION:
; APPLICANT: LA ROBA, Thomas J.
; APPLICANT: KOVALIC, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 270466
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_178264C.1.pap
US-10-425-115-270466

Query Match          30.7%; Score 58; DB 4; Length 118;
Best Local Similarity 34.1%; Pred. No. 18;
Matches 14; Conservative 7; Mismatches 12; Indels 8; Gaps 1;

QY 1 MSPRHLSESSGK-----PLSTKQKASKPPRGCPQANRG 33
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 40 LSPSPQSKNGKNGKFTNGHLFPKNSPKKTFFPPRGKQQTNGG 80

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Search completed: March 3, 2006, 14:18:09
 Job time : 16.8134 secs

100% Pure
Black Ink
(100%)

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OM protein - protein search, using SW model

Run on: March 3, 2006, 14:10:51 ; Search time 1.71429 Seconds
(without alignments)
420.009 Million cell updates/sec

Title: US-10-646-873-43

Perfect score: 1 MSPHLSSESGKPISTKQKSKPPGCGQANRGVVR 36

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New:
1: /cgn2_6/ptodata/1/pubpa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpa/PCT_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubpa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/1/pubpa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/1/pubpa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	27.5	687	US-10-055-877-203	Sequence 203, App
2	51	27.0	514	US-10-821-234-998	Sequence 998, App
3	51	27.0	732	US-11-072-512-3474	Sequence 3474, App
4	50	26.5	258	US-11-072-512-3034	Sequence 3034, App
5	50	26.5	299	US-11-156-084-340	Sequence 340, App
6	50	26.5	501	US-11-173-893-10	Sequence 10, App
7	50	26.5	560	US-11-173-893-4	Sequence 4, App
8	50	26.5	749	US-11-072-512-2622	Sequence 2622, App
9	50	26.5	768	US-11-173-893-2	Sequence 2, App
10	50	26.5	2769	US-11-113-424-14	Sequence 14, App
11	49.5	26.2	459	US-11-087-099-9854	Sequence 9854, App
12	49.5	26.2	473	US-10-131-8264-382	Sequence 382, App
13	49.5	26.2	473	US-10-973-1158-382	Sequence 382, App
14	49.5	26.2	2760	US-11-124-3674-444	Sequence 444, App
15	49.5	26.2	2803	US-11-124-3674-442	Sequence 442, App
16	49.5	26.2	2803	US-11-124-3674-445	Sequence 445, App
17	49.5	26.2	2984	US-11-124-3674-443	Sequence 443, App
18	49.5	26.2	3027	US-11-124-3674-441	Sequence 441, App
19	48.5	25.7	96	US-10-330-773-171	Sequence 171, App
20	48.5	25.7	854	US-11-087-099-5642	Sequence 5642, App
21	48	25.4	218	US-10-467-657-4470	Sequence 4470, App
22	47.5	25.1	451	US-10-330-773-352	Sequence 352, App
23	47.5	25.1	512	US-11-087-099-1062	Sequence 1062, App
24	47.5	25.1	637	US-11-087-099-7996	Sequence 7996, App
25	47	24.9	212	US-11-214-199-4	Sequence 4, App

26	47	24.9	327	5	US-09-978-360A-750	Sequence 750, App
27	47	24.9	388	6	US-10-858-730-83	Sequence 83, App
28	47	24.9	837	7	US-11-094-519A-43	Sequence 43, App
29	47	24.9	845	7	US-11-094-519A-42	Sequence 42, App
30	47	24.9	885	6	US-10-912-971-2	Sequence 2, App
31	47	24.9	1839	7	US-11-087-099-9631	Sequence 9631, App
32	46.5	24.6	355	6	US-10-467-657-5428	Sequence 5428, App
33	46.5	24.3	44	6	US-10-467-657-7398	Sequence 4718, App
34	46	24.3	68	6	US-10-467-657-4718	Sequence 4718, App
35	46	24.3	104	6	US-10-330-773-167	Sequence 173, App
36	46	24.3	107	6	US-10-330-773-173	Sequence 175, App
37	46	24.3	107	6	US-10-330-773-175	Sequence 177, App
38	46	24.3	107	6	US-10-330-773-177	Sequence 157, App
39	46	24.3	279	6	US-10-878-556A-157	Sequence 159, App
40	46	24.3	326	7	US-10-330-773-169	Sequence 33, App
41	46	24.3	338	7	US-11-207-626A-33	Sequence 1094, App
42	46	24.3	702	7	US-11-098-686-10194	Sequence 2398, App
43	46	24.3	951	7	US-11-121-438-14	Sequence 14, App
44	46	24.3	1823	6	US-10-995-561-988	Sequence 988, App
45	46	24.3	2102	6	US-10-995-561-990	Sequence 990, App

ALIGNMENTS

RESULT 1
US-10-055-877-203
Sequence 203, Application US/10055877
Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: Decisiofaro, Marc
APPLICANT: Padigar, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchenev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Szytek, Kimberly
APPLICANT: Rattell, Luca
APPLICANT: Kexuda, Ramesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zerhusen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Patburjan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Elsen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shinkels, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Steacie
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25

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; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 203
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-055-877-203
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Query Match          27.5%; Score 52; DB 6; Length 687;
Best Local Similarity 53.6%; Pred. No. 19;
Matches 15; Conservative 2; Mismatches 7; Indels 4; Gaps 2;
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Oy          9 SSGKPLSTKQKASRPRGCPQANRGVVR 36
             |||||:|||||:|||||:|||||:
Db          11 SSGKPV-TLOELMGP---CPRIIRGVRR 34
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RESULT 2
US-10-821-234-998
; Sequence 998, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
```

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; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 998
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-998
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Query Match          27.0%; Score 51; DB 6; Length 514;
Best Local Similarity 44.8%; Pred. No. 19;
Matches 13; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
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Oy          4 RHLSSESGKPLSTKQKASRPRGCPQANR 32
             |||||:|||||:|||||:|||||:
Db          461 RGLSSSSGSGSKSQSTSPGQALENR 489
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```
RESULT 3
US-11-072-512-3474
; Sequence 3474, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
```

```
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
```

```
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3474
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3474
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Query Match          27.0%; Score 51; DB 7; Length 732;
Best Local Similarity 42.4%; Pred. No. 28;
Matches 14; Conservative 7; Mismatches 8; Indels 4; Gaps 2;
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Oy          1 MSPHLSSESGKPLSTKQKASR-PRGCPQANR 32
             |||||:|||||:|||||:|||||:
Db          1 MTP---PKSSQELLSVRQSEVPEPQGVPRKKER 30
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```
RESULT 4
US-11-072-512-3034
; Sequence 3034, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
```

```
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: HIO, YURI
; APPLICANT: ISONO, YUUKO
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3034
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3034
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Query Match 26.5%; Score 50; DB 7; Length 258;
Best Local Similarity 33.3%; Pred. No. 12;
Matches 14; Conservative 2; Mismatches 16; Indels 10; Gaps 1;

QY 2 SPRHLSSES-----GKPLSTKQASKPPGCPQANR 33
DB 202 SPRHLSSESSTSTSSPSTSSPSSSSPSSSSCPALG 243

RESULT 5
US-11-156-084-340
; Sequence 340, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OR INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: Patent version 3.2
; SEQ ID NO 340
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Prochlorococcus marinus str. MIT 9313
US-11-156-084-340

Query Match 26.5%; Score 50; DB 7; Length 299;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 9 SSGKPLSTKQASKPP 24
DB 170 ATGKPLTQCGSSPPP 185

RESULT 6
US-11-173-893-10
; Sequence 10, Application US/11173893
; Publication No. US20060029602A1
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; TITLE OR INVENTION: Gamma-Heraguin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/173,893
; FILING DATE: 07/01/2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,845
; FILING DATE: 07/10/1997
; CLASSIFICATION:
; APPLICATION NUMBER: 60/021640
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

Query Match 26.5%; Score 50; DB 7; Length 501;
Best Local Similarity 37.9%; Pred. No. 25;
Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 2 SPRHLSSESGKPLSTKQASKPPGCPQA 30
DB 26 SPLFCTTSPGYPLTSTVTSVSPPPPLPRLPS 54

RESULT 7
US-11-173-893-4
; Sequence 4, Application US/11173893
; Publication No. US20060029602A1
; GENERAL INFORMATION:
; APPLICANT: Schaefer, Gabriele M.
; TITLE OR INVENTION: Gamma-Heraguin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/173,893
; FILING DATE: 07/01/2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,845
; FILING DATE: 07/10/1997
; CLASSIFICATION:
; APPLICATION NUMBER: 60/021640
; FILING DATE: 07/12/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

Query Match 26.5%; Score 50; DB 7; Length 560;
Best Local Similarity 37.9%; Pred. No. 28;
Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 2 SPRHLSSESGKPLSTKQASKPPGCPQA 30
DB 293 SPLFCTTSPGYPLTSTVTSVSPPPPLPRLPS 321

RESULT 8
US-11-072-512-2622
Sequence 2622, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2622
LENGTH: 749
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-2622

Query Match 26.5%; Score 50; DB 7; Length 749;
Best Local Similarity 38.1%; Pred. No. 39;
Matches 16; Conservative 4; Mismatches 6; Indels 16; Gaps 3;

QY 7 SESS-----GKPLSTKQKASKPPRCPO-----ANRCV 34
Db 132 SEASLDLQGRVPT--EASVQPVACPOVSVISRPEPVANEGI 171

RESULT 9
US-11-173-893-2
Sequence 2, Application US/11173893
Publication No. US20060029602A1
GENERAL INFORMATION:
APPLICANT: Schaefer, Gabriele M.
APPLICANT: Sliwowski, Mark
TITLE OF INVENTION: Gamma-Heraguilin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Pointe San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/173,893

FILING DATE: 07/01/2005
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/891,845
FILING DATE: 07/10/1997
CLASSIFICATION:
APPLICATION NUMBER: 60/021640
FILING DATE: 07/12/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 768 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-11-173-893-2

Query Match 26.5%; Score 50; DB 7; Length 768;
Best Local Similarity 37.9%; Pred. No. 40;
Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 2 SPRHSSSGKPLSTKQKASKPPRCPOA 30
Db 293 SPFLCTTSPPYPLTSTVSPPPRPLPRS 321

RESULT 10
US-11-113-424-14
Sequence 14, Application US/11113424
Publication No. US20050260713A1
GENERAL INFORMATION:
APPLICANT: Gangoli, et al.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: US/11/113,424
CURRENT FILING DATE: 2005-04-21
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/311,590
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/257,314
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/311,613
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/315,617
PRIOR FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/307,506
PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/322,358
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 60/288,153
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 2769
TYPE: PRT
ORGANISM: Homo sapiens
US-11-113-424-14

Query Match 26.5%; Score 50; DB 7; Length 2769;
Best Local Similarity 37.9%; Pred. No. 1,66+02;
Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 2 SPRHSSSGKPLSTKQKASKPPRCPOA 30

Db 293 SPLCTTSPGYTLSTSTVSPPPPLPKS 321

RESULT 11

US-11-087-099-9854
Sequence 9854, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 9854
LENGTH: 459
TYPE: PRT
ORGANISM: Glycine max
US-11-087-099-9854

Query Match 26.2%; Score 49.5; DB 7; Length 459;
Best Local Similarity 24.5%; Pred. No. 27;
Matches 13; Conservative 9; Mismatches 14; Indels 17; Gaps 1;

Qy 1 MSPRLSSSGKPP-----LSTQKASKPPGCPQANRGVVR 36

Db 166 VTGRRNGSGEGIPRLRYVDQQLRQKALQGLGVNRQAVRPQRLPETSVSVLR 218

RESULT 12

US-10-131-826A-382
Sequence 382, Application US/10131826A
Publication No. US20050245730A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 550
SEQ ID NO 382
LENGTH: 473
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-382

Query Match 26.2%; Score 49.5; DB 6; Length 473;
Best Local Similarity 28.6%; Pred. No. 28;
Matches 14; Conservative 8; Mismatches 8; Indels 19; Gaps 3;

Qy 3 PRHLSS-----SGKP-----LSTQKASKPP-----RGCPQANR 32

Db 376 PRHINDSPFGTLPGSAPPLPLAVRPGSEPPGFTSGPRRRPGGSRKRR 424

RESULT 13

US-10-973-115B-382
Sequence 382, Application US/10973115B
Publication No. US20060040351A1

GENERAL INFORMATION:

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APPLICANT: DeForge, Laura
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APPLICANT: Gurney, Austin L.
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APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING

FILE REFERENCE: 39870-3330R1C300C1

CURRENT APPLICATION NUMBER: US/10/973,115B

CURRENT FILING DATE: 2004-10-22

PRIOR APPLICATION NUMBER: US 10/145,747

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: US 10/028,072

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: PCT/US00/32678

PRIOR FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: US 09/581,742

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: PCT/US00/05746

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 60/135,736

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 60/123,090

PRIOR FILING DATE: 1999-03-05

NUMBER OF SEQ ID NOS: 550
SEQ ID NO 382
LENGTH: 473
TYPE: PRT
ORGANISM: Homo sapiens
US-10-973-115B-382

Query Match 26.2%; Score 49.5; DB 6; Length 473;
Best Local Similarity 28.6%; Pred. No. 28;
Matches 14; Conservative 8; Mismatches 8; Indels 19; Gaps 3;

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 3, 2006, 13:19:17 ; Search time 16.5695 Seconds
(without alignments)
822.038 Million cell updates/sec

Title: US-10-646-873-44

Perfect score: 1 RLKQSQSDLLERERESVLRREQVAEERRN 31

Sequence: 1 RLKQSQSDLLERERESVLRREQVAEERRN 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneeqp19808.*
2: geneeqp19908.*
3: geneeqp20008.*
4: geneeqp20018.*
5: geneeqp20028.*
6: geneeqp20038.*
7: geneeqp20038.*
8: geneeqp20048.*
9: geneeqp20058.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	31	2	AAW79678
2	146	100.0	31	4	AAE07321
3	146	100.0	31	6	ADA26381
4	146	100.0	31	8	ADN17174
5	146	100.0	215	2	AAW79681
6	146	100.0	215	4	AAE07324
7	146	100.0	215	6	ADA26384
8	146	100.0	215	8	ADN17177
9	146	100.0	672	4	AAW79574
10	146	100.0	672	2	AAW79676
11	146	100.0	679	4	AAE07319
12	146	100.0	679	4	AAW78590
13	146	100.0	679	6	ADA26379
14	146	100.0	679	7	ADG14341
15	146	100.0	679	8	ADN17172
16	146	100.0	682	8	ADG97562
17	142	97.3	172	8	AAW73987
18	68	46.6	1439	8	ADR12189
19	68	46.6	1439	9	ADU77050
20	68	46.6	1439	9	ADM00404
21	59	40.4	357	4	ABU53268
22	59	40.4	524	2	AAW32096
23	59	40.4	524	4	AAW73285
24	59	40.4	524	5	AAO19011

25	59	40.4	524	8	ADJ73446	ADJ73446 Swine ret
26	59	40.4	744	8	ADJ73450	ADJ73450 Swine ret
27	58.5	40.1	689	9	ADJ65414	ADJ65414 S. mannon
28	58	39.7	230	9	ADJ65542	ADJ65542 S. mannon
29	58	39.7	524	6	ADJ25645	ADJ25645 Aspergill
30	58	39.7	894	4	ADJ64737	ADJ64737 Drosophill
31	57	39.0	1893	4	ADJ59829	ADJ59829 Drosophill
32	56	38.4	219	8	ADJ94706	ADJ94706 Plant ful
33	56	38.4	322	6	ADJ53441	ADJ53441 Protein e
34	56	38.4	322	8	ADJ05434	ADJ05434 M. catarr
35	56	38.4	828	7	ADJ65842	ADJ65842 Human col
36	56	38.4	828	7	ADJ65842	ADJ65842 Human col
37	56	38.4	828	4	ADJ48365	ADJ48365 Human col
38	56	38.4	985	4	ADJ63557	ADJ63557 Drosophill
39	56	38.4	985	4	ADJ66752	ADJ66752 Drosophill
40	55.5	38.0	500	5	ADJ73751	ADJ73751 Candida a
41	55	37.7	109	4	ADJ53270	ADJ53270 Human tes
42	55	37.7	143	4	ADJ20989	ADJ20989 Novel hum
43	55	37.7	144	4	ADJ53278	ADJ53278 Human tes
44	55	37.7	224	6	ADJ54938	ADJ54938 Human pro
45	55	37.7	224	6	ADJ026229	ADJ026229 MDDT rela
				7	ADJ70695	ADJ70695 Human hea

ALIGNMENTS

RESULT 1
AAW79678 standard; protein; 31 AA.

AAW79678;

11-JAN-1999 (first entry)

Synthetic CS198 derived peptide #2.

Gastrointestinal tract; GI tract; cancer; disease; detection; CS198; human; predisposition; treatment; Barrett's oesophagus; gastric ulcer; gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis; pancreatitis.

Synthetic.

WO9844159-A1.

08-OCT-1998.

30-MAR-1998; 98WO-US006251.

31-MAR-1997; 97US-00828855.

(ABBO) ABBOTT LAB.

Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J; Granada EN, Hayden M, Hodges SC, Klags MR, Kratochvil JD; Roberts-Rapp L, Russell JC, Stroupe SD;

WPI; 1998-542714/46.

New gastrointestinal polynucleotides, CS198, and their detection - used for developing products for the diagnosis and treatment of gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.

Claim 26; Page 102; 127pp; English.

AAW79677-W79680 are synthetic CS198 derived peptide fragments which are used in a method to detect the presence of a target human CS198 polynucleotide in a test sample. The CS198 gene is useful as a marker for gastrointestinal (GI) tract disorders. The methods and products can be used in detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition to diseases and conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus, gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative

CC colitis, and pancreaticitis
XX Sequence 31 AA;
SQ
Query Match 100.0%; Score 146; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RLOKSQSSDLLERERESVLRREQVAAERRN 31
DB 1 RLOKSQSSDLLERERESVLRREQVAAERRN 31
RESULT 2
AAE07321
ID AAE07321 standard; peptide; 31 AA.
XX
AC AAE07321;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human CS 198 peptide #2.
XX
CS CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
KM gastritis; Crohn's disease; ulcerative colitis; pancreaticitis;
KM Barrett's oesophagus; gene therapy; drug screening; human.
XX
OS Homo sapiens.
XX
PN US2001010904-A1.
XX
PD 02-AUG-2001.
XX
PF 30-MAR-1998; 98US-00050516.
XX
PR 31-MAR-1997; 97US-00828855.
XX
PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUSSE/) RUSSELL J C.
PA (STRO/) STROUPE S D.
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
PI Granados EN, Hayden M, Hodges SC, Klaas MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 2001-496163/54.
XX
DR Detecting the presence of target CS 198 polynucleotide, useful for
XX detecting or diagnosing diseases of the gastrointestinal tract, comprises
XX contacting test sample with at least one CS 198-specific polynucleotide.
XX
PS Claim 17; Page 51; 68pp; English.
XX
CC The invention relates to a method of detecting the presence of a target
XX CS 198 polynucleotide comprising contacting the test sample with at least
XX one CS 198-specific polynucleotide. The method is useful for detecting
XX diseases of the gastrointestinal (GI) tract organs, particularly cancer.
XX The CS 198 polynucleotides, polypeptides and antibodies are useful for
XX detecting, diagnosing, staging, monitoring, prognosticating, preventing,
XX treating or determining predisposition to diseases and conditions of the
XX GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
XX ulcerative colitis, pancreaticitis and Barrett's oesophagus. The CS 198
XX polypeptides are useful as standards or reagents in diagnostic

CC immunoassays, as components or as target sites for various therapies.
CC Antibodies directed against at least one epitope contained within these
CC polypeptides are useful as delivery agents for therapeutic agents, in
CC diagnostic tests and for screening for conditions or diseases associated
CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
CC for the generation of chimeric antibodies for therapeutic use. The CS 198
CC polynucleotide is also useful in gene therapy and drug screening. The
CC method of the invention provides an alternative, non-surgical diagnostic
CC method capable of detecting early stage GI tract disease such as cancer.
CC The present sequence is a peptide derived from human CS 198 polypeptide
XX consensus sequence
XX
SQ Sequence 31 AA;
OY
DB 1 RLOKSQSSDLLERERESVLRREQVAAERRN 31
1 RLOKSQSSDLLERERESVLRREQVAAERRN 31
Query Match 100.0%; Score 146; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RLOKSQSSDLLERERESVLRREQVAAERRN 31
DB 1 RLOKSQSSDLLERERESVLRREQVAAERRN 31
RESULT 3
ADA26381
ID ADA26381 standard; protein; 31 AA.
XX
AC ADA26381;
XX
DT 20-NOV-2003 (first entry)
XX
DE Synthetic peptide based on CS198 protein #2.
XX
CS CS198; cancer diagnosis; cancer staging; cancer monitoring;
KM cancer prognosticating; cancer prevention; cancer;
KM gastrointestinal tract disorder; gene therapy.
XX
OS Synthetic.
XX
PN US2003082619-A1.
XX
PD 01-MAY-2003.
XX
PF 23-OCT-2002; 2002US-00279547.
XX
PR 31-MAR-1997; 97US-00828855.
XX
PR 30-MAR-1998; 98US-00050516.
XX
PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M A.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUSSE/) RUSSELL J C.
PA (STRO/) STROUPE S D.
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
PI Granados EN, Hayden MA, Hodges SC, Klaas MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 2003-596961/56.
XX
DR Detecting the presence of a target CS198 polynucleotide in a test sample
XX comprises contacting the sample with a CS198 specific polynucleotide and
XX detecting the presence of the target CS198 polynucleotide in the test
XX sample.

PS Claim 17, Page 51, 67pp; English.

XX The invention describes a method of detecting the presence of a target

CC CS198 polynucleotide in a test sample. The method comprises contacting

CC the test sample with at least one CS198 specific polynucleotide or its

CC complement, and detecting the presence of the target CS198 polynucleotide

CC in the test sample, where the CS198-specific polynucleotide has at least

CC 50% identity to a polynucleotide having any of the 27 fully defined

CC sequences of 34-2894 bp (51-27) given in the specification, or their

CC fragments or complements. The composition and methods are useful in

CC diagnosing, staging, monitoring, prognosticating, preventing or treating,

CC or determining the predisposition of an individual to, diseases and

CC conditions of the gastrointestinal tract, e.g. cancer and in gene

CC therapy. This is the amino acid sequence of a synthetic peptide based on

CC the predicted human CS198 protein sequence derived from the CS198

CC consensus sequence shown in seq id 27.

XX Sequence 31 AA;

SQ

Query Match 100.0%; Score 146; DB 6; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.9e-12;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLOKSQSSDLRERRESVLRROEVAEERRN 31

DB 1 RLOKSQSSDLRERRESVLRROEVAEERRN 31

RESULT 5

ID ADN17174 standard; peptide, 31 AA.

AC ADN17174;

XX

DT 17-JUN-2004 (first entry)

XX

DE CS198 peptide #2.

XX

KW Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.

KW

XX

OS Unidentified.

XX

XX

PN US2004043406-A1.

XX

PD 04-MAR-2004.

XX

PF 22-AUG-2003; 2003US-00646873.

XX

PR 31-MAR-1997; 97US-00828855.

XX

PR 30-MAR-1998; 98US-00050516.

XX

XX

PA (BILL/) BILLINGEL P A.

PA (COHE/) COHEN M.

PA (COLP/) COLPITTS T L.

PA (FRIE/) FRIEDMAN P N.

PA (GORD/) GORDON J.

PA (GRAN/) GRANADOS E N.

PA (HAYD/) HAYDEN M A.

PA (HODG/) HODGES S C.

PA (KLAS/) KLAS M R.

PA (KRAT/) KRATOCHVIL J D.

PA (ROBE/) ROBERTS-RAPP L.

PA (RUSSE/) RUSSELL J C.

PA (STRO/) STROUPE S D.

XX

XX

PI Billington PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,

PI Granados EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;

PI Roberts-Rapp L, Russell JC, Stroupe SD;

XX

DR WPI, 2004-313754/29.

XX

PT Diagnosing diseases such as cancer of the gastrointestinal tract, by

PT detecting aberrant expression or activity of the CS198 polypeptide, and

PT associated treatment methods.

XX

XX Claim 17, SEQ ID NO 44, 67pp; English.

PS

XX The invention relates to reagents and methods for detecting diseases of

CC the gastrointestinal (GI) tract. The method involves detecting the

CC presence of target CS198 polynucleotide in the test sample. The methods

CC and compositions of the present invention are useful for the diagnosis,

CC prevention and/or treatment of diseases or conditions associated with

CC aberrant expression or activity of the CS198 polypeptide, such as cancer

CC of the gastrointestinal tract. These are also useful in gene therapy. The

CC present sequence is a CS198 peptide used to illustrate the method of the

CC invention.

XX

XX Sequence 31 AA;

SQ

Query Match 100.0%; Score 146; DB 8; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.9e-12;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLOKSQSSDLRERRESVLRROEVAEERRN 31

DB 1 RLOKSQSSDLRERRESVLRROEVAEERRN 31

RESULT 5

ID AAW79681 standard; protein, 215 AA.

AC AAW79681;

XX

DT 11-JAN-1999 (first entry)

XX

DE Human CS198 protein C-terminal.

XX

KW Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;

KW human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;

KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;

KW

XX

OS Homo sapiens.

XX

XX

PN WO9844159-A1.

XX

PD 08-OCT-1998.

XX

PF 30-MAR-1998; 98WO-US006251.

XX

PR 31-MAR-1997; 97US-00828855.

XX

XX

PA (ABBO) ABBOTT LAB.

XX

PI Billington PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,

PI Granados EN, Hayden M, Hodges SC, Kلاس MR, Kratochvil JD;

PI Roberts-Rapp L, Russell JC, Stroupe SD;

XX

DR WPI; 1998-542714/46.

XX

PT New gastrointestinal polynucleotides, CS198, and their detection - used

PT for developing products for the diagnosis and treatment of

PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.

XX

XX Claim 26, Page 103, 127pp; English.

XX

CC This sequence represents the C-terminal of the human CS198 protein which

CC is used in a method to detect the presence of a target CS198

CC polynucleotide in a test sample. The CS198 gene is useful as a marker for

CC gastrointestinal (GI) tract disorders. The methods and products can be

CC used in detecting, diagnosing, staging, monitoring, prognosticating,

CC preventing or treating, or determining the predisposition to diseases and

CC conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,

CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative

CC colitis, and pancreatitis

XX Sequence 215 AA;
SQ
Query Match 100.0%; Score 146; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RLOKSSDILLERRESVLRREQEVABERRN 31
Db 73 RLOKSSDILLERRESVLRREQEVABERRN 103

RESULT 6
AAE07324
ID AAE07324 standard; protein; 215 AA.
XX AAE07324;
AC
XX
XX 06-NOV-2001 (first entry)
DT
XX
XX Human CS 198 protein C-terminal portion.
DE
XX CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
KW gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
KW Barrett's oesophagus; gene therapy; drug screening; human.
XX
XX Homo sapiens.
XX
XX US2001010904-A1.
PN
XX 02-AUG-2001.
PD
XX 30-MAR-1998; 98US-00050516.
XX
XX 31-MAR-1997; 97US-00828855.
PR
XX
XX (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUS/) RUSSELL J C.
PA (STRO/) STROUPE S D.
XX
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden M, Hodges SC, KLAS MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
DR WPI, 2001-496163/54.
XX
PT Detecting the presence of target CS 198 polynucleotide, useful for
PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
PT contacting test sample with at least one CS 198-specific polynucleotide.
XX
XX Claim 17; Page 52-53; 68pp; English.
XX
XX The invention relates to a method of detecting the presence of a target
XX CS 198 polynucleotide comprising contacting the test sample with at least
XX one CS 198-specific polynucleotide. The method is useful for detecting
XX diseases of the gastrointestinal (GI) tract organs, particularly cancer.
XX The CS 198 polynucleotides, polypeptides and antibodies are useful for
XX detecting, diagnosing, staging, monitoring, prognosticating, preventing,
XX treating or determining predisposition to diseases and conditions of the
XX GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
XX ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
XX polypeptides are useful as standards or reagents in diagnostic
XX immunoassays, as components or as target sites for various therapies.

CC Antibodies directed against at least one epitope contained within these
CC polypeptides are useful as delivery agents for therapeutic agents, in
CC diagnostic tests and for screening for conditions or diseases associated
CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
CC for the generation of chimeric antibodies for therapeutic use. The CS 198
CC polynucleotide is also useful in gene therapy and drug screening. The
CC method of the invention provides an alternative, non-surgical diagnostic
CC method capable of detecting early stage GI tract disease such as cancer.
CC The present sequence is C-terminal portion of human CS 198 polypeptide
XX
XX Sequence 215 AA;
SQ
Query Match 100.0%; Score 146; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RLOKSSDILLERRESVLRREQEVABERRN 31
Db 73 RLOKSSDILLERRESVLRREQEVABERRN 103

RESULT 7
ADA26384
ID ADA26384 standard; protein; 215 AA.
XX ADA26384;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Synthetic peptide based on CS198 protein #5.
DE
XX CS198; cancer diagnosis; cancer staging; cancer monitoring;
KW cancer prognosticating; cancer prevention; cancer;
KW gastrointestinal tract disorder; gene therapy.
XX
XX Synthetic.
XX
XX US2003082619-A1.
PN
XX 01-MAY-2003.
PD
XX
XX 23-OCT-2002; 2002US-00278547.
XX
XX 31-MAR-1997; 97US-00828855.
XX
XX 30-MAR-1998; 98US-00050516.
PR
XX
XX (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M A.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUS/) RUSSELL J C.
PA (STRO/) STROUPE S D.
XX
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden MA, Hodges SC, KLAS MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
XX WPI, 2003-596961/56.
XX
XX Detecting the presence of a target CS198 polynucleotide in a test sample
XX comprises contacting the sample with a CS198 specific polynucleotide and
XX detecting the presence of the target CS198 polynucleotide in the test
XX sample.
XX
XX Claim 52; Page 52; 67pp; English.

CC The invention describes a method of detecting the presence of a target
CC CS198 polynucleotide in a test sample. The method comprises contacting
CC the test sample with at least one CS198 specific polynucleotide or its
CC complement, and detecting the presence of the target CS198 polynucleotide
CC in the test sample, where the CS198-specific polynucleotide has at least
CC 50% identity to a polynucleotide having any of the 27 fully defined
CC sequences of 34-2894 bp (SI-27) given in the specification, or their
CC fragments or complements. The composition and methods are useful in
CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
CC or determining the predisposition of an individual to, diseases and
CC conditions of the gastrointestinal tract, e.g. cancer and in gene
CC therapy. This is the amino acid sequence of a synthetic peptide based on
CC the predicted human CS198 protein sequence derived from the CS198
CC consensus sequence shown in seq id 27.

CC Sequence 215 AA;

Query Match 100.0%; Score 146; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLOKSSDLEERESVLRREQVAAERRN 31
Db 73 RLOKSSDLEERESVLRREQVAAERRN 103

RESULT 8
ADN17177

ID ADN17177 standard; protein; 215 AA.

AC ADN17177;

DT 17-JUN-2004 (first entry)

DE CS198 protein #2.

XX Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.

XX Unidentified.

XX US2004043406-A1.

XX 04-MAR-2004.

XX 22-AUG-2003; 2003US-00646873.

XX 31-MAR-1997; 97US-00828855.

XX 30-MAR-1998; 98US-00050516.

XX (BILL/) BILLINGEL P A.

XX (COHE/) COHEN M.

XX (COLP/) COLPITS T L.

XX (FRIE/) FRIEDMAN P N.

XX (GORD/) GORDON J.

XX (GRAN/) GRANADOS E N.

XX (HAYD/) HAYDEN M A.

XX (HODG/) HODGES S C.

XX (KLAS/) KLAS M R.

XX (KRAT/) KRATOCHVIL J D.

XX (ROBE/) ROBERTS-RAPP L.

XX (RUSSE/) RUSSELL J C.

XX (STRO/) STROUPE S D.

XX BILLINGEL P A, Cohen M, Colpits TL, Friedman PN, Gordon J;

XX Grandos EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;

XX Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI; 2004-313754/29.

XX Diagnosing diseases such as cancer of the gastrointestinal tract, by

XX PT detecting aberrant expression or activity of the CS198 polypeptide, and

XX PT associated treatment methods.

PS Claim 17; SEQ ID NO 47; 677p; English.

XX The invention relates to reagents and methods for detecting diseases of
CC the gastrointestinal (GI) tract. The method involves detecting the
CC presence of target CS198 polynucleotide in the test sample. The methods
CC and compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the CS198 polypeptide, such as cancer
CC of the gastrointestinal tract. These are also useful in gene therapy. The
CC present sequence is a CS198 protein used to illustrate the method of the
CC invention.

XX Sequence 215 AA;

Query Match 100.0%; Score 146; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLOKSSDLEERESVLRREQVAAERRN 31
Db 73 RLOKSSDLEERESVLRREQVAAERRN 103

RESULT 9
AAM79574

ID AAM79574 standard; protein; 672 AA.

AC AAM79574;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 3220.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;

XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

XX tissue growth factor; immunomodulatory; cancer; leukaemia;

XX nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

XX WO200157190-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US004098.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX 20-JUN-2000; 2000US-00598075.

XX 19-JUL-2000; 2000US-00620325.

XX 01-SEP-2000; 2000US-0064936.

XX 15-SEP-2000; 2000US-00663561.

XX 20-OCT-2000; 2000US-00693325.

XX 30-NOV-2000; 2000US-00728422.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

XX Ma Y, Zhao Qa, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX WPI; 2001-476283/51.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful

XX PT in diagnosis and gene therapy.

XX Claim 20; Page 288; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the

XX CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to

XX CC cytokine, cell proliferation or cell differentiation or which may induce

XX CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication

XX Sequence 672 AA;

Query Match 100.0%; Score 146; DB 4; Length 672;

Best Local Similarity 100.0%; Pred. No. 5,7e-11; Mismatches 0; Indels 0; Gaps 0;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLOKSQSSDLLERERESVLRREQVAERRN 31
 DB 530 RLOKSQSSDLLERERESVLRREQVAERRN 560

RESULT 10

AAW79676 AAW79676 standard; protein; 679 AA.

XX AAW79676;

XX 11-JAN-1999 (first entry)

XX Human CS198 protein.

XX Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
 KW human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
 KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
 KW pancreatitis.

XX Homo sapiens.

XX MO9844159-A1.

XX 08-OCT-1998.

XX 30-MAR-1998; 98WO-US006251.

XX 31-MAR-1997; 97US-00828855.

XX (ABBO) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI; 1998-542714/46.

XX New gastrointestinal polynucleotides, CS198, and their detection - used
 PT for developing products for the diagnosis and treatment of
 PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.

XX Claim 26; Page 100-102; 127pp; English.

XX This sequence represents the human CS198 protein which is used in a
 CC method to detect the presence of a target CS198 polynucleotide in a test
 CC sample. The CS198 gene is useful as a marker for gastrointestinal (GI)
 CC tract disorders. The methods and products can be used in detecting,
 CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
 CC or determining the predisposition to diseases and conditions of the GI
 CC tract, such as GI tract cancer, Barrett's oesophagus, gastric ulcer,
 CC gastritis, leiomyoma, polyps, Crohn's disease, ulcerative colitis, and
 CC pancreatitis

XX Sequence 679 AA;

Query Match 100.0%; Score 146; DB 2; Length 679;

Best Local Similarity 100.0%; Pred. No. 5.8e-11; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLOKSQSSDLLERERESVLRREQVAERRN 31
 DB 537 RLOKSQSSDLLERERESVLRREQVAERRN 567

RESULT 11

AAE07319 AAE07319 standard; protein; 679 AA.

XX AAE07319;

XX 06-NOV-2001 (first entry)

XX Human CS 198 protein.

XX CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
 KW gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
 KW Barrett's oesophagus; gene therapy; drug screening; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 353 /note="Encoded by CCGN"

XX US2001010904-A1.

XX 02-AUG-2001.

XX 30-MAR-1998; 98US-00050516.

XX 31-MAR-1997; 97US-00828855.

XX (BILL/) BILLINGEL P A.

XX (COLE/) COHEN M.

XX (FRIE/) FRIEDMAN P N.

XX (GORD/) GORDON J.

XX (GRAN/) GRANADOS E N.

XX (HAYD/) HAYDEN M.

XX (HODG/) HODGES S C.

XX (KLAS/) KLAS M R.

XX (KRAT/) KRATOCHVIL J D.

XX (ROBE/) ROBERTS-RAPP L.

XX (RUS/) RUSSELL J C.

XX (STRO/) STROUPE S D.

XX Billingel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 DR N-PSDB; AAD13637.

XX Claim 17; Page 49-51; 68pp; English.

XX The invention relates to a method of detecting the presence of a target
 CC CS 198 polynucleotide comprising contacting the test sample with at least
 CC one CS 198-specific polynucleotide. The method is useful for detecting
 CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
 CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
 CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
 CC treating or determining predisposition to diseases and conditions of the
 CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
 CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
 CC polypeptides are useful as standards or reagents in diagnostic

CC immunosassys, as components or as target sites for various therapies.
CC Antibodies directed against at least one epitope contained within these
CC polypeptides are useful as delivery agents for therapeutic agents, in
CC diagnostic tests and for screening for conditions or diseases associated
CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
CC for the generation of chimeric antibodies for therapeutic use. The CS 198
CC polynucleotide is also useful in gene therapy and drug screening. The
CC method of the invention provides an alternative, non-surgical diagnostic
CC method capable of detecting early stage GI tract disease such as cancer.
CC The present sequence is human CS 198 polypeptide
XX
SQ Sequence 679 AA;

Query Match 100.0%; Score 146; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLQKSSDILLERESVLRREQVEAERRN 31
DB 537 RLQKSSDILLERESVLRREQVEAERRN 567

RESULT 12
ID AAM78590 standard; protein; 679 AA.
XX
AC AAM78590;
XX

DT 06-NOV-2001 (first entry)
XX

DE Human protein SEQ ID NO 1252.
XX

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX
XX 27-APR-2000; 2000US-00560875.
XX
XX 20-JUN-2000; 2000US-00598075.
XX
XX 19-JUL-2000; 2000US-00620325.
XX
XX 01-SEP-2000; 2000US-00654936.
XX
XX 15-SEP-2000; 2000US-00663561.
XX
XX 20-OCT-2000; 2000US-00693325.
XX
XX 30-NOV-2000; 2000US-00728422.
XX
XX
XX (HYSE-) HYSEQ INC.
XX

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZM;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX
XX N-PSDB; AAK51723.
XX
XX

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX

XX Claim 20; Page 3512-3514; 6221P; English.
XX

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78333-AAM80302) that exhibit activity relating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or

CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK5282) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 679 AA;

Query Match 100.0%; Score 146; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLQKSSDILLERESVLRREQVEAERRN 31
DB 537 RLQKSSDILLERESVLRREQVEAERRN 567

RESULT 13
ID ADA26379 standard; protein; 679 AA.
XX
AC ADA26379;
XX

DT 20-NOV-2003 (first entry)
XX

DE Predicted amino acid sequence of the CS198 protein.
XX

XX CS198; cancer diagnosis; cancer staging; cancer monitoring;
XX cancer prognosticating; cancer prevention; cancer;
XX gastrointestinal tract disorder; gene therapy.
XX

XX Synthetic;
XX
XX US2003082619-A1.
XX
XX 01-MAY-2003.
XX
XX 23-OCT-2002; 2002US-00278547.
XX
XX 31-MAR-1997; 97US-00828855.
XX
XX 30-MAR-1996; 96US-00050516.
XX
XX
XX (BILL/) BILLINGEL P A.
XX
XX (COH/) COHEN M.
XX
XX (COLP/) COLPITTS T L.
XX
XX (FRIE/) FRIEDMAN P N.
XX
XX (GORD/) GORDON J.
XX
XX (GRAN/) GRANADOS E N.
XX
XX (HAYD/) HAYDEN M A.
XX
XX (HODG/) HODGES S C.
XX
XX (KLAS/) KLAS M R.
XX
XX (KRAT/) KRATOCHVIL J D.
XX
XX (ROBE/) ROBERTS-RAPP L.
XX
XX (RUSSE/) RUSSELL J C.
XX
XX (STRO/) STROUPE S D.
XX
XX
XX Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX Granados EN, Hayden MA, Hodges SC, Kras MR, Kratochvil JD;
XX Roberts-Rapp L, Russell JC, Stroupe SD;
XX
XX WPI; 2003-596961/56.
XX
XX

XX Detecting the presence of a target CS198 polynucleotide in a test sample
XX comprises contacting the sample with a CS198 specific polynucleotide and
XX detecting the presence of the target CS198 polynucleotide in the test
XX sample.
XX

XX Claim 17; Page 49-50; 676P; English.
XX

XX The invention describes a method of detecting the presence of a target

CC CS198 polynucleotide in a test sample. The method comprises contacting
CC the test sample with at least one CS198 specific polynucleotide or its
CC complement, and detecting the presence of the target CS198 polynucleotide
CC in the test sample, where the CS198-specific polynucleotide has at least
CC 50% identity to a polynucleotide having any of the 27 fully defined
CC sequences of 34-2894 bp (SI-27) given in the specification, or their
CC fragments or complements. The composition and methods are useful in
CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
CC or determining the predisposition of an individual to, diseases and
CC conditions of the gastrointestinal tract, e.g. cancer and in gene
CC therapy. This is the predicted amino acid sequence of the human CS198
CC protein derived from the CS198 consensus sequence shown in seq id 27.
XX
XX

SO Sequence 679 AA;

Query Match 100.0%; Score 146; DB 6; Length 679;
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLOKQSSDILRRERESVLRROQVAAERRN 31
Db 537 RLOKQSSDILRRERESVLRROQVAAERRN 567

RESULT 14

ADG14341
ID ADG14341 standard; protein; 679 AA.

AC ADG14341;

DT 26-FEB-2004 (first entry)

XX Human NC2.

DE Human NC2.

KW Human; NC1; NC2; NC3; PHH1; pancreas beta-cell; insulin; antidiabetic;
KW neuroprotective.

OS Homo sapiens.

PN WO2003078631-A1.

XX 25-SEP-2003.

XX 06-MAR-2003; 2003WO-JP002620.

XX 15-MAR-2002; 2002JP-00071592.

PA (KANF) KANEKA CORP.

PI Niwa H, Yamashita K;

XX WPI; 2003-767524/72.

DR N-PSDB; ADG14344.

XX Familial persistent hyperinsulinemic hypoglycemia of infancy (PHH1)
PT patient-expressed genes for detecting and screening e.g. proliferative
PT insulin-producing cells in treatment of PHH1.

XX Claim 1; SEQ ID NO 2; 34pp; Japanese.

XX The present invention relates to human NC1, NC2 and NC3 proteins and
XX coding sequences (ADG14340-ADG14345). The coding sequences are useful for
XX detecting and screening proliferative insulin-producing cells as well as
XX differentiating and proliferation of such cells and their precursors as
XX analogous cells in treatment of e.g. PHH1 and diseases due to
XX differentiation/proliferation abnormality, diseases of the nervous system
XX and pancreas. The coding sequences are also useful as spontaneous
XX proliferation models of pancreas beta-cells. The novel genes NC1, NC2 and
XX NC3 were isolated from the pancreas of PHH1 patients, which were used in
XX testing for the detection of proliferative insulin-producing cells or
XX pancreas beta-cells by Northern analysis.

SO Sequence 679 AA;

Query Match 100.0%; Score 146; DB 7; Length 679;
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLOKQSSDILRRERESVLRROQVAAERRN 31
Db 537 RLOKQSSDILRRERESVLRROQVAAERRN 567

RESULT 15

ADN17172
ID ADN17172 standard; protein; 679 AA.

AC ADN17172;

DT 17-JUN-2004 (first entry)

XX CS198 protein #1.

DE Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.

XX Unidentified.

OS US2004043406-A1.

PN 04-MAR-2004.

XX 22-AUG-2003; 2003US-00646873.

XX 31-MAR-1997; 97US-00828855.

XX 30-MAR-1998; 98US-00050516.

XX (BILL/) BILLINGEL P A.

XX (COHE/) COHEN M.

XX (COLP/) COLPITTS T L.

XX (FRIE/) FRIEDMAN P N.

XX (GORD/) GORDON J.

XX (GRAN/) GRANADOS E N.

XX (HAYD/) HAYDEN M A.

XX (HODG/) HODGES S C.

XX (KLAS/) KLAS M R.

XX (KRAT/) KRATOCHVIL J D.

XX (ROBE/) ROBERTS-RAPP L.

XX (RUSSE/) RUSSELL J C.

XX (STRO/) STROUPE S D.

XX Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

XX Granados EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;

XX Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI; 2004-313754/29.

DR GENBANK; D87440.

XX Diagnosing diseases such as cancer of the gastrointestinal tract, by
PT detecting aberrant expression or activity of the CS198 polypeptide, and
PT associated treatment methods.

XX Claim 17; SEQ ID NO 42; 67pp; English.

XX The invention relates to reagents and methods for detecting diseases of
XX the gastrointestinal (GI) tract. The method involves detecting the
XX presence of target CS198 polynucleotide in the test sample. The methods
XX and compositions of the present invention are useful for the diagnosis,
XX prevention and/or treatment of diseases or conditions associated with
XX aberrant expression or activity of the CS198 polypeptide, such as cancer
XX of the gastrointestinal tract. These are also useful in gene therapy. The
XX present sequence is a CS198 protein used to illustrate the method of the
XX invention.

SO Sequence 679 AA;

Query Match 100.0%; Score 146; DB 8; Length 679;

Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLOKSQSSDILLERERESVLRROQEVAEERRN 31
|||||
Db 537 RLOKSQSSDILLERERESVLRROQEVAEERRN 567

Search completed: March 3, 2006, 13:35:22
Job time : 18.5695 secs

Inside Edge Blank (unpiped)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 3, 2006, 13:26:31 ; Search time 1.95821 Seconds
(without alignments)
1523.185 Million cell updates/sec

Title: US-10-646-873-44

Perfect score: 146

Sequence: 1 RLKSSQSDLLERRESVLRREQVAERERN 31

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	679	2 T00636	hypothetical prote
2	145.2	100.0	679	2 AC0136	heat shock protein
3	145.2	100.0	679	2 T15597	hypothetical prote
4	145.2	100.0	679	2 T15598	hypothetical prote
5	145.2	100.0	679	2 T15599	hypothetical prote
6	145.2	100.0	679	2 T15600	hypothetical prote
7	145.2	100.0	679	2 T15601	hypothetical prote
8	145.2	100.0	679	2 T15602	hypothetical prote
9	145.2	100.0	679	2 T15603	hypothetical prote
10	145.2	100.0	679	2 T15604	hypothetical prote
11	145.2	100.0	679	2 T15605	hypothetical prote
12	145.2	100.0	679	2 T15606	hypothetical prote
13	145.2	100.0	679	2 T15607	hypothetical prote
14	145.2	100.0	679	2 T15608	hypothetical prote
15	145.2	100.0	679	2 T15609	hypothetical prote
16	145.2	100.0	679	2 T15610	hypothetical prote
17	145.2	100.0	679	2 T15611	hypothetical prote
18	145.2	100.0	679	2 T15612	hypothetical prote
19	145.2	100.0	679	2 T15613	hypothetical prote
20	145.2	100.0	679	2 T15614	hypothetical prote
21	145.2	100.0	679	2 T15615	hypothetical prote
22	145.2	100.0	679	2 T15616	hypothetical prote
23	145.2	100.0	679	2 T15617	hypothetical prote
24	145.2	100.0	679	2 T15618	hypothetical prote
25	145.2	100.0	679	2 T15619	hypothetical prote
26	145.2	100.0	679	2 T15620	hypothetical prote
27	145.2	100.0	679	2 T15621	hypothetical prote
28	145.2	100.0	679	2 T15622	hypothetical prote
29	145.2	100.0	679	2 T15623	hypothetical prote

30	51.5	35.3	456	2 T05612	hypothetical prote
31	51.5	35.3	599	2 T51548	hypothetical prote
32	51	34.9	142	2 T05612	hypothetical prote
33	51	34.9	226	2 T24125	hypothetical prote
34	51	34.9	268	2 T24118	hypothetical prote
35	51	34.9	270	2 T24126	hypothetical prote
36	51	34.9	419	2 T24126	hypothetical prote
37	51	34.9	453	2 T24248	hypothetical prote
38	51	34.9	457	2 T50402	hypothetical prote
39	51	34.9	646	2 T19654	hypothetical prote
40	51	34.9	790	2 T25104	hypothetical prote
41	51	34.9	798	2 T25104	hypothetical prote
42	51	34.9	857	2 T25104	hypothetical prote
43	51	34.9	964	2 T25104	hypothetical prote
44	51	34.9	964	2 T25104	hypothetical prote
45	51	34.9	988	2 T25104	hypothetical prote

ALIGNMENTS

RESULT 1

hypothetical protein F21856.2 - human
C.Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C.Accession: T00636
R.Lamerdin, J.B.; McCreedy, P.M.; Skowronski, E.; Adamson, A.W.; Burkhart-Schultz, K.; C
rgescu, A.; Avila, J.; Liu, S.; Bruce, R.; Quan, G.; Montgomery, M.; Ow, D.; Nolan, M.;
submitted to the EMBL Data Library, January 1998
A.Description: Sequence analysis of a 3.5 Mb contig in 19p13.3 between CDC34 and D19S34;
A.Reference number: Z14195
A.Accession: T00636
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-679 <Lam>
A.Cross-references: UNIPROT:Q81VT2; UNIPARC:UPI00000745CD; EMBL:AC004030; NID:G2804590;
C.Genetics:
A.Map position: 19p13.3
A.Introns: 594/1; 637/3; 650/3
A.Note: F21856_2

Query Match 100.0%; Score 146; DB 2; Length 679;

Best Local Similarity 100.0%; Pred. No. 1.1e-09; Mismatches 0; Indels 0; Gaps 0;

Db 1 RLKSSQSDLLERRESVLRREQVAERERN 31
537 RLKSSQSDLLERRESVLRREQVAERERN 567

RESULT 2

heat shock protein grp94 [imported] - Yersinia pestis (strain CO92)
C.Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 03-Jul-2004
C.Accession: AC0136
R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-Taraght, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
H.M.; Rutherford, K.; Skellern, M.; Skellern, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A.Reference number: AB00001; PMID:21470413; PMID:11586360
A.Accession: AC0136
A.Molecule type: DNA
A.Status: preliminary
A.Residues: 1-192 <KUR>
A.Cross-references: UNIPROT:Q8ZHO8; UNIPARC:UPI00000DDCC53; GB:AL590842; PIND:CA089950.1
C.Gene: YP01107
C.Superfamily: heat shock protein grp94

Query Match 45.2%; Score 66; DB 2; Length 192;

Best Local Similarity 60.0%; Pred. No. 0.82;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 6 QSDLLERERSVLRQEQVAEER 30
Db 45 QLSDALQERESLIRAKAEVNIIR 69

RESULT 3

T15597
hypothetical protein C25A11.4b - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C/Accession: T15597

R/Favetto, T.
submitted to the EMBL Data Library, October 1995

A/Description: The sequence of C. elegans cosmid C25A11.

A/Reference number: Z18375

A/Accession: T15597

A/Status: preliminary; translated from GB/EMBL/DBDJ

A/Molecule type: DNA

A/Residues: 1-737 <FAV>

A/Cross-references: UNIPARC:UP100001787B; EMBL:U39650; NID:g1049376; PID:g1049381; PIDN

A/Experimental source: strain Bristol N2

C/Genetics:

A/Gene: CESP:C25A11.4b

A/Introns: 65/3; 88/3; 126/3; 433/2; 494/2; 711/2

Query Match 42.5%; Score 62; DB 2; Length 737;

Best Local Similarity 51.6%; Pred. No. 9.3;

Matches 16; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

Qy 3 QKSQSDLLERERSVLRQEQVAE--ERRN 31
Db 556 EEAQIADLLERERHNLIRENERRAVERAN 586

RESULT 4

T15598
hypothetical protein C25A11.4a - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C/Accession: T15598

R/Favetto, T.
submitted to the EMBL Data Library, October 1995

A/Description: The sequence of C. elegans cosmid C25A11.

A/Reference number: Z18375

A/Accession: T15598

A/Status: preliminary; translated from GB/EMBL/DBDJ

A/Molecule type: DNA

A/Residues: 1-1017 <FAV>

A/Cross-references: UNIPARC:UP100001787B; EMBL:U39650; NID:g1049376; PID:g1049380; PIDN

A/Experimental source: strain Bristol N2

C/Genetics:

A/Gene: CESP:C25A11.4a

A/Introns: 65/3; 88/3; 126/3; 433/2; 494/2; 711/2; 735/1; 792/3; 833/3; 873/2

Query Match 42.5%; Score 62; DB 2; Length 1017;

Best Local Similarity 51.6%; Pred. No. 13;

Matches 16; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

Qy 3 QKSQSDLLERERSVLRQEQVAE--ERRN 31
Db 556 EEAQIADLLERERHNLIRENERRAVERAN 586

RESULT 5

T38881
probable DNA-J-like protein - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T38881

R/Murphy, L.; Harris, D.; Bartrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, February 1996

A/Reference number: Z21807

A/Accession: T38881

A/Status: preliminary; translated from GB/EMBL/DBDJ

A/Molecule type: DNA

A/Residues: 1-392 <MUR>

A/Cross-references: UNIPROT:Q10209; UNIPARC:UP1000013A191; EMBL:Z69380; PIDN:CAA93340.1;

A/Experimental source: strain 972h-; cosmid c4H3

C/Genetics:

A/Gene: SPDB:SPAC4H3.01

A/Map position: 1

A/Introns: 29/2; 53/3; 277/2

F/8-74/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 41.1%; Score 60; DB 2; Length 392;

Best Local Similarity 61.1%; Pred. No. 8.5;

Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 13 RERSVLRQEQVAEER 30
Db 157 RERELAKRQEMIEDRR 174

RESULT 6

E75292
GGDEF family protein - Deinococcus radiodurans (strain R1)

C/Species: Deinococcus radiodurans

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: E75292

R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;

Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A/Reference number: A75250; MUID:20036896; PMID:10567266

A/Accession: E75292

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-856 <WHI>

A/Cross-references: UNIPROT:Q9RS28; UNIPARC:UP1000003F88; GB:AE002061; GB:AE000513; NID

A/Experimental source: strain R1

C/Genetics:

A/Gene: DR2299

A/Map position: 1

Query Match 41.1%; Score 60; DB 2; Length 856;

Best Local Similarity 45.2%; Pred. No. 19;

Matches 14; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 1 RLOKSQSDLLERERSVLRQEQVAEERRN 31
Db 351 RLAEQRGLAEQIRYELRREABLRKRN 381

RESULT 7

S28589
trichohyalin - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 12-Mar-1993 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C/Accession: S28589

R/Fietz, M.J.; Rogers, G.E.

submitted to the EMBL Data Library, December 1992

A/Description: Examination of the gene encoding rabbit trichohyalin.

A/Reference number: S28589

A/Accession: S28589

A/Molecule type: DNA

A/Residues: 1-1407 <FIE>

A/Cross-references: UNIPROT:P37709; UNIPARC:UP1000013738C; EMBL:Z19092; NID:g1746; PIDN:

C/Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root sh

covalent modifications to this protein include conversion of arginine to citrulline and

C/Genetics:

A/Introns: 46/3

C/Superfamily: trichohyalin; calmodulin repeat homology

C.Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat
F149-81/Domin: calmodulin repeat homology <EF2>

Query Match 40.4%; Score 59; DB 1; Length 1407;
Best Local Similarity 42.9%; Pred. No. 40;
Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 LQKSSDILRRERESVLRQEVAAER 29
DB 1153 LQSEERLRQERERERERERERERER 1180

RESULT 8

T36106
hypothetical protein SCE15.03c - Streptomyces coelicolor

C.Species: Streptomyces coelicolor
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C.Accession: T36106
R.Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A.Reference number: 221597
A.Accession: T36106

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-677 <MUR>

A.Cross-references: UNIPROT:Q9X878; UNIPARC:UPI00000DAFF; EMBL:AL049707; PIDD:CA841272.

A.Genetics:

A.Experimental source: strain A3(2)

A.Gene: SCORDB:SCE15.03c

Query Match 39.4%; Score 57.5; DB 2; Length 677;
Best Local Similarity 41.2%; Pred. No. 29;
Matches 14; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 RQKSSDILRRERESVLR--RQEVAAER 31
DB 312 RIKQRMLEAIGERERETELRLAEREAER 345

RESULT 9

T13594
hypothetical protein p6b - fruit fly (Drosophila melanogaster)

C.Species: Drosophila melanogaster

C.Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C.Accession: T13594

R.Perez, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demallie, J.G.

submitted to the EMBL Data Library, October 1998

A.Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A.Reference number: 217692

A.Accession: T13594

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-1891 <PER>

A.Cross-references: UNIPROT:O77275; UNIPARC:UPI000007C242; EMBL:AL031227; NID:el330103;

A.Genetics:

A.Gene: p6b

A.Cross-references: FlyBase:FBgn0003053

A.Introns: 289/3

Query Match 39.0%; Score 57; DB 2; Length 1891;
Best Local Similarity 43.3%; Pred. No. 93;
Matches 13; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 RQKSSDILRRERESVLRQEVAAER 30
DB 1535 RQEAERERERERERERERERERER 1564

RESULT 10

T13893
gene hindlight protein - fruit fly (Drosophila melanogaster)

C.Species: Drosophila melanogaster

C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C.Accession: T13893
R.Yip, M.L.R.; Lamka, M.L.; Lipschitz, H.D.

Development 124, 2129-2141, 1997

A>Title: Control of germ-band retraction in Drosophila by the zinc-finger protein HINDSHI

A.Reference number: 217807; MUID:97330681; PMID:9187140

A.Accession: T13893

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-1920 <YIP>

A.Cross-references: UNIPROT:O46205; UNIPARC:UPI0000078955; EMBL:U86010; NID:g2769709; FI

A.Genetics:

A.Gene: hindlight

A.Cross-references: FlyBase:FBgn0003053

A.Function: probably function as a transcription factor

A.Description: probably function as a transcription factor

A.Keywords: nucleus; zinc finger

Query Match 39.0%; Score 57; DB 2; Length 1920;
Best Local Similarity 43.3%; Pred. No. 95;
Matches 13; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 RQKSSDILRRERESVLRQEVAAER 30
DB 1535 RQEAERERERERERERERERERER 1564

RESULT 11

J6525
processing peptidase (EC 3.4.-.-) beta chain, mitochondrial - shiitake mushroom

C.Species: Lentinula edodes (shiitake mushroom)

C.Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 07-May-1999

C.Accession: J6525

R.Zhang, M.; Xie, W.; Leung, G.S.W.; Deane, E.E.; Kuan, H.S.

Gene 206, 23-27, 1998

A>Title: Cloning and characterization of the gene encoding beta subunit of mitochondrial

A.Reference number: J6525; MUID:98121308; PMID:9461410

A.Accession: J6525

A.Molecule type: mRNA

A.Residues: 1-466 <ZHA>

A.Cross-references: UNIPARC:UPI0000175DBE

C.Comment: This protein belongs to the p17illysin family of endoprotease that conserved

C.Genetics:

A.Gene: beta-mp

A.Introns: 13/3 439/3

C.Superfamily: mitochondrial processing peptidase alpha chain

C.Keywords: hydrolase; mitochondrion; zinc

Query Match 38.7%; Score 56.5; DB 2; Length 466;
Best Local Similarity 46.4%; Pred. No. 26;
Matches 13; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 2 LQKSSDILRRERESVLRQEVAAER 28
DB 133 LQNSLLEGALERERDVLRQEVQKQ 160

RESULT 12

T14286
embryogenic callus protein 98b - carrot

C.Species: Daucus carota (carrot)

C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C.Accession: T14286

R.Yu, Z.; Ueda, K.; Masuda, K.; Itch, A.; Ono, M.; Inoue, M.

submitted to the EMBL Data Library, March 1998

A.Description: A novel nuclear protein with a HMG-box from carrot embryo.

A.Reference number: T14286

A.Accession: T14286

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-502 <XUZ>

A.Cross-references: UNIPROT:O80383; UNIPARC:UPI00000AB396; EMBL:AB012708; NID:g3551256;

A.Experimental source: embryogenic callus

C.Genetics:


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Query Match      100.0%; Score 146; DB 1; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLOKSQSSDLRRERESVLRREOVAAERRN 31
Db 537 RLOKSQSSDLRRERESVLRREOVAAERRN 567

RESULT 2
CS021_PONPY STANDARD; PRT; 685 AA.
ID CS021_PONPY STANDARD; PRT; 685 AA.
AC Q5R8H3;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Protein C19orf21 homolog.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Kidney;
RG The German cDNA consortium;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; CR858675; CAH90887.1; -; mRNA.
KW Coiled coil.
FT COILED 551
SQ SEQUENCE 685 AA; 75892 MW; A3A99F4343396E81 CRC64;

Query Match      97.3%; Score 142; DB 1; Length 685;
Best Local Similarity 96.8%; Pred. No. 4.5e-08;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLOKSQSSDLRRERESVLRREOVAAERRN 31
Db 543 RLOKSQSSDLRRERESVLRREOVAAERRN 573

RESULT 3
CS021_MOUSE STANDARD; PRT; 648 AA.
ID CS021_MOUSE STANDARD; PRT; 648 AA.
AC Q9D275;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Protein C19orf21 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
ID MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
EX Okazaki Y., Futuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
RA Nishikido I., Osato N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
RA Yeai K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirini L.M., Kanapin A., Matzuda H., Batalova S., Beisel K.W.,
RA Blake U.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Datta E., Dregani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guerinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

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RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius U.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sanderlin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wallestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Zircini P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scherz T.E.,
RA Brownstein M.J., Udell T.B., Tohilyuki S., Carninci P., Prange C.,
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalak U., Smalins D.E.,
RA Schermer A., Schein J.B., Jones S.U.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC
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CC -----
DR EMBL; AK020266; BAB32049.1; -; mRNA.
DR EMBL; BC013508; AAH13508.1; -; mRNA.
DR Ensemble; ENSMUSG00000035852; Mus musculus.
DR MGI; MGI:1926156; 9130017M09R1k.
KW Coiled coil.
FT COILED 511
SQ SEQUENCE 648 AA; 72281 MW; 1E395B70763B3D1F CRC64;

Query Match      93.2%; Score 136; DB 1; Length 648;
Best Local Similarity 93.5%; Pred. No. 2.1e-07;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RLOKSQSSDLRRERESVLRREOVAAERRN 31
Db 503 RLOKSQSSDLRRERESVLRREOVAAERRN 533

RESULT 4
GRPE_YERPE STANDARD; PRT; 192 AA.
ID GRPE_YERPE STANDARD; PRT; 192 AA.
AC Q7CH40; Q74W49; Q8ZH08;
DT 25-OCT-2004 (Rel. 45, Created)

```

DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE GRP protein (HSP-70 cofactor)
 GN Name=grp; OrderedLocustNames=yF01107, y3073, yP1049;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 NC NCB1_TaxID=632;
 [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
 RA Parkhill J., Wren B.M., Thomson N.R., Titchall R.W., Holden M.T.G.,
 RA Prentice M.B., Sebatilla M., James K.D., Churcher C.M., Mungall K.L.,
 RA Baker S., Baeham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.-M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,
 RA Leather S., Mole S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."
 RL Nature 413:523-527(2001).
 [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=KIM5 / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RX DOI=10.1128/JB.184.16.4601-4611.2002;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Peterson J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM."
 RL J. Bacteriol. 184:4601-4611(2002).
 [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=91001 / Biovar Mediaevalis;
 RX PubMed=15368893;
 RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
 RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
 RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
 RA Yang H., Wang J., Huang P., Yang R.;
 RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
 avirulent to humans."
 RL DNA Res. 11:179-197(2004).
 -1- FUNCTION: Participates actively in the response to hyperosmotic
 and heat shock by preventing the aggregation of stress-denatured
 proteins, in association with dnaK and grpE. It is the nucleotide
 exchange factor for dnaK and may function as a thermosensor.
 CC Unfolded proteins bind initially to dnaJ; upon interaction with
 the dnaJ-bound protein, dnaK hydrolyzes its bound ATP, resulting
 in the formation of a stable complex. GrpE releases ADP from dnaK;
 ATP binding to dnaK triggers the release of the substrate protein,
 thus completing the reaction cycle. Several rounds of ATP-
 dependent interactions between dnaJ, dnaK and grpE are required
 for fully efficient folding (By similarity).
 -1- SUBUNIT: Homodimer (By similarity).
 -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 -1- SIMILARITY: Belongs to the grpE family.
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 removed.
 CC
 CC EMBL: A414146; CAC8950.1; -; Genomic DNA.
 CC EMBL: AE013908; AAC86623.1; -; Genomic DNA.
 CC EMBL: AE017130; AA561299.1; -; Genomic DNA.
 CC PIR: AC0136; AC0136.
 CC HSSP: P09372; 1DKG.
 CC HAMAP: MF_01151; -; 1.
 CC InterPro: IPR000740; GrpE.
 CC PANTHER: PTHR11697; SFP20; GrpE; 1.

DR Pfam: PF01025; GrpE; 1.
 DR PRINTS: PR00773; GREPROTEIN.
 DR PROSITE: PS01071; GRPE; 1.
 DR Chaperone; Complete proteome; Heat shock.
 SQ SEQUENCE 192 AA; 21557 MW; BA1A165F8AD1062 CRC64;
 Query Match 45.2%; Score 66; DB 1; Length 192;
 Best local similarity 60.0%; Pred. No. 8;
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 6 QSSDLERERESVLRROEVAEERR 30
 DB 45 QLSDLQRERESLRAKAEVENIR 69
 RESULT 5
 ID 066DA8 YERPS PRELIMINARY; PRT; 192 AA.
 AC 066DA8-
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE GrpE protein (HSP-70 cofactor).
 GN Name=grpE; OrderedLocustNames=yP181141;
 OS Yersinia pseudotuberculosis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 NC NCB1_TaxID=633;
 [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=IP32953 / Serotype I;
 RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
 RA Chain P.S.G., Garnier E., Larimer F.W., Lamerdin J., Stoutland P.O.,
 RA Regala W.M., Georgescu A.M., Verges L.M., Land M.L., Motin V.L.,
 RA Brubaker R.R., Fowler J., Himebusch J., Marceau M., Medigue C.,
 RA Simonet M., Chenal-Francois V., Souza B., Dacheux D., Elliott J.M.,
 RA Derise A., Hauser L.J., Garcia E.;
 RT "Insights into the evolution of Yersinia pestis through whole-genome
 comparison with Yersinia pseudotuberculosis."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
 -1- FUNCTION: Participates actively in the response to stress-denatured
 proteins, in association with dnaK and grpE. It is the nucleotide
 exchange factor for dnaK and may function as a thermosensor.
 CC Unfolded proteins bind initially to dnaJ; upon interaction with
 the dnaJ-bound protein, dnaK hydrolyzes its bound ATP, resulting
 in the formation of a stable complex. GrpE releases ADP from dnaK;
 ATP binding to dnaK triggers the release of the substrate protein,
 thus completing the reaction cycle. Several rounds of ATP-
 dependent interactions between dnaJ, dnaK and grpE are required
 for fully efficient folding (By similarity).
 -1- SIMILARITY: Belongs to the grpE family.
 CC EMBL: BX936398; CAH20381.1; -; Genomic DNA.
 CC GO: GO:0000774; F:adenyl-nucleotide exchange factor activity; IEA.
 CC GO: GO:0051087; F:chaperone binding; IEA.
 CC GO: GO:004803; F:protein homodimerization activity; IEA.
 CC GO: GO:0051082; F:unfolded protein binding; IEA.
 CC GO: GO:0006457; P:protein folding; IEA.
 CC GO: GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro: IPR000740; GrpE.
 DR Pfam: PF01025; GrpE; 1.
 DR PRINTS: PR00773; GRPEPROTEIN.
 DR PROSITE: PS01071; GRPE; 1.
 DR Chaperone; Complete proteome; Heat shock.
 SQ SEQUENCE 192 AA; 21545 MW; AFD5FC7AA472062 CRC64;
 Query Match 45.2%; Score 66; DB 2; Length 192;
 Best local similarity 60.0%; Pred. No. 8;
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 6 QSSDLERERESVLRROEVAEERR 30
 DB 45 QLSDLQRERESLRAKAEVENIR 69

RESULT 6	OC61W6_YARLI PRELIMINARY;	PRT; 1229 AA.
ID	OC61W6_YARLI PRELIMINARY;	PRT; 1229 AA.
AC	OC61W6_YARLI PRELIMINARY;	PRT; 1229 AA.
DT	25-OCT-2004 (TREMBLrel. 28, Created)	
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)	
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)	
DE	Similarity.	
GN	OrderedLocusNames=YALIOF128379;	
OS	Yarrowia lipolytica (Candida lipolytica).	
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	
OC	Saccharomycetales; Dipodascaceae; Yarrowia.	
OX	NCBI_TaxID=4952;	
OX	[1]	
RN	NCU1E012E DISEQUENCE [LARGE SCALE GENOMIC DNA].	
RP	PubMed=15292592; DOI=10.1038/nature02579;	
RX	PubMed=15292592; DOI=10.1038/nature02579;	
RA	Dujon B., Sherman D., Fischer G., Durrens P., Casargola S.,	
RA	Lafontaine I., de Montigny J., Marc C., Neuvéglise C., Talla E.,	
RA	Goiffard N., Frangul L., Aigle M., Antchoud V., Badoir A., Barbe V.,	
RA	Batmy S., Blanchin S., Beckerlich J.-M., Beyne E., Bleykaesten C.,	
RA	Bertrame A., Boyer J., Cactolico L., Confalieri F., de Darvar A.,	
RA	Despons L., Fabre E., Faithed C., Ferry-Dumazet H., Gropi A.,	
RA	Dertrave F., Henneguin C., Janniaux N., Joyet P., Kachouri R.,	
RA	Kerret A., Koszul R., Lemaire M., Lest I., Ma L., Muller H.,	
RA	Nicoud J.-M., Nikolaki M., Ozeas S., Ozier-Kalogiropoulos O.,	
RA	Pellens S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,	
RA	Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,	
RA	Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,	
RA	Bouchier C., Candron B., Scarpelli C., Gallardin C., Weissenbach J.,	
RA	Wincker P., Souciet J.-L.,	
RT	"Genome evolution in yeasts."	
RL	Nature 430:35-44(2004).	
DR	EMBL; CR382132; CAG78153.1; -) Genomic DNA.	
DR	InterPro; IPR001670; Pfam-A10.	
DR	InterPro; IPR001670; Pfam-A10.	
DR	PROSITE; PS00060; ADH IRON 2; UNKNOWN 1.	
DR	PROSITE; PS00060; ADH IRON 2; UNKNOWN 1.	
KM	Complete proteome.	
SO	SEQUENCE 1229 AA; 132821 MW; 63DB6815F938F9A9 CRC64;	
Query Match	43.5%; Score 63.5; DB 2; Length 1229;	
Best Local Similarity	45.5%; Pred. No. 1.1e+02;	
Matches	15; Conservative 6; Mismatches 7; Indels 5; Gaps	
OY	3 OKSOSDILERRERSVLRQEQ---VAERR 30	
DB	194 OKOBAERLREERERLREERERERQAWBERQ 226	
RESULT 7		
ID	Q7NL34_GLOVI PRELIMINARY;	PRT; 266 AA.
AC	Q7NL34_GLOVI PRELIMINARY;	PRT; 266 AA.
DT	01-MAR-2004 (TREMBLrel. 26, Created)	
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)	
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
DE	Gli1292 protein.	
GN	OrderedLocusNames=gli1292;	
OS	Gloeobacter violaceus.	
OC	Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacteriales; Gloeobacter.	
OX	NCBI_TaxID=33072;	
OX	[1]	
RN	NCU1E012E DISEQUENCE [LARGE SCALE GENOMIC DNA].	
RP	PubMed=14621292;	
RX	PubMed=14621292;	
RA	Medluna P., Kaneo T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,	
RA	Sakamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,	
RA	Kohara M., Matsuno M., Matsuo A., Nakazaki N., Shimp S.,	
RA	Tsuchi C., Yamada M., Taba S.,	
RT	"Complete genome structure of Gloeobacter violaceus PCC 7421, a	
RT	cyanobacterium that lacks thylakoids."	

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DNA Res. 10;137-145(2003).
DR EMBL; BA000045; BAC69233.1;-; Genomic_DNA.
DR InterPro; IPR008538; DUF820.
DR Pfam; PF05685; DUF820; 1.
RW Complete proteome.
SQ SEQUENCE 266 AA; 30978 MW; 6BE848A5426F5C65 CRC64;

Query Match          42.5%; Score 62; DB 2; Length 266;
Best Local Similarity 46.7%; Pred. No. 33;
Matches 14; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Cy      1 FLQKSSDDLREERESVLRDEQVAEERR 30
        | : | | | | | | | | | | | | | |
Db      218 RQRAEQGERGRRAEQGERGRRAEAEGQVAEERR 247

RESULT 8
O6MY9 ASPFU PRELIMINARY; PRT; 524 AA.
ID O6MY9 ASPFU PRELIMINARY; PRT; 524 AA.
AC Q6MY9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE RNA export mediator gle1 homologue, putative.
GN ORNames=Af24A6.110;
OS Aspergillus fumigatus (Sartorya fungigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxId=5085; [1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=14998527; DOI=10.1016/j.fgb.2003.12.003;
RX Pain A., Woodward J., Quail M.A., Anderson M.J., Clark R., Collins M.,
   RA Foster N., Fraser A., Harris D., Lake N., Murphy L., Humphray S.,
   RA O'Neill S., Perlea M., Price C., Rabdinowitch E., Rajandream M.-A.,
   RA Salzberg S., Saunders D., Seeger K., Sharp S., Warren T.,
   RA Denning D.W., Bartrell B., Hall N.;
   RT "Insight into the genome of Aspergillus fumigatus: analysis of a 922
   RT kb region encompassing the nitrate assimilation gene cluster.";
   RL Fungal Genet. Biol. 41:443-453(2004).
   DR EMBL; BX649605; CA647870.1;-; Genomic DNA.
   SQ SEQUENCE 524 AA; 60627 MW; DP9108335A8BDJ3 CRC64;

Query Match          42.5%; Score 62; DB 2; Length 524;
Best Local Similarity 56.3%; Pred. No. 67;
Matches 14; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Cy      6 QSDLLRERSRVLRDEQVAEER 29
        | :: ||||| ||||| |||||
Db      103 QEAERLERERAKLRDEQVAARR 126

RESULT 9
O4MSW1 ASPFU PRELIMINARY; PRT; 524 AA.
ID O4MSW1 ASPFU PRELIMINARY; PRT; 524 AA.
AC Q4MSW1;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE RNA export mediator (Gle1), putative.
GN ORNames=Afu1g11440;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxId=330879; [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Niernman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Arroyo J., Bertman M., Ade K., Archer D.B., Bernhejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,

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RA Goldman G.H., Goni K., Griffith-Jones S., Williams R., Haas B.,
 RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
 RA Keller N., Khouri H., Kikuchi K., Kobayashi T., Kulkarni R.,
 RA Kumagai T., Lafont A., Latge J.-P., Li W., Lord A., Lu C.,
 RA Majora W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
 RA Mounay I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
 RA Penava M.A., Petrea M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitz E., Rawlin N., Rajendram M.A., Reichard U.,
 RA Renaud H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Rensing C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Taveuch M., Tekla F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J., Yu J.-H., Frazer C., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrett B., Denning D.W.,
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
 RT *Aspergillus fumigatus*.";
 RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL, AAF0100004; EAL90471.1; -!- Genomic DNA.
 SQ SEQUENCE 524 AA; 60627 MW; DF9108335A8BD3 CRC64;

Query Match 42.5%; Score 62; DB 2; Length 524;
 Best Local Similarity 58.3%; Pred. No. 67;
 Matches 14; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 6 OSDDLREBSVLRREGEVAER 29
 DB 103 QEAERLRERAKLRREGEVAER 126

RESULT 10
 ID 018137_CABEL PRELIMINARY; PRT; 944 AA.
 AC 018137;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Apical junction molecule protein 1, isoform b.
 GN Name=ajm-1; ORFNames=C25A11.4;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodertinae; Caenorhabditis.
 OC NCBI_Taxid=6239;
 RX NCBI_Taxid=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Brictol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2016(1998).
 DR EMBL, U39650; AAK39186.1; -!- Genomic DNA.
 DR HSSP, P05412; 1FOS.
 DR Ensemble, C25A11.4; Caenorhabditis elegans.
 DR WormBase, WBGene0000100; ajm-1.
 DR WormPeP, C25A11.4b; CE27084.
 KW Complete proteome.
 SQ SEQUENCE 944 AA; 113558 MW; 6C4FBC0CFAD3B03 CRC64;

Query Match 42.5%; Score 62; DB 2; Length 944;
 Best Local Similarity 51.6%; Pred. No. 1.3e+02;
 Matches 16; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

QY 3 QKSQSDLLERRESVLRREGEVAE--ERRN 31
 DB 687 EEAQLADLLERERHNOILRENERREVAERAN 717

RESULT 11
 OS82W2_9TRYP
 ID 0582W2_9TRYP PRELIMINARY; PRT; 963 AA.

AC OS82W2;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=tb927.3.2490;
 OS Trypanosoma brucei.
 OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OC NCBI_Taxid=5691;
 RX NCBI_Taxid=5691;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GUTat10.1;
 RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
 RA Shalom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
 RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
 RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
 RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
 RA Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GUTat10.1;
 RA El-Sayed N.M., Khalak H., Adams M.D.;
 RA Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GUTat10.1;
 RA Haas B., Blandin G., El-Sayed N.,
 RA Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AC091330; AAK80727.1; -!- Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 963 AA; 110072 MW; 341C60AD1FFFPF28 CRC64;

Query Match 42.5%; Score 62; DB 2; Length 963;
 Best Local Similarity 43.3%; Pred. No. 1.3e+02;
 Matches 13; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 RUKSQSDLLERRESVLRREGEVAER 30
 DB 526 KLDKSGRDVAVEROSIQAKRYLVEER 555

RESULT 12
 ID 0952Y7_CABEL PRELIMINARY; PRT; 1148 AA.
 AC 0952Y7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Apical junction molecule protein 1, isoform c.
 GN Name=ajm-1; ORFNames=C25A11.4;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodertinae; Caenorhabditis.
 OC NCBI_Taxid=6239;
 RX NCBI_Taxid=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Brictol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2016(1998).
 DR EMBL, U39650; AAK39186.1; -!- Genomic DNA.
 DR HSSP, P05412; 1FOS.
 DR Ensemble, C25A11.4; Caenorhabditis elegans.
 DR WormBase, WBGene0000100; ajm-1.
 DR WormPeP, C25A11.4c; CE27085.
 KW Complete proteome.
 SQ SEQUENCE 1148 AA; 137473 MW; 432F662CC8E20729 CRC64;

Query Match 42.5%; Score 62; DB 2; Length 1148;
 Best Local Similarity 51.6%; Pred. No. 1.5e+02;
 Matches 16; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

OY 3 QKSQSDLLERRESVLRREQVAE--ERRN 31
DB 687 EEAQLADLLERHRNQLIRENREAVERRAN 717

RESULT 13
OY 08MOC7 CAEEL PRELIMINARY; PRT; 1439 AA.
ID 08MOC7 CAEEL PRELIMINARY; PRT; 1439 AA.
AC 08MOC7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Apical junction molecule protein 1, isoform d.
GN Name=ajm-1; ORFNames=C25A11.4;
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodermine; Caenorhabditis.
OX NCBI_TaxID=6239;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Bristol N2;
RC MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT Investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; U39650; AAM51517.1; -; Genomic_DNA.
DR HSSP; P05412; 1FOS.
DR Ensemble; C25A11.4; Caenorhabditis elegans.
DR WormBase; WBGene0000100; ajm-1.
DR InterPro; IPR002893; Znf_MYND.
DR PROSITE; PS50865; ZF_MYND_2; 1.
KW Complete proteome.
SQ SEQUENCE 1439 AA; 170263 MW; 30753B0B6FB749F CRC64;

Query Match 42.5%; Score 62; DB 2; Length 1439;
Best Local Similarity 51.6%; Pred. No. 2e+02;
Matches 16; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

OY 3 QKSQSDLLERRESVLRREQVAE--ERRN 31
DB 687 EEAQLADLLERHRNQLIRENREAVERRAN 717

RESULT 14
OY 018138 CAEEL PRELIMINARY; PRT; 1480 AA.
ID 018138 CAEEL PRELIMINARY; PRT; 1480 AA.
AC 018138;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Apical junction molecule protein 1, isoform a.
GN Name=ajm-1; ORFNames=C25A11.4;
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodermine; Caenorhabditis.
OX NCBI_TaxID=6239;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Bristol N2;
RC MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT Investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; U39650; AAK39187.1; -; Genomic_DNA.
DR HSSP; P05412; 1FOS.
DR Ensemble; C25A11.4; Caenorhabditis elegans.
DR WormBase; WBGene0000100; ajm-1.
DR WormPep; C25A11.4a; CE27083.
DR InterPro; IPR002893; Znf_MYND.

DR PROSITE; PS50865; ZF_MYND_2; 1.
KW Complete proteome.
SQ SEQUENCE 1480 AA; 175237 MW; EC9FAA97040EC7BA CRC64;

Query Match 42.5%; Score 62; DB 2; Length 1480;
Best Local Similarity 51.6%; Pred. No. 2e+02;
Matches 16; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

OY 3 QKSQSDLLERRESVLRREQVAE--ERRN 31
DB 687 EEAQLADLLERHRNQLIRENREAVERRAN 717

RESULT 15
OY 04S6V2 TENTG PRELIMINARY; PRT; 1484 AA.
ID 04S6V2 TENTG PRELIMINARY; PRT; 1484 AA.
AC 04S6V2;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 14 SCAR14723, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0023112001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallou O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Maucel E., Bouneau L., Fischer C., Ozouf-Coenaz C., Bernot A.,
RA Maucel S., Jaffe D., Fisher S., Luchaila G., Dossat C., Segreus B.,
RA Daelva C., Salenouat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,
RA Cnaut C., Duprat S., Brottier P., Couranceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kella M., Volt DN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander B.S., Weissenbach J., Roest Crolious H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL; CAE01014723; CAG03630.1; -; Genomic_DNA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR00219; RhGEF.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhGEF; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhGEF; 1.
DR PROSITE; PSS0010; DH 2; 1.
DR PROSITE; PSS0003; PH_DOMAIN; 1.
FT NON_TER 1
FT NON_TER 1484
SQ SEQUENCE 1484 AA; 165189 MW; 4BD39AFAD2C48FAF CRC64;

Query Match 41.8%; Score 61; DB 2; Length 1484;
Best Local Similarity 41.4%; Pred. No. 2.6e+02;
Matches 12; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

OY 2 LKQSSDLLERRESVLRREQVAEERR 30

Mon Mar 6 11:39:02 2006

us-10-646-873-44.rup

Page 7

Db 838 LKTTEDDKKKERDLSLASEQDLTESLR 866

Search completed: March 3, 2006, 13:26:09
Job time : 14.8397 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 13:35:46 ; Search time 4.15743 Seconds
(without alignments)
616.473 Million cell updates/sec

Title: US-10-646-873-44

Perfect score: 166
Sequence: 1 RLOKSGSSDLERERESVLRREQVAEERRN 31

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents, AA:
1: /cgn2_6/ptodata/1/1aa/5-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCUTS-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	31	2	US-09-050-516-44
2	146	100.0	31	2	US-10-278-547-44
3	146	100.0	215	2	US-09-050-516-47
4	146	100.0	215	2	US-10-278-547-47
5	146	100.0	679	2	US-09-050-516-42
6	146	100.0	679	2	US-10-278-547-42
7	56	38.4	322	2	US-09-540-236-310
8	56	38.4	828	2	US-10-092-138A-26
9	56	38.4	828	2	US-08-681-219A-26
10	55.5	38.0	513	2	US-09-248-796A-18714
11	55	37.7	461	2	US-09-949-016-8508
12	54.5	37.3	737	2	US-09-543-681A-6489
13	54.5	37.3	1898	1	US-08-056-200-94
14	54.5	37.3	1898	1	US-08-800-644-94
15	54.5	37.3	1898	2	US-09-538-092-1280
16	54	37.0	166	1	US-08-365-103B-14
17	54	37.0	166	1	US-08-365-103B-12
18	54	37.0	320	1	US-08-365-103B-10
19	54	37.0	321	1	US-08-365-103B-8
20	53.5	36.6	205	2	US-09-270-767-36272
21	53.5	36.6	205	2	US-09-270-767-51489
22	52.5	36.0	638	2	US-09-949-016-9984
23	52.5	36.0	734	2	US-09-134-000C-5602
24	52.5	36.0	761	2	US-09-046-894-35
25	52.5	36.0	811	2	US-08-933-750C-45
26	52.5	36.0	811	1	US-09-234-613-45
27	52	35.6	447	2	US-09-248-796A-14846

28	52	35.6	482	2	US-09-538-092-1345	Sequence 1345, Ap
29	52	35.6	538	2	US-09-370-368-9	Sequence 9, Appl
30	52	35.6	712	2	US-09-949-016-10600	Sequence 10600, A
31	52	35.6	859	2	US-09-199-637A-281	Sequence 281, App
32	52	35.6	859	2	US-09-252-991A-21413	Sequence 21413, A
33	52	35.6	919	2	US-09-949-016-6954	Sequence 6954, Ap
34	52	35.6	1487	2	US-09-489-039A-12113	Sequence 12113, A
35	51	34.9	373	2	US-09-270-767-42838	Sequence 42838, A
36	51	34.9	868	2	US-09-543-681A-5357	Sequence 5357, Ap
37	51	34.9	1003	2	US-09-198-452A-17	Sequence 17, Appl
38	51	34.9	1003	2	US-09-438-185A-8	Sequence 8, Appl
39	50.5	34.6	550	2	US-09-538-092-1259	Sequence 1259, Ap
40	50	34.2	149	2	US-09-270-767-42544	Sequence 42544, A
41	50	34.2	255	2	US-09-227-357-488	Sequence 488, App
42	50	34.2	255	2	US-09-973-278-386	Sequence 386, App
43	50	34.2	495	2	US-09-538-092-224	Sequence 224, App
44	50	34.2	538	2	US-09-309-572-12	Sequence 12, Appl
45	50	34.2	538	2	US-09-718-096-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-050-516-44
Sequence 44, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828, 855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-44

Query Match 100.0%; Score 146; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RLOKSSDDLREERSVLRREQVAEERRN 31
Db 1 RLOKSSDDLREERSVLRREQVAEERRN 31

RESULT 2

US-10-278-547-44
Sequence 44, Application US/10278547
Patent No. 6660834
GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 44:

US-10-278-547-44

Query Match 100.0%; Score 146; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RLOKSSDDLREERSVLRREQVAEERRN 31
Db 1 RLOKSSDDLREERSVLRREQVAEERRN 31

RESULT 3

US-09-050-516-47
Sequence 47, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
KRATOCHVIL, LISA
APPLICANT: ROBERTS-RAP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-47

Query Match 100.0%; Score 146; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 7.6e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLOKSSDILLERRESVLRREQVAAERRN 31
Db 73 RLOKSSDILLERRESVLRREQVAAERRN 103

RESULT 4

US-10-278-547-47
Sequence 47, Application US/10278547
Patent No. 6660834

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSER: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547

FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065, US, P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6660834e

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-10-278-547-47

Query Match 100.0%; Score 146; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 7.6e-12;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. 6627414

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSER: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065, US, P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 679 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6627414e

US-09-050-516-42

Query Match 100.0%; Score 146; DB 2; Length 679;

Best Local Similarity 100.0%; Pred. No. 2.7e-11;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

US-10-278-547-42

Sequence 42, Application US/10278547

Patent No. 6660834

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-278-547-42
Query Match 100.0%; Score 146; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 2,7e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 RLOKSSSDLLERRESVLRREQVAAERRN 31
Db 537 RLOKSSSDLLERRESVLRREQVAAERRN 567
RESULT 7
US-09-540-236-3120
Sequence 3120, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3120

LENGTH: 322
TYPE: PRT
ORGANISM: M.catarhalis
US-09-540-236-3120
Query Match 38.4%; Score 56; DB 2; Length 322;
Best Local Similarity 46.7%; Pred. No. 8.8;
Matches 14; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
Cy 1 RLOKSSSDLLERRESVLRREQVAAERR 30
Db 134 QLAIQEORLEQERLENERREQERLEQER 163
RESULT 8
US-10-092-138A-26
Sequence 26, Application US/10092138A
Patent No. 6743630
GENERAL INFORMATION:
APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
FILE REFERENCE: 65823/JPW/PT
CURRENT APPLICATION NUMBER: US/10/092,138A
CURRENT FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 828
TYPE: PRT
ORGANISM: human
US-10-092-138A-26
Query Match 38.4%; Score 56; DB 2; Length 828;
Best Local Similarity 40.0%; Pred. No. 25;
Matches 14; Conservative 7; Mismatches 8; Indels 6; Gaps 1;
Cy 1 RLOKSSSDLLER-----RESVLRREQVAAER 29
Db 38 RLOQTEREDLLERKLAQAQCEQSHLMREHDVQER 72

RESULT 9
US-08-681-219A-26
Sequence 26, Application US/08681219A
Patent No. 6911526
GENERAL INFORMATION:
APPLICANT: Sato, Taka-Aki
APPLICANT: Yanagisawa, Jun
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
TITLE OF INVENTION: DOMAIN AND USES THEREOF
FILE REFERENCE: 48962
CURRENT APPLICATION NUMBER: US/08/681,219A
CURRENT FILING DATE: 1996-07-22
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 828
TYPE: PRT
ORGANISM: human
US-08-681-219A-26
Query Match 38.4%; Score 56; DB 2; Length 828;
Best Local Similarity 40.0%; Pred. No. 25;
Matches 14; Conservative 7; Mismatches 8; Indels 6; Gaps 1;
Cy 1 RLOKSSSDLLER-----RESVLRREQVAAER 29
Db 38 RLOQTEREDLLERKLAQAQCEQSHLMREHDVQER 72
RESULT 10

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Query Match Similarity 37.7% Score 55; DB 2; Length 461;
Best Local Similarity 46.9% Pred. No. 18;
Matches 15; Conservative 4; Mismatches 9; Indels 4; Gaps 1;

Cy 3 OKSQSDLLRRERSV---LRREQVAEERR 30
      | | | | | | | | | | | | | |
Db 43 OOLEERKLLRRERERLHEEWILLREQKAOEEFR 74

RESULT 12
US-09-543-681A-6489
; Sequence 6489, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001

```

Query Match	37.3%	Score 54.5	DB 1	Length 1898
Best Local Similarity	44.1%	Pred. No. 98		
Matches 15	Conservative 6	Mismatches 8	Indels 5	Gaps 2

QY	1	R	L	O	K	S	S	D	L	E	---	R	E	S	T	V	R	E	E	V	A	E	R	R	30
DB	677	R	K	R	E	E	E	E	R	L	E	R	K	R	E	E	E	E	R	E	E	E	E	E	709

```

US-08-800-644-94
; Sequence 94 Application US/08800644
; Patent No. 5958752
; GENERAL INFORMATION:
; APPLICANT: Steinert, Peter M.
; APPLICANT: Lee, Seung-Chul
; APPLICANT: Kim, In-Gyu
; APPLICANT: Chung, Soo-Il
; APPLICANT: Park, Sang-Chul
; TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,644
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/056,200
; FILING DATE: 30-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedtich, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH054.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1898 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-800-644-94

Query Match          37.3% Score 54.5; DB 1; Length 1898;
Best Local Similarity 44.1%; Pred. No. 98;
Matches 15; Conservative 6; Mismatches 8; Indels 5; Gaps 2;

QY      1 RLRKSSDLLE---RERSVLRREGEVAERR 30
        ||:::|||||::|||::|||::|||:
Db       677 RLKRREERERLRLRKREHREE-RREQELAESEQ 709

RESULT 15
US-09-538-092-1280
; Sequence 1280, Application US/09538092
; Patent No. 6753114
; GENERAL INFORMATION:
; APPLICANT: Gioc, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurafastSeqFormatter Version 0.9

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; SEQ ID NO 1280
; LENGTH: 1898
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number Q07283
US-09-538-092-1280

Query Match          37.3%; Score 54.5; DB 2; Length 1898;
Best Local Similarity 44.1%; Pred. No. 98;
Matches 15; Conservative 6; Mismatches 8; Indels 5; Gaps 2.

QY      1 RLQKSSDLIE---RRRESVLRQDFVAERR 30
          |||::: ||| ||| ||| |||:::
Db      677 RLKREERERLECRLEKREHEEE-RRQELABEEQ 709

Search completed: March 3, 2006, 13:38:53
Job time : 5.3241 secs

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Query Match 37.3%, Score 54.5; DB 2; Length 1898;
 Best Local Similarity 44.1%, Pred. No. 98;
 Matches 15; Conservative 6; Mismatches 8; Indels 5; Gaps 2;

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QY      1 RLQKQSSDLE----RERSVLRREQEVAEERR 30
        ||:::  :  ||  ||  |||||::|||  :
Db      677 RLKREEREERLEQLKREHEEE--RREQETAEBO 709

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Search completed: March 3, 2006, 13:38:53
Job time : 5.3241 secs

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 3, 2006, 14:09:14 ; Search time 13.6171 Seconds
(without alignments)
951.209 Million cell updates/sec

Title: US-10-646-873-44

Perfect score: 146
Sequence: 1 RLQKSSQSLLEERERESYLRRQVAEERRN 31

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.dep.*
- 2: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.dep.*
- 3: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.dep.*
- 4: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.dep.*
- 5: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.dep.*
- 6: /cgn2_6/ptodata/1/pubppa/US11_PUBCOMB.dep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	31	3	US-09-050-516-44
2	146	100.0	31	4	US-10-278-547-44
3	146	100.0	31	4	US-10-646-873-44
4	146	100.0	215	3	US-09-050-516-47
5	146	100.0	215	4	US-10-278-547-47
6	146	100.0	215	4	US-10-646-873-47
7	146	100.0	679	3	US-09-050-516-42
8	146	100.0	679	4	US-10-278-547-42
9	146	100.0	679	4	US-10-646-873-42
10	142	97.3	172	4	US-10-106-698-4761
11	68	46.6	1439	5	US-10-754-079-157
12	59	40.4	293	4	US-10-425-115-367723
13	59	40.4	1407	5	US-10-732-923-3359
14	58.5	40.1	527	5	US-10-732-923-19024
15	58.5	40.1	689	6	US-11-097-143-14634
16	58	39.7	524	4	US-10-128-714-3303
17	58	39.7	894	6	US-11-097-143-21003
18	57.5	39.4	161	4	US-10-424-599-176239
19	57	39.0	184	4	US-10-424-599-17876
20	57	39.0	1893	6	US-11-097-143-6279
21	56.5	38.7	487	4	US-10-425-115-358829
22	56.5	38.7	656	4	US-10-437-963-147007
23	56	38.4	219	4	US-10-425-114-57370
24	56	38.4	322	4	US-10-382-1228-63265
25	56	38.4	322	4	US-10-437-963-111187
26	56	38.4	828	2	US-08-681-219-28
27	56	38.4	828	3	US-09-230-111C-26

28	56	38.4	828	4	US-10-092-138-26	Sequence 26, Appl
29	56	38.4	828	5	US-10-820-403-26	Sequence 26, Appl
30	56	38.4	985	6	US-11-097-143-17463	Sequence 17463, A
31	56	38.4	985	6	US-11-097-143-27048	Sequence 27048, A
32	55.5	38.0	500	4	US-10-032-585-7588	Sequence 7588, Ap
33	55	37.7	143	5	US-10-450-763-51348	Sequence 51348, A
34	55	37.7	224	4	US-10-094-749-2506	Sequence 2506, Ap
35	55	37.7	224	4	US-10-408-765A-2501	Sequence 2501, Ap
36	55	37.7	478	4	US-10-437-963-142690	Sequence 142690, A
37	55	37.7	527	4	US-10-450-763-51352	Sequence 51352, A
38	55	37.7	691	4	US-10-369-493-20148	Sequence 20148, A
39	55	37.7	827	4	US-10-437-963-152005	Sequence 152005, A
40	55	37.7	1100	5	US-10-494-940-22	Sequence 22, Appl
41	55	37.7	1391	4	US-10-437-963-128235	Sequence 128235, A
42	54.5	37.3	105	4	US-10-425-115-248030	Sequence 248030, A
43	54.5	37.3	274	4	US-10-767-701-38902	Sequence 38902, A
44	54	37.0	165	4	US-10-425-115-233920	Sequence 233920, A
45	54	37.0	166	5	US-10-473-127-1945	Sequence 1945, Ap

ALIGNMENTS

RESULT 1
US-09-050-516-44
Sequence 44, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-PAPE, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-44

Query Match 100.0%; Score 146; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 8,4e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLOKSQSSDILLERRESVLRREQVVAERRN 31
DB 1 RLOKSQSSDILLERRESVLRREQVVAERRN 31

RESULT 2
US-10-278-547-44
Sequence 44, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KCLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 44:

US-10-278-547-44

Query Match 100.0%; Score 146; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 8,4e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLOKSQSSDILLERRESVLRREQVVAERRN 31
DB 1 RLOKSQSSDILLERRESVLRREQVVAERRN 31

RESULT 3
US-10-646-873-44
Sequence 44, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KCLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-646-873-44

Query Match 100.0%; Score 146; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 8,4e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLOKSQSSDLRERESVLRREQVAAERRN 31
Db 1 RLOKSQSSDLRERESVLRREQVAAERRN 31

RESULT 4

US-09-050-516-47
Sequence 47, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20010010904A1e
US-09-050-516-47

Query Match 100.0%; Score 146; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.6e-10;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLOKSQSSDLRERESVLRREQVAAERRN 31
Db 73 RLOKSQSSDLRERESVLRREQVAAERRN 103

RESULT 5

US-10-278-547-47
Sequence 47, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-278-547-47

Query Match 100.0%; Score 146; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.6e-10;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLOKSQSSDLRERESVLRREQVAAERRN 31
Db 73 RLOKSQSSDLRERESVLRREQVAAERRN 103

RESULT 6
US-10-646-873-47
Sequence 47, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE

COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-646-873-47
Query Match 100.0%; Score 146; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.6e-10;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 RLOKSSDILLERRESVLRREQVAEERRN 31
Db 73 RLOKSSDILLERRESVLRREQVAEERRN 103
RESULT 7
US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANDOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.

APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-42
Query Match 100.0%; Score 146; DB 3; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 RLOKSSDILLERRESVLRREQVAEERRN 31
Db 537 RLOKSSDILLERRESVLRREQVAEERRN 567
RESULT 8
US-10-278-547-42
Sequence 42, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANDOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASCSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>

REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.

INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-278-547-42

Query Match 100.0%; Score 146; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLOKSSDILLERESVLRREQVAAERRN 31
DB 537 RLOKSSDILLERESVLRREQVAAERRN 567

RESULT 9
US-10-646-873-42
Sequence 42, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASCSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-646-873-42

Query Match 100.0%; Score 146; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLOKSSDILLERESVLRREQVAAERRN 31
DB 537 RLOKSSDILLERESVLRREQVAAERRN 567

RESULT 10
US-10-106-698-4761
Sequence 4761, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 4761
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (55)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (116)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-4761

Query Match 97.3%; Score 142; DB 4; Length 172;
Best Local Similarity 96.8%; Pred. No. 1.6e-09;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RLOKSSDLELRERESVLRREQVAAERRN 31
Db 30 RLOKSSDLELRERESVLRREQVAAERRN 60

RESULT 11

US-10-754-079-157
Sequence 157, Application US/10754079
Publication No. US2005008602A1
GENERAL INFORMATION:

APPLICANT: Hirai, Yohel
TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
FILE REFERENCE: 46739200222
CURRENT FILING DATE: 2004-01-07
PRIOR APPLICATION NUMBER: US 10/155,922
PRIOR FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: PCT/JP01/04691
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: JP 2000-166903
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: JP 2001-347340
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: JP 2001-347338
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: JP 2001-371175
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: JP 2001-371336
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: JP 2003-1891
PRIOR FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 162
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 157
LENGTH: 1439
TYPE: PRT
ORGANISM: Mus Musculus
US-10-754-079-157

Query Match 46.6%; Score 68; DB 5; Length 1439;
Best Local Similarity 44.7%; Pred. No. 15;
Matches 17; Conservative 5; Mismatches 8; Indels 8; Gaps 1;

Oy 1 RLOKSSDLELRERESVLRREQVAAERR 30
Db 218 RLOKSSDLELRERESVLRREQVAAERR 255

RESULT 12

US-10-425-115-367723
Sequence 367723, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 367723
LENGTH: 293
TYPE: PRT
ORGANISM: Zea mays
FEATURE:

NAME/KEY: unsure
LOCATION: (1)-(293)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: M74577_98535C.1.pep
US-10-425-115-367723

Query Match 40.4%; Score 59; DB 4; Length 293;
Best Local Similarity 70.0%; Pred. No. 33;
Matches 14; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

Oy 11 LERERESVLRREQVAAERR 30
Db 116 LERERESVLRREQVAAERR 133

RESULT 13

US-10-732-923-3359
Sequence 3359, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 3359
LENGTH: 1407
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-10-732-923-3359

Query Match 40.4%; Score 59; DB 5; Length 1407;
Best Local Similarity 42.9%; Pred. No. 1.8e+02;
Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Oy 2 LOKSSDLELRERESVLRREQVAAERR 29
Db 1153 LOKSSDLELRERESVLRREQVAAERR 1180

RESULT 14

US-10-732-923-19024
Sequence 19024, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 19024
LENGTH: 527
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-10-732-923-19024

Query Match 40.1%; Score 58.5; DB 5; Length 527;
Best Local Similarity 45.2%; Pred. No. 72;
Matches 14; Conservative 7; Mismatches 7; Indels 3; Gaps 1;

Oy 1 RLOKSSDLELRERESVLRREQVAAERR 28
Db 370 RLOKSSDLELRERESVLRREQVAAERR 400

RESULT 15

US-11-097-143-14634
 ; Sequence 14634, Application US/11097143
 ; Publication No. US20050208558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig
 ; APPLICANT: et al.
 ; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
 ; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
 ; FILE REFERENCE: DROSOPHILA GENES.
 ; FILE REFERENCE: CLO00728
 ; CURRENT APPLICATION NUMBER: US/11/097,143
 ; CURRENT FILING DATE: 2005-04-04
 ; PRIOR APPLICATION NUMBER: 60/157,832
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: 60/160,191
 ; PRIOR FILING DATE: 1999-10-19
 ; PRIOR APPLICATION NUMBER: 60/161,932
 ; PRIOR FILING DATE: 1999-10-28
 ; PRIOR APPLICATION NUMBER: 60/164,769
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: 60/173,383
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR APPLICATION NUMBER: 60/175,693
 ; PRIOR FILING DATE: 2000-01-12
 ; PRIOR APPLICATION NUMBER: 60/184,831
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/191,637
 ; PRIOR FILING DATE: 2000-03-23
 ; NUMBER OF SEQ ID NOS: 43008
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 14634
 ; LENGTH: 689
 ; TYPE: PR1
 ; ORGANISM: DROSOPHILA
 US-11-097-143-14634

Query Match 40.1%; Score 58.5; DB 6; Length 689;
 Best Local Similarity 45.2%; Pred. No. 95;
 Matches 14; Conservative 7; Mismatches 7; Indels 3; Gaps 1;

QY 1 RLOKSSDL---LRRRESVLRREQVABE 28
 |::|||:|||||:|:|
 DB 370 RIEQEQLELRERLEKRESDLKAOQOQASE 400

Search completed: March 3, 2006, 14:18:10
 Job time : 14.6171 secs

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Best Local Similarity 37.9%; Pred. No. 5.9;
Matches 11; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

Qy 1 RLOKSQSDLLERRESVLRREQVAAER 29
Db 84 RLEKKAEMV-RERDEVIRKKEIEIETR 111

RESULT 3

US-11-087-099-8879
; Sequence 8879, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8879
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Daucus carota
US-11-087-099-8879

Query Match 38.7%; Score 56.5; DB 7; Length 502;
Best Local Similarity 42.9%; Pred. No. 6.1;
Matches 12; Conservative 9; Mismatches 6; Indels 1; Gaps 1;

Qy 2 LQKSQSDLLERRESVLRREQVAAER 29
Db 98 LKAKTEEMV-KERREARKEIEIETR 124

RESULT 4

US-10-467-657-4618
; Sequence 4618, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqwIn9, version 1.04
; SEQ ID NO 4618
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4618

Query Match 37.0%; Score 54; DB 6; Length 263;
Best Local Similarity 38.5%; Pred. No. 6.1;
Matches 10; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 5 QSSQSDLLERRESVLRREQVAAER 30
Db 56 SQOODILORORKEQKLRQVQPEQDVR 81

RESULT 5
US-11-087-099-4004
; Sequence 4004, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.

; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4004
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(235)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-4004

Query Match 36.6%; Score 53.5; DB 7; Length 235;
Best Local Similarity 41.7%; Pred. No. 6.2;
Matches 10; Conservative 10; Mismatches 3; Indels 1; Gaps 1;

Qy 1 RLOKSQSDLLERRESVLRREQ 24
Db 85 RLEKKAEMV-RERDEVIRKKE 107

RESULT 6

US-11-087-099-1159
; Sequence 1159, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1159
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-11-087-099-1159

Query Match 36.6%; Score 53.5; DB 7; Length 499;
Best Local Similarity 42.9%; Pred. No. 14;
Matches 12; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 3 QKSQSDLLERRESVLRREQVAAER 30
Db 319 KQEEERBAQREAOA-RREERAEKRR 345

RESULT 7

US-11-087-099-4574
; Sequence 4574, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4574
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Glibberella fujikuroi
US-11-087-099-4574

Query Match 34.6%; Score 50.5; DB 7; Length 451;
Best Local Similarity 41.9%; Pred. No. 30;
Matches 13; Conservative 4; Mismatches 11; Indels 3; Gaps 1;

Qy 3 QKSQSDLLERRESVLRREQVAAER 30
Db 3 QKSQSDLLERRESVLRREQVAAER 30

Db 47 KKGEEBOKOREEERLIREQLEAPAEAR 77

RESULT 8

US-11-087-099-8238
 ; Sequence 8238, Application US/11087099
 ; Publication No. US20060041961A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement
 ; FILE REFERENCE: 38-21(53450)B EP
 ; CURRENT APPLICATION NUMBER: US/11/087,099
 ; PRIOR FILING DATE: 2005-03-22
 ; NUMBER OF SEQ ID NOS: 12464
 ; SEQ ID NO 8238
 ; LENGTH: 1197
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-11-087-099-8238

Query Match 34.2%; Score 50; DB 7; Length 1197;
 Best Local Similarity 32.4%; Pred. No. 1.1e+02;
 Matches 11; Conservative 10; Mismatches 7; Indels 6; Gaps 1;

Qy 2 LKQSQSDLLERRESVL-----RREQVAER 29

Db 619 LERKEKEAEEREROKTIRAEERERKEKEAEER 652

RESULT 9

US-11-072-512-2316
 ; Sequence 2316, Application US/11072512
 ; Publication No. US2006002945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAOHICO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTOYUKI
 ; APPLICANT: NAGAHARA, KENJI
 ; APPLICANT: MASUHO, YASUHIRO
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: 084335-0191
 ; CURRENT APPLICATION NUMBER: US/11/072,512
 ; PRIOR FILING DATE: 2005-03-07
 ; PRIOR APPLICATION NUMBER: US 60/350,978
 ; PRIOR FILING DATE: 2002-01-25
 ; PRIOR APPLICATION NUMBER: JP 2001-379298
 ; PRIOR FILING DATE: 2001-11-05
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 2316
 ; LENGTH: 226
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-072-512-2316

Query Match 33.6%; Score 49; DB 7; Length 226;
 Best Local Similarity 38.5%; Pred. No. 22;
 Matches 10; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 4 KQSQSDLLERRESVLREQVAER 29

Db 62 KAQFSQLEERHAKVTELEQVPAQAK 87

RESULT 10

US-10-821-234-1180
 ; Sequence 1180, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crafin, Birgit
 ; APPLICANT: Andaman, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; PRIOR FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: PE_SEQ_genes Version 1.0
 ; SEQ ID NO 1180
 ; LENGTH: 410
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-1180

Query Match 33.6%; Score 49; DB 6; Length 410;
 Best Local Similarity 39.3%; Pred. No. 42;
 Matches 11; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 3 OKQSQSDLLERRESVLREQVAER 30

Db 227 EAEQSNVALQREEDREVEQKEAEVGELO 254

RESULT 11

US-11-087-099-370
 ; Sequence 370, Application US/11087099
 ; Publication No. US20060041961A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement
 ; FILE REFERENCE: 38-21(53450)B EP
 ; CURRENT APPLICATION NUMBER: US/11/087,099
 ; PRIOR FILING DATE: 2005-03-22
 ; NUMBER OF SEQ ID NOS: 12464
 ; SEQ ID NO 370
 ; LENGTH: 446
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-11-087-099-370

Query Match 33.6%; Score 49; DB 7; Length 446;
 Best Local Similarity 34.5%; Pred. No. 46;
 Matches 10; Conservative 13; Mismatches 4; Indels 2; Gaps 2;

Qy 1 RLKQSQSDLLERRESVLREQVAER 29

Db 58 KIEKETEDLL-KEKDEILRK-KEVEQEK 84

RESULT 12

US-11-129-442-47
 ; Sequence 47, Application US/11129442
 ; Publication No. US20060002951A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kleiman, Lawrence
 ; APPLICANT: CEN, Shan
 ; APPLICANT: GUO, Fei
 ; TITLE OF INVENTION: Inhibition of the tRNAlys3-Primed Initiation of Reverse
 ; TITLE OF INVENTION: Transcription in HIV-1 by APOBEC3G
 ; FILE REFERENCE: 11168.257

```
;; CURRENT APPLICATION NUMBER: US/11/129,442
;; CURRENT FILING DATE: 2005-05-16
;; PRIOR APPLICATION NUMBER: CA 2,467,312
;; PRIOR FILING DATE: 2004-05-14
;; NUMBER OF SEQ ID NOS: 47
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 47
;; LENGTH: 537
;; TYPE: PRT
;; ORGANISM: Murine leukemia virus
US-11-129-442-47
```

```
Query Match          33.6%; Score 49; DB 7; Length 537;
Best Local Similarity 64.7%; Pred. No. 57;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy          14 ERESVLRREQVAEER 30
Db          438 EREVRRETEKEERR 454
```

```
RESULT 13
US-11-072-512-3378
; Sequence 3378, Application US/11072512
; Publication No. US2006002945A1
; GENERAL INFORMATION:
```

```
;; APPLICANT: ISOGAI, TAKAO
;; APPLICANT: SUGIYAMA, TOMOYASU
;; APPLICANT: OTSUKI, TETSUJI
;; APPLICANT: WAKAMATSU, AI
;; APPLICANT: SATO, HIROYUKI
;; APPLICANT: ISHII, SHIZUKO
;; APPLICANT: YAMAMOTO, JUN-ICHI
;; APPLICANT: ISONO, YUUKO
;; APPLICANT: HIO, YURI
;; APPLICANT: OTSUKA, KAORU
;; APPLICANT: NAGAI, KEIICHI
;; APPLICANT: IRIE, RYOTARO
;; APPLICANT: TAMECHIKA, ICHIRO
;; APPLICANT: SEKI, NAOHICO
;; APPLICANT: YOSHIKAWA, TSUTOMU
;; APPLICANT: OTSUKA, MOTOYUKI
;; APPLICANT: NAGAHARI, KENJI
;; APPLICANT: MASUHO, YASUHIKO
;; TITLE OF INVENTION: Novel full length cDNA
;; FILE REFERENCE: 084335-0191
;; CURRENT APPLICATION NUMBER: US/11/072,512
;; CURRENT FILING DATE: 2005-03-07
;; PRIOR APPLICATION NUMBER: US 60/350,978
;; PRIOR FILING DATE: 2002-01-25
;; PRIOR APPLICATION NUMBER: JP 2001-379238
;; PRIOR FILING DATE: 2001-11-05
;; NUMBER OF SEQ ID NOS: 4096
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3378
;; LENGTH: 623
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-072-512-3378
```

```
Query Match          33.6%; Score 49; DB 7; Length 623;
Best Local Similarity 48.1%; Pred. No. 67;
Matches 13; Conservative 5; Mismatches 7; Indels 2; Gaps 1;
```

```
Qy          3 OKSQSSDLLERRESVLRREQVAEER 29
Db          292 OKVQWT--LERRRRLRLRSQSGEQWQEK 316
```

```
RESULT 14
US-10-770-726-77
; Sequence 77, Application US/10770726
; Publication No. US20050266409A1
```

```
;; GENERAL INFORMATION:
;; APPLICANT: Wyeth
;; APPLICANT: Brown, Eugene
;; APPLICANT: Liu, Wei
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
```

```
;; FILE REFERENCE: AM101079 (031896-010000)
;; CURRENT APPLICATION NUMBER: US/10/770,726
;; CURRENT FILING DATE: 2004-02-04
;; NUMBER OF SEQ ID NOS: 48640
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 77
;; LENGTH: 4128
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-770-726-77
```

```
Query Match          33.6%; Score 49; DB 6; Length 4128;
Best Local Similarity 48.1%; Pred. No. 5,6e+02;
Matches 13; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
```

```
Qy          2 LKQSQSSDLLERRESVLRREQVAEER 28
Db          1750 LKLSQSPMLLEMTVEVLCREQOHVMEER 1776
```

```
RESULT 15
US-11-098-686-10232
; Sequence 10232, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
```

```
;; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
;; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
;; FILE REFERENCE: 09531-128001
;; CURRENT APPLICATION NUMBER: US/11/098,686
;; CURRENT FILING DATE: 2005-04-04
;; PRIOR APPLICATION NUMBER: PCT/US03/31318
;; PRIOR FILING DATE: 2003-10-01
;; PRIOR APPLICATION NUMBER: US 60/416,395
;; PRIOR FILING DATE: 2002-10-04
;; NUMBER OF SEQ ID NOS: 11433
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 10232
;; LENGTH: 8746
;; TYPE: PRT
;; ORGANISM: Lawsonia intracellularis
US-11-098-686-10232
```

```
Query Match          33.6%; Score 49; DB 7; Length 8746;
Best Local Similarity 40.5%; Pred. No. 1,3e+03;
Matches 15; Conservative 8; Mismatches 2; Indels 12; Gaps 3;
```

```
Qy          1 RLQSQSSDLLERRESVLRREQ--EVAEER 30
Db          1213 KLQKKQ-----QRRKXTLLMQRTKQEQDLDEIGERR 1244
```

```
Search completed: March 3, 2006, 14:19:04
Job time : 2.47619 secs
```

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OM protein - protein search, using SW model

Run on: March 3, 2006, 13:19:17 / Search time 18.7075 Seconds
(without alignments)
822.038 Million cell updates/sec

Title: US-10-646-873-45

Sequence: 1 ALPEVPSPPDENSDONSRSQAAGITGSYSVS 35

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

A_Geneseq_21:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*
- 9: geneeqp2005s:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	35	2	AAW79679 Synthetic
2	175	100.0	35	4	AAE07322 Human CS
3	175	100.0	35	6	ADA26382 Synthetic
4	175	100.0	35	8	ADN17175 CS198 pep
5	175	100.0	172	4	AAW73987 Human col
6	175	100.0	215	2	AAW79681 Human CS1
7	175	100.0	215	4	AAE07324 Human CS
8	175	100.0	215	6	ADA26384 Synthetic
9	175	100.0	215	8	ADN17177 CS198 pro
10	175	100.0	672	4	AAW79574 Human pro
11	175	100.0	679	2	AAW79676 Human CS1
12	175	100.0	679	4	AAE07319 Human CS
13	175	100.0	679	4	AAW78590 Human pro
14	175	100.0	679	6	ADA26379 Predicted
15	175	100.0	679	6	ADA26379 Predicted
16	175	100.0	679	8	ADN17172 CS198 pro
17	175	100.0	692	8	ADN17172 CS198 pro
18	175	100.0	692	8	ADN17172 CS198 pro
19	175	100.0	692	8	ADN17172 CS198 pro
20	175	100.0	692	8	ADN17172 CS198 pro
21	175	100.0	692	8	ADN17172 CS198 pro
22	175	100.0	692	8	ADN17172 CS198 pro
23	175	100.0	692	8	ADN17172 CS198 pro
24	175	100.0	692	8	ADN17172 CS198 pro

25	55.5	31.7	346	7	ADM04107 Human pro
26	55.5	31.7	531	7	ADM04077 Human pro
27	55.5	31.4	406	4	ABE0211 Drosophila
28	55.5	31.4	581	8	ADN17236 Plant ful
29	55.5	31.4	679	6	ABU50304 Protein e
30	55.5	31.4	789	4	AAW41735 Human pol
31	55.5	31.4	942	4	AAW39949 Human pol
32	55.5	31.4	958	7	ADN17272 Human nov
33	55.5	31.4	958	7	ADN17272 Human nov
34	55.5	31.4	958	7	ADN17272 Human nov
35	55.5	31.4	1277	6	ABU52893 Protein e
36	55.5	31.4	1277	6	ABU52893 Protein e
37	54.5	31.1	1158	5	ABU52893 Protein e
38	54.5	31.1	1158	7	ADD14177 Human src
39	54.5	31.1	1158	7	ADD14177 Human src
40	54.5	31.1	1158	9	ADN17272 Human nov
41	54.5	31.1	1158	9	ADN17272 Human nov
42	53.5	30.6	583	4	ABU04816 Novel hum
43	53.5	30.6	701	6	ABU34205 Protein e
44	53.5	30.3	80	2	AAW27130 Equine rh
45	53.5	30.3	362	7	ABO68987 Pseudomon

ALIGNMENTS

RESULT 1
ID AAW79679 standard; protein; 35 AA.
AAW79679;
11-JAN-1999 (first entry)
Synthetic CS198 derived peptide #3.
Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
pancreatitis;
Synthetic.
WO9844159-A1.
08-OCT-1998.
30-MAR-1998; 98WO-US006251.
31-MAR-1997; 97US-00828855.
(ABBO) ABBOT LAB.
Billing-Medell PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
Granados EN, Hayden M, Hodges SC, Klaes MR, Kratochvil JD;
Roberts-Rapp L, Russell JC, Scroupe SD;
WPI; 1998-542714/46.
New gastrointestinal polynucleotides, CS198, and their detection - used
for developing products for the diagnosis and treatment of
gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
Claim 26; Page 103; 127pp; English.
AAW79679-W79680 are synthetic CS198 derived peptide fragments which are
used in a method to detect the presence of a target human CS198
polynucleotide in a test sample. The CS198 gene is useful as a marker for
gastrointestinal (GI) tract disorders. The methods and products can be
used in detecting, diagnosing, staging, monitoring, prognosticating,
preventing or treating, or determining the predisposition to diseases and
conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative

CC colitis, and pancreatitis
 XX Sequence 35 AA:
 Query Match 100.0%; Score 175; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 5.1e-17;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ALPPEVFSPTPDENSQNSRSSQASGITGSYSVS 35
 Db 1 ALPPEVFSPTPDENSQNSRSSQASGITGSYSVS 35
 RESULT 2
 AAE07322
 ID AAE07322 standard; peptide; 35 AA.
 AC AAE07322;
 XX
 XX 06-NOV-2001 (first entry)
 DE Human CS 198 peptide #3.
 XX
 XX CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
 KW gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
 KW Barrett's oesophagus; gene therapy; drug screening; human.
 XX
 OS Homo sapiens.
 XX
 XX US2001010904-A1.
 XX
 PD 02-AUG-2001.
 XX
 XX 30-MAR-1998; 98US-00050516.
 PP
 PR 31-MAR-1997; 97US-00828855.
 XX
 PA (BILL/) BILLINGEL P A.
 PA (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HAYD/) HAYDEN M.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUSSE/) RUSSELL J C.
 PA (STRO/) STROUPE S D.
 PA
 PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
 PI Granados EN, Hayden M, Hodges SC, Klaas MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX WPI, 2001-496163/54.
 DR
 XX
 PT Detecting the presence of target CS 198 polynucleotide, useful for
 PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
 PT contacting test sample with at least one CS 198-specific polynucleotide.
 XX
 PS Claim 17; Page 52; 68pp; English.
 XX
 CC The invention relates to a method of detecting the presence of a target
 CC CS 198 polynucleotide comprising contacting the test sample with at least
 CC one CS 198-specific polynucleotide. The method is useful for detecting
 CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
 CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
 CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
 CC treating or determining predisposition to diseases and conditions of the
 CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
 CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
 CC polypeptides are useful as standards or reagents in diagnostic

CC immunoassays, as components or as target sites for various therapies.
 CC Antibodies directed against at least one epitope contained within these
 CC polypeptides are useful as delivery agents for therapeutic agents, in
 CC diagnostic tests and for screening for conditions or diseases associated
 CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
 CC for the generation of chimeric antibodies for therapeutic use. The CS 198
 CC polynucleotide is also useful in gene therapy and drug screening. The
 CC method of the invention provides an alternative, non-surgical diagnostic
 CC method capable of detecting early stage GI tract disease such as cancer.
 CC The present sequence is a peptide derived from human CS 198 polypeptide
 CC consensus sequence
 XX
 XX Sequence 35 AA:
 SO
 Query Match 100.0%; Score 175; DB 4; Length 35;
 Best Local Similarity 100.0%; Pred. No. 5.1e-17;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ALPPEVFSPTPDENSQNSRSSQASGITGSYSVS 35
 Db 1 ALPPEVFSPTPDENSQNSRSSQASGITGSYSVS 35
 RESULT 3
 ADA26382
 ID ADA26382 standard; protein; 35 AA.
 AC ADA26382;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX
 DE Synthetic peptide based on CS198 protein #3.
 XX
 XX CS198; cancer diagnosis; cancer staging; cancer monitoring;
 KW cancer prognosticating; cancer prevention; cancer;
 KW gastrointestinal tract disorder; gene therapy.
 XX
 OS Synthetic.
 XX
 XX US2003082619-A1.
 FN
 XX
 PD 01-MAY-2003.
 XX
 XX 23-OCT-2002; 2002US-00278547.
 PF
 XX 31-MAR-1997; 97US-00828855.
 PR 30-MAR-1998; 98US-00050516.
 PR
 XX
 PA (BILL/) BILLINGEL P A.
 PA (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HAYD/) HAYDEN M A.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUSSE/) RUSSELL J C.
 PA (STRO/) STROUPE S D.
 PA
 PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
 PI Granados EN, Hayden MA, Hodges SC, Klaas MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX WPI, 2003-596961/56.
 DR
 XX
 PT Detecting the presence of a target CS198 polynucleotide in a test sample
 PT comprises contacting the sample with a CS198 specific polynucleotide and
 PT detecting the presence of the target CS198 polynucleotide in the test
 PT sample.
 XX

PS Claim 17, page 51; 67pp; English.
XX
CC The invention describes a method of detecting the presence of a target
CC CS198 polynucleotide in a test sample. The method comprises contacting
CC the test sample with at least one CS198 specific polynucleotide or its
CC complement, and detecting the presence of the target CS198 polynucleotide
CC in the test sample, where the CS198-specific polynucleotide has at least
CC 50% identity to a polynucleotide having any of the 27 fully defined
CC sequences of 34-2894 bp (SI-27) given in the specification, or their
CC fragments or complements. The composition and methods are useful in
CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
CC or determining the predisposition of an individual to, diseases and
CC conditions of the gastrointestinal tract, e.g. cancer and in gene
CC therapy. This is the amino acid sequence of a synthetic peptide based on
CC the predicted human CS198 protein sequence derived from the CS198
CC consensus sequence shown in seq id 27.
SQ Sequence 35 AA;
Query Match 100.0%; Score 175; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 5.1e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALPPEVFSPPTDENSDONSRRSSSQASGITGSYSVS 35
DB 1 ALPPEVFSPPTDENSDONSRRSSSQASGITGSYSVS 35
RESULT 4
ADN17175 standard; peptide; 35 AA.
XX
AC ADN17175;
XX
DT 17-JUN-2004 (first entry)
XX
DE CS198 peptide #3.
XX
KM Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.
XX
OS Unidentified.
XX
PN US2004043406-A1.
XX
PD 04-MAR-2004.
XX
PF 22-AUG-2003; 2003US-00646873.
XX
PR 31-MAR-1997; 97US-00828855.
XX
PR 30-MAR-1998; 98US-00050516.
XX
PA (BILL/) BILLINGEL P A.
XX
PA (COHE/) COHEN M.
XX
PA (COLP/) COLPITTS T L.
XX
PA (FRIE/) FRIEDMAN P N.
XX
PA (GORD/) GORDON J.
XX
PA (GRAN/) GRANADOS E N.
XX
PA (HAYD/) HAYDEN M A.
XX
PA (HODG/) HODGES S C.
XX
PA (KLAG/) KLAGS M R.
XX
PA (KRAT/) KRATOCHVIL J D.
XX
PA (ROBE/) ROBERTS-RAPP L.
XX
PA (RUSSE/) RUSSELL J C.
XX
PA (STROU/) STROUPE S D.
XX
PI Billingsel PA, Cohen M, Colpitts TV, Friedman PN, Gordon J,
PI Grandos EN, Hayden MA, Hodges SC, Klags MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
DR WPI; 2004-313754/29.
XX
PT Diagnosing diseases such as cancer of the gastrointestinal tract, by
PT detecting aberrant expression or activity of the CS198 polypeptide, and

PT associated treatment methods.
XX
XX Claim 17, SEQ ID NO 45; 67pp; English.
XX
XX The invention relates to reagents and methods for detecting diseases of
XX the gastrointestinal (GI) tract. The method involves detecting the
XX presence of target CS198 polynucleotide in the test sample. The methods
XX and compositions of the present invention are useful for the diagnosis,
XX aberrant expression or activity of the CS198 polypeptide, such as cancer
XX of the gastrointestinal tract. These are also useful in gene therapy. The
XX present sequence is a CS198 peptide used to illustrate the method of the
XX invention.
SQ Sequence 35 AA;
Query Match 100.0%; Score 175; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 5.1e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALPPEVFSPPTDENSDONSRRSSSQASGITGSYSVS 35
DB 1 ALPPEVFSPPTDENSDONSRRSSSQASGITGSYSVS 35
RESULT 5
AAG73987 standard; protein; 172 AA.
XX
AC AAG73987;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:4751.
XX
KM Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
XX
PR 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
XX WPI; 2001-235357/24.
XX
DR N-PSDB; AAG73987.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 11; Page 6550-6551; 9803pp; English.
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where the
XX proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene therapy
XX and vaccine production. N and P may be used in the prevention, diagnosis
XX and treatment of diseases associated with inappropriate P expression. For
XX example, N and P may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of P by expressing inactive proteins or to
XX supplement the patient's own production of P. Additionally, N may be used
XX to produce the colon cancer-associated Ps, by inserting the nucleic acids
XX into a host cell and culturing the cell to express the proteins. N and P

CC can be used in the prevention, diagnosis and treatment of colorectal
 CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
 CC sequences used in the exemplification of the present invention. N.B.
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027
 CC to 1052, 7921 and 7922

XX Sequence 172 AA;

Query Match 100.0%; Score 175; DB 4; Length 172;
 Best Local Similarity 100.0%; Pred. No. 3.5e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPFEVFSPTPDNSDQNSRSSQASGITGSYSVS 35
 Db 61 ALPFEVFSPTPDNSDQNSRSSQASGITGSYSVS 95

RESULT 6
 AA79681

ID AA79681 standard; protein; 215 AA.

AC AA79681;

DT 11-JAN-1999 (first entry)

DE Human CS198 protein C-terminal.

XX Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
 KW human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
 KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
 KW pancreatitis.

OS Homo sapiens.

PN WO9844159-A1.

PD 08-OCT-1998.

XX 30-MAR-1998; 98WO-US006251.

PR 31-MAR-1997; 97US-00828855.

PA (ABBO) ABBOTT LAB.

PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;

DR WPI; 1998-542714/46.

XX New gastrointestinal polynucleotides, CS198, and their detection - used
 PT for developing products for the diagnosis and treatment of
 PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.

XX Claim 26; Page 103; 127pp; English.

CC This sequence represents the C-terminal of the human CS198 protein which
 CC is used in a method to detect the presence of a target CS198
 CC polynucleotide in a test sample. The CS198 gene is useful as a marker for
 CC gastrointestinal (GI) tract disorders. The methods and products can be
 CC used in detecting, diagnosing, staging, monitoring, prognosticating, preventing
 CC or treating, or determining the predisposition to diseases and conditions of the
 CC GI tract, such as GI tract cancer, Barrett's oesophagus, and
 CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative
 CC colitis, and pancreatitis

XX Sequence 215 AA;

Query Match 100.0%; Score 175; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 4.6e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPFEVFSPTPDNSDQNSRSSQASGITGSYSVS 35
 Db 104 ALPFEVFSPTPDNSDQNSRSSQASGITGSYSVS 138

RESULT 7
 AA07324

ID AA07324 standard; protein; 215 AA.

AC AA07324;

DT 06-NOV-2001 (first entry)

DE Human CS 198 protein C-terminal portion.

XX CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
 KW gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
 KW Barrett's oesophagus; gene therapy; drug screening; human.

OS Homo sapiens.

PN US2001010904-A1.

PD 02-AUG-2001.

XX 30-MAR-1998; 98US-00050516.

PR 31-MAR-1997; 97US-00828855.

PA (BILL) BILLINGEL P A.

PA (COHE) COHEN M.

PA (COLP) COLPITTS T L.

PA (FRIE) FRIEDMAN P N.

PA (GORD) GORDON J.

PA (GRAN) GRANADOS E N.

PA (HAYD) HAYDEN M.

PA (HODG) HODGES S C.

PA (KLAS) KLAS M R.

PA (KRAT) KRATOCHVIL J D.

PA (ROBE) ROBERTS-RAPP L.

PA (RUSSE) RUSSELL J C.

PA (STRO) STROUPE S D.

PI Billingel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;

DR WPI; 2001-496163/54.

XX Detecting the presence of target CS 198 polynucleotide, useful for
 PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
 PT contacting test sample with at least one CS 198-specific polynucleotide.

XX Claim 17; Page 52-53; 68pp; English.

CC The invention relates to a method of detecting the presence of a target
 CC CS 198 polynucleotide comprising contacting the test sample with at least
 CC one CS 198-specific polynucleotide. The method is useful for detecting
 CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
 CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
 CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
 CC treating or determining predisposition to diseases and conditions of the
 CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
 CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
 CC polypeptides are useful as standards or reagents in diagnostic
 CC immunoassays, as components or as target sites for various therapies.
 CC Antibodies directed against at least one epitope contained within these
 CC polypeptides are useful as delivery agents for therapeutic agents, in
 CC diagnostic tests and for screening for conditions or diseases associated
 CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
 CC for the generation of chimeric antibodies for therapeutic use. The CS 198
 CC polynucleotide is also useful in gene therapy and drug screening. The
 CC method of the invention provides an alternative, non-surgical diagnostic

CC method capable of detecting early stage GI tract disease such as cancer.
 CC The present sequence is C-terminal portion of human CS 198 polypeptide
 XX
 XX
 SQ Sequence 215 AA;

Query Match 100.0%; Score 175; DB 4; Length 215;
 Best Local Similarity 100.0%; Pred. No. 4.6e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALPPEVFSPTPDNSQNRSSSQASGITGSYSVS 35
 DB 104 ALPPEVFSPTPDNSQNRSSSQASGITGSYSVS 138

RESULT 8
 ADA26384
 ID ADA26384 standard; protein; 215 AA.

ADA26384;

20-NOV-2003 (first entry)

DE Synthetic peptide based on CS198 protein #5.

XX CS198; cancer diagnosis; cancer staging; cancer monitoring;
 KW cancer prognosticating; cancer prevention; cancer;
 KW gastrointestinal tract disorder; gene therapy.

OS Synthetic.

PN US2003082619-A1.

PD 01-MAY-2003.

PF 23-OCT-2002; 2002US-00278547.

PR 31-MAR-1997; 97US-00828855.

PR 30-MAR-1998; 98US-00050516.

PA (BILL/) BILLINGEL P A.

PA (COHE/) COHEN M.

PA (COLP/) COLPITTS T L.

PA (FRIE/) FRIEDMAN P N.

PA (GORD/) GORDON J.

PA (GRAN/) GRANADOS E N.

PA (HAYD/) HAYDEN M A.

PA (HODG/) HODGES S C.

PA (KLAS/) KLAS M R.

PA (KRAT/) KRATOCHVIL J D.

PA (ROBE/) ROBERTS-RAPP L.

PA (RUSSE/) RUSSELL J C.

PA (STROU/) STROUPE S D.

PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

PI Grandos EN, Hayden MA, Hodges SC, Klaas MR, Kratochvil JD;

PI Roberts-Rapp L, Russell JC, Stroupe SD;

DR WPI; 2003-596961/56.

PT Detecting the presence of a target CS198 polynucleotide in a test sample
 PT comprises contacting the sample with a CS198 specific polynucleotide and
 PT detecting the presence of the target CS198 polynucleotide in the test
 PT sample.

PS Claim 52; Page 52; 67pp; English.

XX The invention describes a method of detecting the presence of a target
 CC CS198 polynucleotide in a test sample. The method comprises contacting
 CC the test sample with at least one CS198 specific polynucleotide or its
 CC complement, and detecting the presence of the target CS198 polynucleotide
 CC in the test sample, where the CS198-specific polynucleotide has at least
 CC 50% identity to a polynucleotide having any of the 27 fully defined
 CC sequences of 34-2894 bp (81-27) given in the specification, or their

CC fragments or complements. The composition and methods are useful in
 CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
 CC or determining the predisposition of an individual to, diseases and
 CC conditions of the gastrointestinal tract, e.g. cancer and in gene
 CC therapy. This is the amino acid sequence of a synthetic peptide based on
 CC the predicted human CS198 protein sequence derived from the CS198
 CC consensus sequence shown in seq id 27.

SQ Sequence 215 AA;

Query Match 100.0%; Score 175; DB 6; Length 215;
 Best Local Similarity 100.0%; Pred. No. 4.6e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALPPEVFSPTPDNSQNRSSSQASGITGSYSVS 35
 DB 104 ALPPEVFSPTPDNSQNRSSSQASGITGSYSVS 138

RESULT 9
 ADN17177

ID ADN17177 standard; protein; 215 AA.

ADN17177;

DT 17-JUN-2004 (first entry)

DE CS198 protein #2.

XX Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.

OS Unidentified.

PN US2004043406-A1.

PD 04-MAR-2004.

PF 22-AUG-2003; 2003US-00646873.

PR 31-MAR-1997; 97US-00828855.

PR 30-MAR-1998; 98US-00050516.

PA (BILL/) BILLINGEL P A.

PA (COHE/) COHEN M.

PA (COLP/) COLPITTS T L.

PA (FRIE/) FRIEDMAN P N.

PA (GORD/) GORDON J.

PA (GRAN/) GRANADOS E N.

PA (HAYD/) HAYDEN M A.

PA (HODG/) HODGES S C.

PA (KLAS/) KLAS M R.

PA (KRAT/) KRATOCHVIL J D.

PA (ROBE/) ROBERTS-RAPP L.

PA (RUSSE/) RUSSELL J C.

PA (STROU/) STROUPE S D.

PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

PI Grandos EN, Hayden MA, Hodges SC, Klaas MR, Kratochvil JD;

PI Roberts-Rapp L, Russell JC, Stroupe SD;

DR WPI; 2004-313754/29.

PT Diagnosing diseases such as cancer of the gastrointestinal tract, by
 PT detecting aberrant expression or activity of the CS198 polypeptide, and
 PT associated treatment methods.

PS Claim 17; SEQ ID NO 47; 67pp; English.

XX The invention relates to reagents and methods for detecting diseases of
 CC the gastrointestinal (GI) tract. The method involves detecting the
 CC presence of target CS198 polynucleotide in the test sample. The methods
 CC and compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of diseases or conditions associated with

CC aberrant expression or activity of the CS198 polypeptide, such as cancer
 CC of the gastrointestinal tract. These are also useful in gene therapy. The
 CC present sequence is a CS198 protein used to illustrate the method of the
 CC invention.

XX Sequence 215 AA;

Query Match 100.0%; Score 175; DB 8; Length 215;
 Best Local Similarity 100.0%; Pred. No. 4.6e-15;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPPEVSPPTDENSDQNSRSSQASGITGSYSVS 35
 |||||
 Db 104 ALPPEVSPPTDENSDQNSRSSQASGITGSYSVS 138

RESULT 10
 AAW79574
 ID AAW79574 standard; protein; 672 AA.

XX AAW79574;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 3220.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KM tissue growth factor; immunomodulatory; cancer; leukaemia;
 KM nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

XX WO200157190-A2.

XX 09-AUG-2001.

PE 05-FEB-2001; 2001WO-US004098.

XX 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663551.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Dmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX WPI; 2001-476283/51.

DR N-P8DB; AAK52707.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.

XX Claim 20; Page 288; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAW79323-AAW80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibit activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111

CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication

XX Sequence 672 AA;

Query Match 100.0%; Score 175; DB 4; Length 672;
 Best Local Similarity 100.0%; Pred. No. 1.8e-15;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPPEVSPPTDENSDQNSRSSQASGITGSYSVS 35
 |||||
 Db 561 ALPPEVSPPTDENSDQNSRSSQASGITGSYSVS 595

RESULT 11
 AAW79676
 ID AAW79676 standard; protein; 679 AA.

XX AAW79676;

DT 11-JAN-1999 (first entry)

DE Human CS198 protein.

XX Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
 KM human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
 KM gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
 KM pancreatitis.

XX Homo sapiens.

XX WO9844159-A1.

XX 08-OCT-1998.

PE 30-MAR-1998; 98WO-US006251.

PR 31-MAR-1997; 97US-00828855.

XX (ABBO) ABBOTT LAB.

XX Billig-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI; 1998-542714/46.

XX New gastrointestinal polynucleotides, CS198, and their detection - used
 PT for developing products for the diagnosis and treatment of
 PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.

XX Claim 26; Page 100-102; 127pp; English.

XX This sequence represents the human CS198 protein which is used in a
 CC method to detect the presence of a target CS198 polynucleotide in a test
 CC sample. The CS198 gene is useful as a marker for gastrointestinal (GI)
 CC tract disorders. The methods and products can be used in detecting,
 CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
 CC or determining the predisposition to diseases and conditions of the GI
 CC tract, such as GI tract cancer, Barrett's oesophagus, gastric ulcer,
 CC gastritis, leiomyoma, polyps, Crohn's disease, ulcerative colitis, and
 CC pancreatitis

XX Sequence 679 AA;

Query Match 100.0%; Score 175; DB 2; Length 679;
 Best Local Similarity 100.0%; Pred. No. 1.8e-15;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPPEVSPPTDENSDQNSRSSQASGITGSYSVS 35
 |||||
 Db 568 ALPPEVSPPTDENSDQNSRSSQASGITGSYSVS 602

XX	AAE07319	standard; protein; 679 AA.
AC	AAE07319,	
XX	06-NOV-2001	(first entry)
DE	Human CS 198 protein.	
XX	CS 198, gastrointestinal tract disease; GI tract; cancer; gastric ulcer;	
KW	gastritis; Crohn's disease; ulcerative colitis; pancreatitis;	
KW	Barrett's oesophagus; gene therapy; drug screening; human.	
XX	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Misc-difference 353	
FT	/note= "Encoded by CCGN"	
XX	US2001010904-A1.	
PX	02-AUG-2001.	
PD	30-MAR-1998;	98US-00050516.
XX	31-MAR-1997;	97US-00828855.
PA	(BILL./ BILLINGEL P A.	
PA	(COHE./ COHEN M.	
PA	(COLP./ COLPITTS T L.	
PA	(FRIE./ FRIEDMAN P N.	
PA	(GORD./ GORDON J.	
PA	(GRAN./ GRANADOS E N.	
PA	(HAYD./ HAYDEN M.	
PA	(HODG./ HODGES S C.	
PA	(KLAS./ KLAS M R.	
PA	(KRAT./ KRATOCHVIL J D.	
PA	(ROBE./ ROBERTS-RAPP L.	
PA	(RUSSE./ RUSSELL J C.	
PA	(STRO./ STROUPE S D.	
PX	Billingel PA., Cohen M, Colpitts TL, Friedman PN, Gordon J;	
PI	Granados EN, Hayden M, Hodges SC, Klas MR, Kratochvil JD;	
PI	Roberts-Rapp L, Russell JC, Stroupe SD,	
PX	WPI, 2001-496163/54.	
DR	N-PSDB; AAD13637.	
PT	Detecting the presence of target CS 198 polynucleotide, useful for	
PT	detecting or diagnosing diseases of the gastrointestinal tract, comprises	
XX	contacting test sample with at least one CS 198-specific polynucleotide.	
PS	Claim 17, Page 49-51; 68pp; English.	
CC	The invention relates to a method of detecting the presence of a target	
CC	CS 198 polynucleotide comprising contacting the test sample with at least	
CC	one CS 198-specific polynucleotide. The method is useful for detecting	
CC	diseases of the gastrointestinal (GI) tract organs, particularly cancer.	
CC	The CS 198 polynucleotides, polypeptides and antibodies are useful for:	
CC	detecting, diagnosing, staging, monitoring, prognosticating, preventing,	
CC	treating or determining predisposition to diseases and conditions of the	
CC	GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,	
CC	ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198	
CC	polypeptides are useful as standards or reagents in diagnostic	
CC	immunoassays, as components or as target sites for various therapies.	
CC	Antibodies directed against at least one epitope contained within these	
CC	polypeptides are useful as delivery agents for therapeutic agents, in	
CC	diagnostic tests and for screening for conditions or diseases associated	
CC	with CS 198, particularly cancer. Monoclonal antibodies may also be used	
CC	for the generation of chimeric antibodies for therapeutic use. The CS 198	
CC	polynucleotide is also useful in gene therapy and drug screening. The	

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CC method of the invention provides an alternative, non-surgical diagnostic
CC method capable of detecting early stage GI tract disease such as cancer.
CC The present sequence is human CS 198 polypeptide
XX
SQ Sequence 679 AA;
Query Match 100.0%; Score 175; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 1,8e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY 1 ALPFEVFSPTPDENSESDONSRRSSQASGITGSYSVS 35
Db 568 ALPFEVFSPTPDENSESDONSRRSSQASGITGSYSVS 602

RESULT 13
ID AAM78590
AC AAM78590;
DT 06-NOV-2001 (first entry)
DE Human protein SEQ ID NO 1252.
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
OS Homo sapiens.
PN WO200157190-A2.
PD 09-AUG-2001.
PE 05-FEB-2001; 2001WO-US004098.
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00653561.
PR 20-OCT-2000; 2000US-00653525.
PR 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX MPI: 2001-476283/51.
XX N-PSDB; AAKS1723.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX
XX Claim 20; Page 3512-3514; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAH80302) that exhibit activity relating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activating/inhibiting activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
XX (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the

```

CC sequence listing were missing at the time of publication
XX
SQ Sequence 679 AA;
Query Match 100.0%; Score 175; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ALPPEVFSPTPDENDONSRRSSSQASGITGSYSVS 35
DB 568 ALPPEVFSPTPDENDONSRRSSSQASGITGSYSVS 602
RESULT 14
ADA26379 standard; protein; 679 AA.
XX
AC ADA26379;
XX
DT 20-NOV-2003 (first entry)
XX
DE Predicted amino acid sequence of the CS198 protein.
XX
KW CS198; cancer diagnosis; cancer staging; cancer monitoring;
KW cancer prognosticating; cancer prevention; cancer;
KW gastrointestinal tract disorder; gene therapy.
XX
OS Synthetic;
XX
PN US2003082619-A1.
XX
PD 01-MAY-2003.
XX
PF 23-OCT-2002; 2002US-00278547.
XX
PR 31-MAR-1997; 97US-00828855.
PR 30-MAR-1998; 98US-00050516.
XX
PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M A.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUS/) RUSSELL J C.
PA (STRO/) STROUDE S D.
XX
PI Billingsel PA, Cohen M, Colpitts TU, Friedman PN, Gordon J;
PI Granados EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
WP1; 2003-596961/56.
XX
DR
XX
PT Detecting the presence of a target CS198 polynucleotide in a test sample
PT comprises contacting the sample with a CS198 specific polynucleotide and
PT detecting the presence of the target CS198 polynucleotide in the test
PT sample.
XX
PS Claim 17; Page 49-50; 67pp; English.
XX
CC The invention describes a method of detecting the presence of a target
CC CS198 polynucleotide in a test sample. The method comprises contacting
CC the test sample with at least one CS198 specific polynucleotide or its
CC complement, and detecting the presence of the target CS198 polynucleotide
CC in the test sample, where the CS198-specific polynucleotide has at least
CC 50% identity to a polynucleotide having any of the 27 fully defined
CC sequences of 34-2894 bp (SI-27) given in the specification, or their
CC fragments or complements. The composition and methods are useful in

CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
CC or determining the predisposition of an individual to, diseases and
CC conditions of the gastrointestinal tract, e.g. cancer and in gene
CC therapy. This is the predicted amino acid sequence of the human CS198
CC protein derived from the CS198 consensus sequence shown in seq id 27.
XX
SQ Sequence 679 AA;
Query Match 100.0%; Score 175; DB 6; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ALPPEVFSPTPDENDONSRRSSSQASGITGSYSVS 35
DB 568 ALPPEVFSPTPDENDONSRRSSSQASGITGSYSVS 602
RESULT 15
ADG14341 standard; protein; 679 AA.
XX
AC ADG14341;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human NC2.
XX
KW Human; NC1; NC2; NC3; PHH1; pancreas beta-cell; insulin; antidiabetic;
KW neuroprotective.
XX
OS Homo sapiens.
XX
PN WO2003078631-A1.
XX
PD 25-SEP-2003.
XX
PF 06-MAR-2003; 2003WO-JP002620.
XX
PR 15-MAR-2002; 2002JP-00071592.
XX
PA (KANF) KANEKA CORP.
XX
PI Niwa H, Yamashita K;
XX
DR WP1; 2003-767524/72.
DR N-PSDB; ADG14344.
XX
PT Familial persistent hyperinsulinemic hypoglycemia of infancy (PHH1)
PT patient-expressed genes for detecting and screening e.g. proliferative
PT insulin-producing cells in treatment of PHH1.
XX
PS Claim 1; SEQ ID NO 2; 34pp; Japanese.
XX
CC The present invention relates to human NC1, NC2 and NC3 proteins and
CC coding sequences (ADG14340-ADG14345). The coding sequences are useful for
CC detecting and screening proliferative insulin-producing cells as well as
CC differentiation and proliferation of such cells and their precursors as
CC analogous cells in treatment of e.g. PHH1 and diseases due to
CC differentiation/proliferation abnormality, diseases of the nervous system
CC and pancreas. The coding sequences are also useful as spontaneous
CC and proliferation models of pancreas beta-cells. The novel genes NC1, NC2 and
CC NC3 were isolated from the pancreas of PHH1 patients, which were used in
CC testing for the detection of proliferative insulin-producing cells or
CC pancreas beta-cells by Northern analysis.
XX
SQ Sequence 679 AA;
XX
CC
XX
Query Match 100.0%; Score 175; DB 7; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ALPPEVFSPTPDENDONSRRSSSQASGITGSYSVS 35
XXXXXX

Db 568 ALPPEVPSFTPPENDQNSRSSQASGITGYSYS 602

Search completed: March 3, 2006, 13:35:23
Job time : 19.7075 secs

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 3, 2006, 13:26:31, Search time 2.21088 Seconds
(without alignments)
1523.185 Million cell updates/sec

Title: US-10-646-873-45

Perfect score: 175
Sequence: 1 ALFPEVFSPTPDENSQSSQASGITGSYSVS 35

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	679	2 T00636	hypothetical prote
2	57	32.6	419	2 B85035	hypothetical prote
3	57	32.6	574	2 S37762	225k protein - Bab
4	57	32.6	661	2 S80734	WHI3 protein - yea
5	55	31.4	679	2 AC0333	probable membrane
6	55	31.4	1277	2 S53043	probable membrane
7	54.5	31.1	1158	2 S57348	nuclear factor RIP
8	54	30.9	1695	2 A56921	kinesin family pro
9	53	30.3	335	2 D83332	hypothetical prote
10	53	30.3	370	2 S27779	major retroviral su
11	53	30.3	750	2 S73829	probable ABC trans
12	53	30.3	1145	2 A59251	myosin - Acatubula
13	52.5	30.0	546	2 AB0088	probable flagellar
14	52	29.7	182	2 T08125	gas-vesticle operon
15	52	29.7	182	2 T08237	gas-vesticle operon
16	52	29.7	571	2 D96516	FLN3.14 [imported
17	52	29.7	1428	2 T13926	probable protein p
18	52	29.7	1428	2 F88640	protein F52C12.4 l
19	51.5	29.4	1029	2 T30351	mucin-like protein
20	51	29.1	139	2 S31941	penicillin-binding
21	51	29.1	344	2 T29264	hypothetical prote
22	51	29.1	362	2 A30901	lymphocyte adhesio
23	51	29.1	578	2 T41715	hypothetical prote
24	51	29.1	879	2 B84765	hypothetical prote
25	51	29.1	1063	2 D86731	hypothetical prote
26	51	29.1	1596	2 A35927	190k DNA-binding p
27	50.5	28.9	170	2 S69465	hypothetical prote
28	50.5	28.9	479	2 G82114	sigma-54 dependent
29	50.5	28.9	1872	2 T30888	vitellinogen - Ath

30	50	28.6	491	1 ZNBPMU
31	50	28.6	517	2 H86452
32	50	28.6	550	2 T03714
33	50	28.6	581	2 B84715
34	50	28.6	616	2 B84463
35	50	28.6	633	2 B84463
36	50	28.6	633	2 B84463
37	50	28.6	972	2 T16094
38	50	28.6	1211	2 T42230
39	49.5	28.3	359	2 S24240
40	49.5	28.3	480	2 T34294
41	49.5	28.3	489	2 B82275
42	49.5	28.3	544	2 B97166
43	49.5	28.3	716	2 H84421
44	49	28.0	896	2 S48761
45	49	28.0	266	2 A82851
			288	2 B40722

ALIGNMENTS

RESULT 1
T00636
hypothetical protein F21856.2 - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C/Accession: T00636
R:Name: J.B.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhart-Schultz, K.; C
rgescu, A.; Avila, J.; Liu, S.; Bruce, R.; Quan, G.; Montgomery, M.; Ow, D.; Nolan, M.;
submitted to the EMBL Data Library, January 1998.
A:Description: Sequence analysis of a 3.5 Mb contig in 19p13.3 between CDC34 and D19S342
A:Reference number: Z14195
A/Accession: T00636
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A:Residues: 1-679 <IAM>
A/Cross-references: UNIPROT:Q81V72; UNIPARC:UPI00000745CD; EMBL:AC004030; NID:G2804590;
C/Genetics:
A/Map position: 19p13.3
A/Introns: 594/1; 637/3; 650/3
A>Note: F21856_2

Query Match 100.0%; Score 175; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALFPEVFSPTPDENSQSSQASGITGSYSVS 35
DB 568 ALFPEVFSPTPDENSQSSQASGITGSYSVS 602

RESULT 2
B85035
hypothetical protein AT4902760 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: B85035
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
g Nature 402, 769-777, 1999
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A/Reference number: B85001; MWID:20083488; PMID:10617198
A/Accession: B85035
A/Status: preliminary
A/Molecule type: DNA
A:Residues: 1-419 <STO>
A/Cross-references: UNIPROT:Q9SV03; UNIPARC:UPI00000A6D56; GB:NC_001268; NID:G7269761; F

Query Match 32.6%; Score 57; DB 2; Length 419;
Best Local Similarity 41.4%; Pred. No. 7.5;
Matches 12; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Oy 5 EVFSPDPDNDQNSRSSQASGITGSYS 33
Db 379 DVRSPPSSSSSDSSSSSSSSSSSSGESS 407

RESULT 3

S37762
225K protein - Babesia bovis (fragment)
C/Species: Babesia bovis
C/Date: 19-May-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C/Accession: S37762
R/Jammer, D.P.; Redeker, D.W.; Perryman, L.E.; McGuire, T.C.
Mol. Biochem. Parasitol. 52, 263-270, 1992
A/Title: A Babesia bovis 225-Kilodalton protein located on the cytoplasmic side of the
A/Reference number: S37762; MUID:92319010; PMID:1377786
A/Accession: S37762
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-574 <JMS>
A/Cross-references: UNIPROT:Q00708; UNIPARC:UPI00000836E2; EMBL:M80466; NID:g155856; PID

Query Match 32.6%; Score 57; DB 2; Length 574;
Best Local Similarity 37.5%; Pred. No. 11;
Matches 12; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Oy 4 PEVFSPTPDNSDQNSRSSQASGITGSYS 35
Db 193 PEIRDTNDENMDTDSKPAQVTPPTSPSIR 224

RESULT 4

S50734
WHI3 protein - yeast (Saccharomyces cerevisiae)

N/Alternate names: protein N1382; protein YNL197C
C/Species: Saccharomyces cerevisiae
C/Date: 27-Jan-1995 #sequence_revision 16-Feb-1996 #text_change 05-Oct-2004
C/Accession: S50734; S49872; S56045; S63154
R/Jomiaux, J.L.; Cosser, F.; Purnelle, B.; Goffeau, A.
Yeast 10, 1639-1645, 1994
A/Title: A 21.7 kb DNA segment on the left arm of yeast chromosome XIV carries WHI3, GCR
A/Reference number: S50712; MUID:95242839; PMID:7725799
A/Accession: S50734
A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-661 <JON>

A/Cross-references: UNIPROT:P34761; UNIPARC:UPI0000138F03; EMBL:X78898; NID:g600045; PID

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994

R/Jomiaux, J.L.; Cosser, F.; Purnelle, B.; Goffeau, A.
submitted to the EMBL Data Library, April 1994

A/Description: A 21.7 kb DNA segment on the left arm of yeast chromosome XIV carries WHI

A/Reference number: S49850

A/Accession: S49872

A/Molecule type: DNA

A/Residues: 1-661 <JON>

A/Cross-references: UNIPARC:UPI0000138F03; EMBL:X78898; NID:g600045; PID:g600068

R/Naeh, R.S.; Futcher, A.B.
submitted to the EMBL Data Library, August 1993

A/Description: Characterization of WHI3, a new size control gene of Saccharomyces cerevi

A/Reference number: S56045

A/Accession: S56045

A/Molecule type: DNA

A/Residues: 1-661 <NAS>

A/Cross-references: UNIPARC:UPI0000138F03; EMBL:U01095; NID:g393076; PID:g393077

R/Cotter, F.; Jomiaux, J.L.; Goffeau, A.; Purnelle, B.; Van Dyc, L.
submitted to the Protein Sequence Database, April 1996

A/Reference number: S63154

A/Accession: S63154

A/Molecule type: DNA

A/Residues: 1-661 <COS>

A/Cross-references: UNIPARC:UPI0000138F03; EMBL:Z71473; NID:g1302194; PID:g1302195; MIPS

A/Experimental source: strain S288C

C/Genetics:

A/Gene: SGD:WHI3
A/Cross-references: SGD:S0005141; MIPS:YNL197C
A/Map position: 14L
A/Superfamily: RNA-binding protein Rnp24p; ribonucleoprotein repeat homology
F;539-609/Domain: ribonucleoprotein repeat homology <RRM1>

Query Match 32.6%; Score 57; DB 2; Length 661;
Best Local Similarity 34.1%; Pred. No. 12;
Matches 15; Conservative 9; Mismatches 10; Indels 10; Gaps 1;

Oy 2 LPEVFSPTPDE-----NSDQNSRSSQASGITGSYS 35
Db 471 MYVPGNSNTPOKVPARLSSRRSHKNNSTTSLSNITGSASIS 514

RESULT 5

AC0333
probable membrane protein YPO2731 [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AC0333
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, T
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AC0333

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-679 <KUR>

A/Cross-references: UNIPROT:Q8ZD61; UNIPARC:UPI00000CD961; GB:AL590842; PIDN:CAC92970.1;

C/Genetics:

A/Gene: YPO2731

Query Match 31.4%; Score 55; DB 2; Length 679;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Oy 10 TPDENSDQNSRSSQASGITGSYS 33
Db 643 TPSSSDSSSSSSSSSSSSSSSSSSGSGS 666

RESULT 6

S53043
probable membrane protein YMR012w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein YMR270.16
C/Species: Saccharomyces cerevisiae
C/Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C/Accession: S53043
R/Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, March 1995
A/Reference number: S53028
A/Accession: S53043
A/Molecule type: DNA

A/Residues: 1-1277 <DEV>

A/Cross-references: UNIPROT:Q03690; UNIPARC:UPI0000052EF5; EMBL:Z48613; NID:g728645; PID

A/Experimental source: strain AB972

C/Genetics:

A/Gene: SGD:CUU1

A/Cross-references: SGD:S0004614; MIPS:YMR012w

A/Map position: 13R

C/Keywords: transmembrane protein

F;835-851/Domain: transmembrane #status predicted <TMM>

Query Match 31.4%; Score 55; DB 2; Length 1277;
Best Local Similarity 56.2%; Pred. No. 48;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 7 FSPPTDNDQNSRSS 22
Db 270 FDPSPKENTDENASS 285

RESULT 7

557348
nuclear factor R1P140 - human
C/Species: Homo sapiens (man)
C/Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C/Accession: S57348
R/Cavallier, V.; Dauvois, S.; L'Hozet, F.; Lopez, G.; Hoare, S.; Kushner, P.J.; Parker, E.M.O. J. 14, 3741-3751, 1995
A/Title: Nuclear factor R1P140 modulates transcriptional activation by the estrogen receptor
A/Reference number: S57348; MUID:95569246; PMID:7641693
A/Accession: S57348
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1158 <CAV>
A/Cross-references: UNIPROT:P48552; UNIPARC:UPI0000160253; EMBL:X64373; NID:G940538; PID

Query Match

Best Local Similarity 31.1%; Score 54.5; DB 2; Length 1158;
Matches 14; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY 1 ALFPEVSPPT-DENSNDNRSSSQASGITGSYS 33
DB 403 STPEESSTPTTIDYSDNNPSTDDSSGDESSYS 436

RESULT 8

A56921
Kinesin family protein KIF1A - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: A56921
R/Okada, Y.; Yamazaki, H.; Sekine-Aizawa, Y.; Hirokawa, N.
Cell 81, 769-780, 1995
A/Title: The neuron-specific kinesin superfamily protein KIF1A is a unique monomeric motor
A/Reference number: A56921; MUID:95282344; PMID:7539720
A/Accession: A56921
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1695 <RES>
A/Cross-references: UNIPROT:P33173; UNIPARC:UPI000007220C; GB:D29951; NID:G976234; PID:
C/Species: Kinesin-related protein unc-104; Kinesin motor domain homology; Pleckstrin
C/KeyWords: nucleotide binding; P-loop
P/6-360/Domain: kinesin motor domain homology <KNOT>
P/97-104/Region: nucleotide-binding motif A (P-loop)

Query Match 30.9%; Score 54; DB 2; Length 1695;

Best Local Similarity 60.9%; Pred. No. 89;
Matches 14; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 4 PEVFSPTPDNSQNRSSSQAS 26
DB 1414 PEVLSPASSEDSE--SRSSSGAS 1434

DB 1414 PEVLSPASSEDSE--SRSSSGAS 1434

RESULT 9

DB3232
hypothetical protein PA3313 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: DB3232
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Ryan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Lam,
J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
gen
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: DB3232
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-335 <STO>
A/Cross-references: UNIPROT:Q9HYT1; UNIPARC:UPI00000C59AA; GB:AE004753; GB:AE004091; NID

A/Experimental source: strain PA01

C/Genetics: PA3313

Query Match 30.3%; Score 53; DB 2; Length 335;
Best Local Similarity 43.8%; Pred. No. 20;
Matches 14; Conservative 3; Mismatches 15; Indels 0; Gaps 0;

QY 4 PEVFSPTPDNSQNRSSSQASGITGSYS 35
DB 38 PRVFSALPENSFWLKRSLAAGIALSLAA 69

RESULT 10

S27779
major merozoite surface antigen 1 homolog (5'end) - Babesia bovis (fragment)
N/Alternate names: variable antigen 1
C/Species: Babesia bovis
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C/Accession: S27779
R/Dalrymple, B.P.; Peters, J.M.
Submitted to the EMBL Data Library, March 1992
A/Description: Sequence of a Babesia bovis gene encoding a protein with regions of amino
acid homology to the S27779
A/Reference number: S27779
A/Accession: S27779
A/Molecule type: mRNA
A/Residues: 1-370 <DAL>
A/Cross-references: UNIPROT:Q17117; UNIPARC:UPI00007AA73; EMBL:M87623; NID:G155927; PID

C/Keywords: surface antigen

Query Match 30.3%; Score 53; DB 2; Length 370;

Best Local Similarity 34.4%; Pred. No. 22;
Matches 11; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 4 PEVFSPTPDNSQNRSSSQASGITGSYS 35
DB 193 PEIINDNDENDTNDNSKPAEVTPTTPSPST 224

RESULT 11

S73829
probable ABC transport permease - Mycoplasma pneumoniae (strain ATCC 29342)
N/Alternate names: hypothetical protein P10_crf750
C/Species: Mycoplasma pneumoniae
A/Variety: ATCC 29342
C/Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: S73829
R/Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A/Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A/Reference number: S73829; MUID:97105885; PMID:8948633
A/Accession: S73829
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-750 <HIM>
A/Cross-references: UNIPROT:P75445; UNIPARC:UPI000013A815; EMBL:AE000049; GB:U00089; NID

C/Genetics: A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C/Genetic code: SGC3

Query Match 30.3%; Score 53; DB 2; Length 750;

Best Local Similarity 39.3%; Pred. No. 49;
Matches 11; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 8 SPTPDNSQNRSSSQASGITGSYS 35
DB 389 SPPEKSGDENTKGDNSSEKTDIVSVS 416

RESULT 12

A59251
myosin - Acetabularia cliftonii
C/Species: Acetabularia cliftonii

C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
 C:Accession: J59251
 R:Vugrek, O.; Menzel, D.
 Submitted to GenBank, March 1997
 A:Description: Molecular analysis of the cDNA coding for an unconventional myosin from *Vibrio*
 A:Reference number: J59251
 A:Accession: J59251
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-1145 <VUG>
 A:Cross-references: UNIPROT:O04146; UNIPARC:UPI00000A9550; GB:U94398; NID:G2051982; PIDN
 C:Genetics:
 A:Gene: myo2
 A:Genetic code: SGCS
 F:97-799/Domain: myosin motor domain homology <MMO>
 Query Match 30.3%; Score 53; DB 2; Length 1145;
 Best Local Similarity 37.0%; Pred. No. 78;
 Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
 Oy 2 LPPEVFSTPDNSDQNSRSSQASGI 28
 Db 635 LVLVLFESDDQNSDQNSSENSNANV 661
 RESULT 13
 AB0088
 Probable flagellar M-ring protein fljF [Imported] - *Yersinia pestis* (strain CO92)
 C:Species: *Yersinia pestis*
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
 C:Accession: AB0088
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.B.
 demo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AB0088
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-546 <KUN>
 A:Cross-references: UNIPROT:Q82108; UNIPARC:UPI00000DCD2A; GB:AL590842; PIDN:CAC89565.1;
 C:Genetics:
 A:Gene: fljF
 C:Superfamily: Probable flagellar basal-body M ring protein
 Query Match 30.0%; Score 52.5; DB 2; Length 546;
 Best Local Similarity 40.6%; Pred. No. 40;
 Matches 13; Conservative 3; Mismatches 13; Indels 3; Gaps 1;
 Oy 5 EVFSEFTPDNSDQNSRSSQASGITGYS 33
 Db 279 EHYGDPRIENDIQEENSNDMAWIGISLS 310
 RESULT 14
 J01125
 Gas-vesicle operon protein gyph - *Halobacterium salinarum* plasmid pNRC100
 C:Species: *Halobacterium salinarum*
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Jan-2000
 C:Accession: J01125; S15187
 R:Jones, J.G.; Young, D.C.; DasSarma, S.
 Gene 102, 117-122, 1991
 A:Title: Structure and organization of the gas vesicle gene cluster on the *Halobacterium*
 A:Reference number: J01122; MUID:91323716; PMID:1864501
 A:Accession: J01125
 A:Molecule type: DNA
 A:Residues: 1-182 <JON>
 A:Cross-references: UNIPARC:UPI000012BE2C; GB:M58557; NID:G150406; PID:G455302
 A:Experimental source: strain NRC-1, plasmid pNRC100
 A:Genetics: NRC
 A>Note: the source is designated as *Halobacterium halobium*
 R:Horne, M.; Englert, C.; Wimmer, C.; Pfeifer, F.

Mol. Microbiol. 5, 1159-1174, 1991
 A:Title: A DNA region of 9 kbp contains all genes necessary for gas vesicle synthesis in
 A:Reference number: S15183; MUID:92055812; PMID:1956294
 A:Accession: S15187
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-182 <HOR>
 A:Cross-references: UNIPARC:UPI000012BE2C; EMBL:X55648; NID:G43516; PID:G43521
 A:Experimental source: plasmid pNRC100
 A:Genetics: PHH
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1990
 A>Note: the source is designated as *Halobacterium halobium*
 C:Genetics: <NRC>
 A:Gene: gyph
 A:Genome: plasmid pNRC100
 C:Genetics: <PHH>
 A:Gene: gyph
 A:Genome: plasmid pNRC100
 C:Superfamily: *Halobacterium* gyph protein
 Query Match 29.7%; Score 52; DB 2; Length 182;
 Best Local Similarity 55.6%; Pred. No. 14;
 Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Oy 11 PDNSDQNSRSSQASGI 28
 Db 3 PDENDASDDQSSQSGI 20
 RESULT 15
 T08237
 Gas-vesicle operon protein gyph - *Halobacterium* sp. (strain NRC-1) plasmid pNRC100
 N:Alternate names: hypothetical protein H0237
 C:Species: *Halobacterium* sp.
 A:Variety: strain NRC-1
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: T08237
 R:Ng, W.V.; Clufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baeklin, D.; Faust, J.; Hall, B.; I
 Genome Res. 8, 1131-1141, 1998
 A:Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or m
 A:Reference number: Z16408; MUID:99063795; PMID:9847077
 A:Accession: T08237
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-182 <NGW>
 A:Cross-references: UNIPROT:P24372; UNIPARC:UPI000012BE2C; EMBL:AF016485; NID:G2822278; I
 A:Experimental source: strain NRC-1
 C:Genetics:
 A:Gene: gyph; HALOSP:H0237
 A:Genome: plasmid pNRC100
 C:Superfamily: *Halobacterium* gyph protein
 Query Match 29.7%; Score 52; DB 2; Length 182;
 Best Local Similarity 55.6%; Pred. No. 14;
 Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Oy 11 PDNSDQNSRSSQASGI 28
 Db 3 PDENDASDDQSSQSGI 20
 Search completed: March 3, 2006, 13:36:34
 Job time: 3.21088 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 13:19:17 ; Search time 13.3673 Seconds

(without alignment)
1847.299 Million cell updates/sec

Title: US-10-646-873-45

Perfect score: 175

Sequence: 1 ALPPEVFSPTDENSDONSRSQASGITGSYSVS 35

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : uniprot_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	679	1 CS021_HUMAN	081VC2 homo sapien
2	165	94.3	685	1 CS021_MOUSE	051Bh3 pongo pygma
3	132	75.4	648	1 CS021_MOUSE	09d279 mus musculu
4	64	36.6	746	2 Q4OR28_LEIMA	049E28 leishmania
5	61	34.9	545	2 Q8MP25_DICDI	08MP25 dictyostell
6	61	34.9	855	2 Q55M66_DICDI	055M66 dictyostell
7	60	34.3	1201	2 Q54VVI_DICDI	054VVI dictyostell
8	60	34.3	3071	2 Q54CF8_DICDI	054CF8 dictyostell
9	59.5	34.0	363	2 Q5CNV9_CRYHO	05CNV9 cryptospori
10	59.5	34.0	2418	2 Q585F7_EMENI	0585F7 aspergillus
11	59	33.7	669	2 Q6Y115_ORYSA	06Y115 oryza sativ
12	59	33.7	1044	2 Q4WK00_ASFPU	04WK00 aspergillus
13	58	33.1	275	2 Q5ZJAI_CHICK	05ZJAI gallus gall
14	58	33.1	1331	2 Q54T97_DICDI	054T97 dictyostell
15	58	33.1	1377	2 Q9VJ42_DROME	09VJ42 drosophila
16	57.5	32.9	568	2 Q4T095_TETNG	04T095 tetraodon n
17	57	32.6	285	2 Q85ZB9_ORYSA	085ZB9 oryza sativ
18	57	32.6	419	2 Q9S703_ARATH	09S703 arabidopsis
19	57	32.6	574	2 Q00708_BABBO	000708 babesia bov
20	57	32.6	607	2 Q71T12_MOMCH	071T12 momordica c
21	57	32.6	607	2 Q71T13_MOMCH	071T13 momordica c
22	57	32.6	661	1 WH13_YEAST	W14761 saccharomyc
23	57	32.6	893	2 Q527C2_MAGAR	0527C2 magnaporthe
24	56.5	32.3	826	2 Q417X8_GIBZE	0417X8 gibberella
25	56	32.0	296	2 Q9C1C4_AJBEA	09C1C4 ajellomyces
26	56	32.0	349	2 Q7Y0C1_ORYSA	07Y0C1 oryza sativ
27	56	32.0	460	2 Q76P28_DICDI	076P28 dictyostell
28	56	32.0	598	2 Q6BK24_DEBNA	06BK24 debaryomyce
29	56	32.0	749	2 Q54KT6_DICDI	054KT6 dictyostell
30	56	32.0	893	2 Q81ZX0_STRAM	081ZX0 streptomyce
31	56	32.0	917	2 Q4SENI_TETNG	04SENI tetraodon n

32	55.5	31.7	132	2 Q5UTV9_HUMAN	05UTV9 homo sapien
33	55.5	31.7	191	2 Q5C1P1_SCHUA	05C1P1 schistosoma
34	55.5	31.7	216	2 Q51TW1_HUMAN	051TW1 homo sapien
35	55.5	31.7	506	2 Q8K383_MOUSE	08K383 mus musculu
36	55.5	31.7	1017	2 Q52BV0_MAGGR	052BV0 magnaporthe
37	55.5	31.7	1393	2 Q5CXH8_CRYPV	05CXH8 cryptospori
38	55.5	31.7	1754	2 Q8OU37_MOUSE	08OU37 mus musculu
39	55.5	31.7	2607	2 Q8BT18_MOUSE	08BT18 mus musculu
40	55	31.4	406	2 Q9W404_DROME	09W404 drosophila
41	55	31.4	437	2 Q5LW22_SILPO	05LW22 silicibacte
42	55	31.4	503	2 Q84D78_LISSE	084D78 listeria se
43	55	31.4	524	2 Q84DU1_LISSE	084DU1 listeria se
44	55	31.4	525	2 Q84DU2_LISSE	084DU2 listeria se
45	55	31.4	679	2 Q82D61_YERPE	082D61 yersinia pe

ALIGNMENTS

RESULT 1	CS021_HUMAN	STANDARD;	PRT;	679 AA.
AC	Q81VT2;			
DT	13-SEP-2005 (Rel. 48, Created)			
DT	13-SEP-2005 (Rel. 48, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Protein C19orf121.			
GN	Name=C19orf121;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Carnivora; Homiidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	TISSUE=Brain, and Colon;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uebli T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,			
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,			
RA	Scherech A., Schein J.B., Jones S.J.M., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	EMBL: BC042125; AAH42125.1; -; mRNA.			
CC	EMBL: BC052236; AAH52236.1; -; mRNA.			
DR	PIR; T00636; T00636.			
DR	Ensembl; ENSG0000009812; Homo sapiens.			
DR	HGNC; HGNC:27000; C19orf121.			
FT	Coiled coil.			
KM	Coiled coil.			
SO	SEQUENCE 679 AA; 75357 MW; D2881CF5087E61F8 CRC64;			

Query Match 100.0%; Score 175; DB 1; Length 679;
 Best Local Similarity 100.0%; Pred. No. 1e-13;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPPEVFPPTDENDONSRRSSQASGITGSYSVS 35
 |||||
 Db 568 ALPPEVFPPTDENDONSRRSSQASGITGSYSVS 602

RESULT 2
 CS021_PONPY STANDARD; PRT; 685 AA.
 ID Q5RBH3;
 AC Q5RBH3;
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Protein C19orf21 homolog.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Pongo.
 NCBI_TaxID=9600;
 OX NCBI [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Kidney;
 RG The German cDNA consortium;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; CR858675; CAH90887.1; -; mRNA.
 DR Colled coll.
 KW COILED 551 575 Potential.
 FT SEQUENCE 685 AA; 75892 MW; A3A99FA343396E81 CRC64;
 SQ

Query Match 94.3%; Score 165; DB 1; Length 685;
 Best Local Similarity 94.3%; Pred. No. 2e-12;
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALPPEVFPPTDENDONSRRSSQASGITGSYSVS 35
 |||||
 Db 574 ALPPEVFPPTDENDONSRRSSQASGITGSYSVS 608

RESULT 3
 CS021_MOUSE STANDARD; PRT; 648 AA.
 ID Q9D279;
 AC Q9D279;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Protein C19orf21 homolog.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 OX NCBI [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikiyado I., Otsu N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Bruscia V., Chochia I., Cousins S.,
 RA Dalia E., Dregani T.A., Fletcher C.F., Forrest L.E., Cousins S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedziercki R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Leinhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagasima T., Numata K., Okido T., Pavan W.J., Perlee G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Waples C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yangisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shitaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yamashita A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pirange C.,
 RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Melek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulik S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallov D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AK020266; BAB32049.1; -; mRNA.
 DR EMBL; BC013508; AAH13508.1; -; mRNA.
 DR Ensembl; ENSMUSG00000035852; Mus musculus.
 DR MGI; MGI:1926156; 9130017N09Rik.
 KW Colled coll. 511 534 Potential.
 FT SEQUENCE 648 AA; 72281 MW; 1B395B70763B3D1F CRC64;
 SQ

Query Match 75.4%; Score 132; DB 1; Length 648;
 Best Local Similarity 75.4%; Pred. No. 3.3e-08;
 Matches 28; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Qy 1 ALPPEVFPPTDENDONSRRSSQASGITGSYSVS 35
 |||||
 Db 534 ALPPEVFPPTDENDONSRRSSQASGITGSYSVS 570

RESULT 4
 Q4QE28_LEIMA PRELIMINARY; PRT; 746 AA.
 ID Q4QE28;
 AC Q4QE28;
 DT 13-SEP-2005 (TRENBLrel. 31, Created)

RA Farbrother P., Desany B., Just B., Morio T., Rost R., Churcher C.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Murry D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardrop A., Felder M., Thangaveilu M., Johnson D., Knights A.,
 RA Loulsged H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
 RA Shaulsky G., Schleichner M., Weinstein G., Rosenthal A., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Barrett B., Kuspa A.,
 RA "The genome of the social amoeba Dictyostelium discoideum";
 RL Nature 0:0-0(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL/AAP10100066; EAL67286.1; -; Genomic_DNA.
 DR EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 KM Hypothetical protein.
 SQ SEQUENCE 1201 AA; 136978 MW; DDE248A641817D4 CRC64;
 Query Match 34.3%; Score 60; DB 2; Length 1201;
 Best Local Similarity 43.3%; Pred. No. 1.2e+02;
 Matches 13; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
 Oy 6 VFSPPTDENSQNSRSSQASGINGSVS 35
 Db 84 IISPTQKSSSSSSSSSSSSSSSSSSSSSS 113
 RESULT 8
 ID Q54CF8_DICDI PRELIMINARY; PRT; 3071 AA.
 AC Q54CF8;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE CHD gene family protein containing chromodomain, hellicase domain, and
 DE DNA-binding domain.
 GN Name=DD80220643; ORFNames=DD80220643;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AK4;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugang R., Bertrman M., Song J., Olsen R., Szafranski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pletcher K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Kethornou A., Nie X., Hall N., Angard C., Hemphill L., Bason N.,
 RA Faibrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Murry D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardrop A., Felder M., Thangaveilu M., Johnson D., Knights A.,
 RA Loulsged H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
 RA Shaulsky G., Schleichner M., Weinstein G., Rosenthal A., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Barrett B., Kuspa A.,
 RA "The genome of the social amoeba Dictyostelium discoideum";
 RL Nature 0:0-0(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL/AAP10100074; EAL60858.1; -; Genomic_DNA.
 DR EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 KM DNA-binding; Hellicase.
 SQ SEQUENCE 3071 AA; 345579 MW; 71AD7343CD66B8 CRC64;

Query Match 34.3%; Score 60; DB 2; Length 3071;
 Best Local Similarity 43.5%; Pred. No. 3.7e+02;
 Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 Oy 4 PEVSPPTDENSQNSRSSQAS 26
 Db 2253 PNTFSPPTSNQNNNNNNNNNS 2275
 RESULT 9
 ID Q5CNV9_CRYHO PRELIMINARY; PRT; 363 AA.
 AC Q5CNV9;
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE RNA-binding protein.
 GN ORFNames=Chro.80392;
 OS Cryptosporidium hominis.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 OC Cryptosporididae; Cryptosporidium.
 OX NCBI_TaxID=237895;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=TU502;
 RA Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G.,
 RA Puiu D., Mangue P., Aktyoshi D., Mackey A.J., Pearson W.R., Dear P.H.,
 RA Bankier A.T., Peterson D.L., Abrahamson M.S., Kapur V., Tzipori S.,
 RA Buck G.A.;
 RT "The genome of Cryptosporidium hominis";
 RL Nature 431:1107-1112(2004).
 DR EMBL/AAL01000005; EAL38288.1; -; Genomic_DNA.
 DR InterPro: IPR007109; Brix.
 DR Pfam: PF04427; Brix; 1.
 DR PROSITE: PSS0833; Brix; 1.
 SQ SEQUENCE 363 AA; 40988 MW; F42649CBF10B86CD CRC64;
 Query Match 34.0%; Score 59.5; DB 2; Length 363;
 Best Local Similarity 50.0%; Pred. No. 36;
 Matches 16; Conservative 2; Mismatches 13; Indels 1; Gaps 1;
 Oy 5 EVSPPTDENSQNSRSSQASGI-TGSYSVS 35
 Db 259 EVKPTSGNRDENQWGLSERSGIYTKVSVS 290
 RESULT 10
 ID Q5B5F7_EMENI PRELIMINARY; PRT; 2418 AA.
 AC Q5B5F7;
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=AN423.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FGSC A4;
 RA Birren B., Nusbaum C., Abouelell A., Allen N., Anderson S.,
 RA Arachchi H.M., Barria N., Bastien V., Bloom T., Boguslavsky L.,
 RA Boukhalter B., Butler J., Calvo S.B., Camarata J., Chang J.,
 RA Choquel Y., Collymore A., Cook A., Cooke P., Corum B., Deatellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Fero S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Haefer N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamat M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,

RA Matthews C., Maucelli E., McCarthy M., Meldrum J., Meneus L.,
 RA Milnova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunhkhong P., Piere N., Purcell S.,
 RA Rachupa A., Ramsay U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman U., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talama J., Testaye S., Theodore J., Topham K., Travers M.,
 RA Vasilev H., Venkaterman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zaimoun J., Zembek L., Zimmer A., Zody M.,
 RA Zander E.,
 RT "Genome Sequence of *Aspergillus nidulans*,"
 DR Submitted (JAN-2004) to the EMBL/Genbank/DBJ databases.
 RA EMBL; AAC00100068; EAA59322.1; -; Genomic_DNA.
 DR InterPro; IPR000074; APOA1 A4 E.
 DR InterPro; IPR011992; EF-Hand_Type.
 KW Hypothetical protein. Repeat
 SQ SEQUENCE 2418 AA; 267172 MW; 0165HC08CC056B0 CRC64;

Query Match 34.0%; Score 59.5; DB 2; Length 2418;
 Best Local Similarity 40.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 7; Mismatches 11; Indels 3; Gaps 2;

QY 3 PPEVPSPTPDEN--SDONSRSQASGITGSYS 35
 DB 2287 PPEVFPEDENQSGDEPTGTERRTSYGTAAES 2320

RESULT 11
 O6Y15_ORYSA PRELIMINARY; PRT; 669 AA.

AC O6Y15;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 GN Name=OSUNBD056122.34;
 OS *Oryza sativa* (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 OC NCBI_TaxID=39447;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.,
 RL Submitted (AUG-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF005644; BAD17485.1; -; Genomic_DNA.
 DR Gramene; O6Y15; -;
 KW Hypothetical protein.
 SQ SEQUENCE 669 AA; 68389 MW; 6B3B83B6DA44D89 CRC64;

Query Match 33.7%; Score 59; DB 2; Length 669;
 Best Local Similarity 50.0%; Pred. No. 85;
 Matches 13; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 8 SPTPDNSDNRSSQASGITGSYS 33
 DB 415 SPESDSDSDNRSSSSSSSSSSSSSSSS 440

RESULT 12
 Q4WK00_ASPFU PRELIMINARY; PRT; 1044 AA.

AC Q4WK00;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=Afu1901700;
 OS *Aspergillus fumigatus* Af293.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
 OC NCBI_TaxID=330879;

RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC SYRINAF293;
 RC Niemann W., Pain A., Anderson M.J., Wortman J., Kim H., Stanley,
 RA Arroya J., Bertrian M., Abe K., Archer D.B., Barmajo C., Bennett J.,
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
 RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Goni K., Griffith-Jones S., Guilliam R., Haas B.,
 RA Haas H., Harris D., Hrtutchi H., Huang J., Humphrey S., Jimenez J.,
 RA Keller N., Khouri H., Kikuchi K., Kobayashi T., Kulxarni R.,
 RA Kumagai T., Lafon A., Latge J.-P., Li W., Lord A., Lu C.,
 RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
 RA Mounya I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
 RA Penava M.A., Pertea W., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J., Yu J.-H., Frazer C., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrett B., Denning D.W.,
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
Aspergillus fumigatus,"
 RL Submitted (May-2005) to the EMBL/Genbank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAH01000007; EAL67882.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 1044 AA; 113308 MW; C3B1D83A1826E529 CRC64;

Query Match 33.7%; Score 59; DB 2; Length 1044;
 Best Local Similarity 42.9%; Pred. No. 1.4e+02;
 Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 6 VSPPTDNRSSQASGITGSYS 33
 DB 983 TSPSDSDSDNRSSSSSSSSSSSSSSSES 1010

RESULT 13
 O5ZJAI_CHICK PRELIMINARY; PRT; 275 AA.

AC O5ZJAI;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=RCMB04.19110;
 OS *Gallus gallus* (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CB; TISSUE=Bursa;
 RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
 RA Pledier P., Kuter S., Haysenizaki Y., Kostovska D.J., Koter M.,
 RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
 gene function analysis,"
 RL Genome Biol. 6:R6-R6(2005).
 DR EMBL; AJ720533; CAG32192.1; -; mRNA.
 DR InterPro; IPR000717; PCI.
 DR Pfam; PF01399; PCI; 1.
 DR SMART; SM00088; PINT; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 275 AA; 30404 MW; 506BAE2AE80CFEE CRC64;

Query Match 33.1%; Score 58; DB 2; Length 275;
 Best Local Similarity 36.7%; Pred. No. 41;

```
Matches 11: Conservative 6; Mismatches 13; Indels 0; Gaps 0;
Oy 5 EVFSPTRPNDQNSRSSQASGRTGSV 34
Db 241 ELREPAFGTNRQTSKTSKAKJLNGSAXI 270

RESULT 14
054197 D1CDI
ID 054197 D1CDI PRELIMINARY; PRT; 1331 AA.
AC 054197;
DT 13-SEP-2005 (TRMBLrel. 31, Created)
DT 13-SEP-2005 (TRMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TRMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD80204281;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugeng R., Bertman M., Song J., Olsen R., Szafarski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankler A.T., Lehmann R., Hamlin N., Davies R., Gauder P., Fey P.,
RA Plicher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kethorou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., Van Driessche N., Cronin A., Goodhead I.,
RA Hansen D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Oulles M., Mohan M.B., Salto T., Buchrieser C.,
RA Wardoper A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louisgeed H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmons M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shuley G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.,
RA Williams J., Dear P.H., Noegel A.A., Barrett B., Kuypa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAF10100076; EAL66513.1; -; Genomic DNA.
CC DR Hypothetical protein.
CC KW
SQ SEQUENCE 1331 AA; 154245 MW; D9CE76799F45D15 CRC64;

Query Match 33 1%; Score 58; DB 2; Length 1331;
Best Local Similarity 52.2%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Oy 4 PEVFSPTDENSQNSRSSQAS 26
Db 438 PFFSPPPPPQSSSTNSSSSS 460

RESULT 15
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ID 09V742 DROME PRELIMINARY; PRT; 1377 AA.
AC 09V742;
DT 01-MAY-2000 (TRMBLrel. 13, Created)
DT 01-OCT-2002 (TRMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
DE CG10600-PA.
GN Name=CG10600; ORFNames=CG10600;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoekins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bakendale U., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Burtis K.C., Butam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mikhlov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclio J.M.,
RA Palazzolo M., Plittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shie B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2242605; PubMed=12537568;
RA Celnik S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoekins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Paclio J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnik S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochownik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bertencourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Ruoco S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
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RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celinker S., Carlson J., Man K., Pfeiffer B., Friese E., George R.,
RA Hoskins R., Stapleton M., Pacled J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003660; AAF53715.3; -; Genomic_DNA.
DR Inctact; Q9VJ42; -;
DR Ensembl; CG10600; Drosophila melanogaster.
DR FlyBase; Fggn0032717; CG10600.
SQ SEQUENCE 1377 AA; 150552 MW; 9FBC2436A9BD6ABA CRC64;

Query Match 33.1%; Score 58; DB 2; Length 1377;
Best Local Similarity 46.4%; Pred. No. 2.6e+02;
Matches 13; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

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Db 930 PAAGSSPSQONENNSSSQSGAGSVS 957

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 Job time : 16.3673 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 13:35:46 ; Search time 4.69388 Seconds
(without alignments)
616.473 Million cell updates/sec

Title: US-10-646-873-45

Perfect score: 175
Sequence: 1 ALFPEVSPRPDENSDNRSSSQASGITGSYSVS 35

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents, AA:*
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6: /cgn2_6/prodata/1/1aa/backfill501.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	35	US-09-050-516-45	Sequence 45, Appl
2	175	100.0	35	US-10-278-547-45	Sequence 45, Appl
3	175	100.0	215	US-09-050-516-47	Sequence 47, Appl
4	175	100.0	215	US-10-278-547-47	Sequence 47, Appl
5	175	100.0	679	US-09-050-516-42	Sequence 42, Appl
6	175	100.0	679	US-10-278-547-42	Sequence 42, Appl
7	57	32.6	661	US-09-487-558B-422	Sequence 422, App
8	54.5	31.1	1163	US-09-949-016-11047	Sequence 11047, A
9	54	30.9	642	US-09-248-796A-15380	Sequence 15380, A
10	53	30.3	80	US-09-091-219-6	Sequence 6, Appl1
11	53	30.3	80	US-09-660-541-6	Sequence 6, Appl1
12	53	30.3	362	US-09-252-991A-17733	Sequence 17733, A
13	53	30.3	437	US-09-921-099A-17	Sequence 17, Appl
14	53	30.3	2232	US-09-091-219-25	Sequence 25, Appl
15	53	30.3	2232	US-09-660-541-25	Sequence 25, Appl
16	53	30.3	2247	US-09-091-219-2	Sequence 2, Appl1
17	53	30.3	2247	US-09-660-541-2	Sequence 2, Appl1
18	52	29.7	341	US-09-248-796A-14575	Sequence 14575, A
19	52	29.7	393	US-09-248-796A-18493	Sequence 18493, A
20	51.5	29.4	266	US-09-589-287B-19	Sequence 19, Appl
21	51.5	29.4	266	US-09-879-919-24	Sequence 24, Appl
22	51.5	29.4	266	US-09-589-287A-19	Sequence 19, Appl
23	51.5	29.4	266	US-09-589-286A-19	Sequence 19, Appl
24	51.5	29.4	266	US-09-255-794A-19	Sequence 19, Appl
25	51.5	29.4	266	US-09-507-968D-19	Sequence 19, Appl
26	51.5	29.4	266	US-09-589-285-19	Sequence 19, Appl
27	51	29.1	362	US-09-194-2	Patent No. 5504194

28	51	29.1	1596	2	US-09-538-092-887	Sequence 887, App
29	50.5	28.9	252	2	US-09-248-796A-23055	Sequence 23055, A
30	50.5	28.9	505	2	US-09-248-796A-14299	Sequence 14299, A
31	50	28.6	410	2	US-09-248-796A-19654	Sequence 19654, A
32	50	28.6	548	2	US-09-398-395A-2	Sequence 2, Appl1
33	50	28.6	548	2	US-09-398-395A-4	Sequence 4, Appl1
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36	50	28.6	548	2	US-09-398-395A-10	Sequence 10, Appl
37	50	28.6	548	2	US-09-398-395A-12	Sequence 12, Appl
38	50	28.6	548	2	US-09-887-586A-2	Sequence 2, Appl1
39	50	28.6	548	2	US-09-887-586A-4	Sequence 4, Appl1
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45	50	28.6	548	2	US-09-895-752-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-050-516-45
Sequence 45, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: ROSSBELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF INVENTIONS: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-45

Query Match 100.0%; Score 175; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 8.8e-18;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ALPPEVPSPTDENSDONSRSSSQASGITGSYSVS 35

RESULT 2
US-10-278-547-45

Sequence 45, Application US/10278547
Patent No. 6660834

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL

COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-10-278-547-45

Query Match 100.0%; Score 175; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 8.8e-18;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ALPPEVPSPTDENSDONSRSSSQASGITGSYSVS 35

RESULT 3
US-09-050-516-47

Sequence 47, Application US/09050516
Patent No. 6627414

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA

APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL

COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-47

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Best Local Similarity 100.0%; Pred. No. 8.3e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 104 ALPPEVFSPTPDNSDONSRSQASGITGSYSVS 138

RESULT 4

US-10-278-547-47
Sequence 47, Application US/10278547
Patent No. 6660834

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITTS, TRACEY L.

FRIEDMAN, PAULA N.

GORDON, JULIAN

GRANADOS, EDWARD N.

HAYDEN, MARK

HODGES, STEVEN C.

KLASS, MICHAEL R.

KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSER: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547

FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065.US.PI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6660834e

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-10-278-547-47

RESULT 5

Query Match 100.0%; Score 175; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.3e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPPEVFSPTPDNSDONSRSQASGITGSYSVS 35
DB 104 ALPPEVFSPTPDNSDONSRSQASGITGSYSVS 138

US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. 6627414

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITTS, TRACEY L.

FRIEDMAN, PAULA N.

GORDON, JULIAN

GRANADOS, EDWARD N.

HAYDEN, MARK

HODGES, STEVEN C.

KLASS, MICHAEL R.

KRATOCHVIL, JON D.

ROBERTS-RAPP, LISA

RUSSELL, JOHN C.

STROUPE, STEPHEN D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSER: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065.US.PI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 679 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6627414e

US-09-050-516-42

Query Match 100.0%; Score 175; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPPEVFSPTPDNSDONSRSQASGITGSYSVS 35
DB 568 ALPPEVFSPTPDNSDONSRSQASGITGSYSVS 602

RESULT 6

US-10-278-547-42
Sequence 42, Application US/10278547
Patent No. 6660834

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

```
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/938-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-278-547-42
Query Match 100.0%; Score 175; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.130
CURRENT APPLICATION NUMBER: US/09/487,558B
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/487,558
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 446
SOFTWARE: PatentIn version 3.0
SEQ ID NO 422
LENGTH: 661
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-422
Query Match 32.6%; Score 57; DB 2; Length 661;
Best Local Similarity 34.1%; Pred. No. 14;
Matches 15; Conservative 9; Mismatches 10; Indels 10; Gaps 1;
2 LPEVFSPTPDENSDNRSRSGASGITGSYSVS 35
471 MYFVNGNTFQKVPARLSSSRSHKNNSTTSLSSNITGSASIS 514
RESULT 8
US-09-949-016-11047
Sequence 11047, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11047
LENGTH: 1163
TYPE: PRT
ORGANISM: Human
US-09-949-016-11047
Query Match 31.1%; Score 54.5; DB 2; Length 1163;
Best Local Similarity 41.2%; Pred. No. 63;
Matches 14; Conservative 5; Mismatches 14; Indels 1; Gaps 1;
1 ALPEVFSPTPDENSDNRSRSGASGITGSYSVS 33
408 SIFESSPTTIDYSDNPSFTDSSGDESSYS 441
RESULT 9
US-09-248-796A-15380
Sequence 15380, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
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; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15380
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15380

Query Match          30.3%; Score 54; DB 2; Length 642;
Best Local Similarity 52.4%; Pred. No. 35;
Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 7 PSEPDPENDSDNRSRSSQASGYS 27
DB 441 PSEPDPENDSDNRSNSDGD 461

RESULT 10
US-09-091-219-6
; Sequence 6, Application US/09091219
; Patent No. 6171592
; GENERAL INFORMATION:
; APPLICANT: STUDEBERT, Michael J.
; APPLICANT: CRAB, Brendan S.
; APPLICANT: PENG, Li
; TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS
; FILE REFERENCE: 040268/0151
; CURRENT APPLICATION NUMBER: US/09/091,219
; EARLIER FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: PCT/AU96/00815
; EARLIER FILING DATE: 1996-12-18
; EARLIER APPLICATION NUMBER: AU PN7201
; EARLIER FILING DATE: 1995-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 80
; TYPE: PRT
; ORGANISM: equine rhinovirus 1
US-09-091-219-6

Query Match          30.3%; Score 53; DB 2; Length 80;
Best Local Similarity 42.9%; Pred. No. 3.7;
Matches 12; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 6 VFSPTDENDSDNRSRSSQASGIGYS 33
DB 42 VISPEGGSNTSSSTSSQSSGLGWFS 69

RESULT 11
US-09-660-541-6
; Sequence 6, Application US/09660541
; Patent No. 6531136
; GENERAL INFORMATION:
; APPLICANT: STUDEBERT, Michael J.
; APPLICANT: CRAB, Brendan S.
; APPLICANT: PENG, Li
; TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS
; FILE REFERENCE: 040268/0151
; CURRENT APPLICATION NUMBER: US/09/660,541
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/091,219
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN7201
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 80
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; TYPE: PRT
; ORGANISM: equine rhinovirus 1
US-09-660-541-6

Query Match          30.3%; Score 53; DB 2; Length 80;
Best Local Similarity 42.9%; Pred. No. 3.7;
Matches 12; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 6 VFSPTDENDSDNRSRSSQASGIGYS 33
DB 42 VISPEGGSNTSSSTSSQSSGLGWFS 69

RESULT 12
US-09-252-991A-17733
; Sequence 17733, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,768
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17733
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (295)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-17733

Query Match          30.3%; Score 53; DB 2; Length 362;
Best Local Similarity 43.8%; Pred. No. 24;
Matches 14; Conservative 3; Mismatches 15; Indels 0; Gaps 0;

QY 4 PVSFPTDENDSDNRSRSSQASGIGYS 35
DB 65 PVSFSAIBPENSPLMKRSIALAAGIALSLISAA 96

RESULT 13
US-09-921-099A-17
; Sequence 17, Application US/09921099A
; Patent No. 6602707
; GENERAL INFORMATION:
; APPLICANT: Hefenider, Steven
; APPLICANT: Watkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seis, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/09/921,099A
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-921-099A-17

Query Match          30.3%; Score 53; DB 2; Length 437;
Best Local Similarity 45.8%; Pred. No. 30;
Matches 11; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
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QY      7  FSPPTDENSDQNSRRSSSQASGITG 30
      ||| ::::| | | | |
Db     231 FSPKSNQSSNQSSNSSSSSSSSSGG 254

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US-09-091-219-25
RESULT 14
US-09-091-219-25
Sequence 25, Application US/09091219
Patent No. 6171592
GENERAL INFORMATION:
APPLICANT: STUDDERT, Michael J.
APPLICANT: CRABB, Brendan S.
APPLICANT: PENG, Li
TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS
FILE REFERENCE: 040268/0151
CURRENT APPLICATION NUMBER: US/09/091,219
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: PCT/AU96/00815
EARLIER FILING DATE: 1996-12-18
EARLIER APPLICATION NUMBER: AU PNT201
EARLIER FILING DATE: 1995-12-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 2232
TYPE: PR1
ORGANISM: equine rhinovirus 1
US-09-091-219-25

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	Query Match	30.3%	Score 53	DB 2	Length 2232
	Best Local Similarity	42.9%	Pred. No.	2.3e+02	
	Matches	12	Conservative	6	Mismatches 10; Indels 0; Gaps 0
Oy	6	VFSPTPDSNDONSSSSQASGITSYS	33		
	:	::	::		
Db	249	VISPEGGQNTSTTSSSQSSSLGWFS	276		

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RESULT 15
US-09-660-541-25
: Sequence 25, Application US/09660541
: Patent No. 6531136
: GENERAL INFORMATION:
: APPLICANT: STUDDERT, Michael J.
: APPLICANT: CRAIB, Brendan S.
: APPLICANT: FENG, Li
: TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS
: FILE REFERENCE: 040268/01s1
: CURRENT APPLICATION NUMBER: US/09/660,541
: PRIORITY FILING DATE: 2000-09-12
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/091,219
: PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-05
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PNT201
: PRIOR FILING DATE: EARLIER FILING DATE: 1995-12-18
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 25
: LENGTH: 2232
: TYPE: PRT
: ORGANISM: equine rhinovirus 1
: US-09-660-541-25

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	Query Match Similarity	30.3%	Score 53	DB 2:	length 223;
	Best Local Similarity	42.9%	Pred No. 2	3e+02;	
	Matches	12;	Mismatches	10;	Indels 0; Gaps 0
Qy		6 VPSPTDENSDONSRSSSQASGRTSYS	33		
		: : : : : :			
b		249 VISPEGGQNTNSTRSSSQSGSLGWFS	276		

GenCore version 5.1.7
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OM protein - protein search, using bw model

Run on: March 3, 2006, 14:09:14 ; Search time 15.3741 Seconds
(without alignments)
951.209 Million cell updates/sec

Title: US-10-646-873-45

Perfect score: 175
Sequence: 1 ALPFRVSPDPDSDNSRSSQASGITGSYSVS 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.Main:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	35	3 US-09-050-516-45	Sequence 45, Appl
2	175	100.0	35	4 US-10-278-547-45	Sequence 45, Appl
3	175	100.0	35	4 US-10-646-873-45	Sequence 45, Appl
4	175	100.0	172	4 US-10-106-698-4761	Sequence 47, Appl
5	175	100.0	215	3 US-09-050-516-47	Sequence 47, Appl
6	175	100.0	215	4 US-10-278-547-47	Sequence 47, Appl
7	175	100.0	215	4 US-10-646-873-47	Sequence 47, Appl
8	175	100.0	679	3 US-09-050-516-42	Sequence 42, Appl
9	175	100.0	679	4 US-10-278-547-42	Sequence 42, Appl
10	175	100.0	679	4 US-10-646-873-42	Sequence 42, Appl
11	175	100.0	300	4 US-10-424-599-219343	Sequence 219343, Appl
12	63	36.0	300	4 US-10-425-114-37734	Sequence 37734, A
13	63	36.0	329	4 US-11-097-143-42681	Sequence 42681, A
14	58	33.1	285	4 US-10-437-963-127884	Sequence 127884, A
15	57	32.6	661	3 US-09-801-368-422	Sequence 422, App
16	56.5	32.3	651	4 US-10-425-114-45324	Sequence 45324, A
17	56	32.0	359	4 US-10-437-963-187082	Sequence 187082, A
18	56	32.0	893	4 US-10-156-761-12540	Sequence 12540, A
19	55.5	31.7	346	4 US-10-108-260A-2792	Sequence 2792, Ap
20	55.5	31.7	531	4 US-10-108-260A-2762	Sequence 2762, Ap
21	55	31.4	406	6 US-11-097-143-7425	Sequence 7425, Ap
22	55	31.4	581	4 US-10-425-114-46602	Sequence 46602, A
23	55	31.4	679	4 US-10-282-122A-78228	Sequence 78228, A
24	55	31.4	958	4 US-10-408-765A-1768	Sequence 1768, Ap
25	54.5	31.1	1158	5 US-10-756-149-5250	Sequence 5250, Ap
26	54	30.9	806	4 US-10-437-963-203995	Sequence 203995, A
27	53.5	30.6	583	5 US-10-450-763-35175	Sequence 35175, A

28	53.5	30.6	701	4 US-10-282-122A-62129	Sequence 62129, A
29	53	30.3	300	4 US-10-437-963-150328	Sequence 150328, A
30	53	30.3	437	5 US-10-619-992-17	Sequence 17, Appl
31	53	30.3	448	6 US-11-097-143-2595	Sequence 2595, Ap
32	52.5	30.0	213	6 US-11-097-143-35148	Sequence 35148, A
33	52	29.7	46	5 US-10-450-763-53161	Sequence 53161, A
34	52	29.7	62	4 US-10-424-599-254465	Sequence 254465, A
35	52	29.7	93	4 US-10-767-701-32997	Sequence 32997, A
36	52	29.7	109	4 US-10-425-115-332428	Sequence 332428, A
37	52	29.7	163	4 US-10-425-114-71060	Sequence 71060, A
38	52	29.7	173	4 US-10-437-963-115260	Sequence 115260, A
39	52	29.7	185	4 US-10-424-599-242244	Sequence 242244, A
40	52	29.7	233	4 US-10-425-115-204469	Sequence 204469, A
41	52	29.7	250	3 US-09-978-360A-473	Sequence 473, App
42	52	29.7	252	4 US-10-437-963-141437	Sequence 141437, A
43	52	29.7	275	5 US-10-220-335-295	Sequence 295, App
44	52	29.7	297	5 US-10-220-335-639	Sequence 639, App
45	52	29.7	298	5 US-10-450-763-53184	Sequence 53184, A

ALIGNMENTS

RESULT 1
US-09-050-516-45
Sequence 45, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET INFORMATION: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-45

Query Match 100.0%; Score 175; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPEVESPDPDENSQNSRSSQASGITGSYSVS 35
Db 1 ALPEVESPDPDENSQNSRSSQASGITGSYSVS 35

RESULT 2

US-10-278-547-45
Sequence 45, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.

HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL

COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: No. US20030082619A1e

SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-10-278-547-45

Query Match 100.0%; Score 175; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPEVESPDPDENSQNSRSSQASGITGSYSVS 35
Db 1 ALPEVESPDPDENSQNSRSSQASGITGSYSVS 35

RESULT 3

US-10-646-873-45
Sequence 45, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.

HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL

COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: No. US20040043406A1e

SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-646-873-45

Query Match 100.0%; Score 175; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPPEVFSPTPDNSDONSRSSSQASGITGSYSVS 35
DB 1 ALPPEVFSPTPDNSDONSRSSSQASGITGSYSVS 35

RESULT 4

US-10-106-698-4761
Sequence 4761, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 4761
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: MISC_FEATURE
LOCATION: (55)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (116)
NAME/KEY: MISC_FEATURE
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-699-4761

Query Match 100.0%; Score 175; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPPEVFSPTPDNSDONSRSSSQASGITGSYSVS 35
DB 61 ALPPEVFSPTPDNSDONSRSSSQASGITGSYSVS 95

RESULT 5

US-09-050-516-47
Sequence 47, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA

ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065-US-P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623

TELEX:
INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids

TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e

US-09-050-516-47

Query Match 100.0%; Score 175; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.1e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPPEVFSPTPDNSDONSRSSSQASGITGSYSVS 35
DB 104 ALPPEVFSPTPDNSDONSRSSSQASGITGSYSVS 138

RESULT 6

US-10-278-547-47
Sequence 47, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-278-547-47

Query Match 100.0%; Score 175; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 2,1e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPEVFPSPDPENDQNSRSSSQASGITGSYSVS 35
Db 104 ALPEVFPSPDPENDQNSRSSSQASGITGSYSVS 138

RESULT 7
US-10-646-873-47
Sequence 47, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-AUG-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-646-873-47

Query Match 100.0%; Score 175; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 2,1e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPEVFPSPDPENDQNSRSSSQASGITGSYSVS 35
Db 104 ALPEVFPSPDPENDQNSRSSSQASGITGSYSVS 138

RESULT 8
US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-42

Query Match 100.0%; Score 175; DB 3; Length 679;
Best Local Similarity 100.0%; Pred. No. 8.1e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPPEVFSPTDENSDQNSRSSQASGITGSYSVS 35
Db 568 ALPPEVFSPTDENSDQNSRSSQASGITGSYSVS 602

RESULT 9
US-10-278-547-42
Sequence 42, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065, US, P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-278-547-42

Query Match 100.0%; Score 175; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 8.1e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPPEVFSPTDENSDQNSRSSQASGITGSYSVS 35
Db 568 ALPPEVFSPTDENSDQNSRSSQASGITGSYSVS 602

RESULT 10
US-10-646-873-42
Sequence 42, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065, US, P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-646-873-42

US-10-437-963-127884

Query Match 32.6%; Score 57; DB 4; Length 285;
Best Local Similarity 45.8%; Pred. No. 28;
Matches 11; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 7 RSPPTDENSRRSSQASGITS 30
Db 162 YVPTPEERIESNGIASWAGING 185

RESULT 15

US-09-801-368-422
; Sequence 422, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Call, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methode for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 422
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-422

Query Match 32.6%; Score 57; DB 3; Length 661;
Best Local Similarity 34.1%; Pred. No. 74;
Matches 15; Conservative 9; Mismatches 10; Indels 10; Gaps 1;

QY 2 LRPPEVSPPTDE-----NSDONSRRSSQASGITSYSVS 35
Db 471 MYPVNOSNTPOKVPARLSSRRSHONSTTSLSSNITTSASIS 514

Search completed: March 3, 2006, 14:18:10
Job time : 15.3741 secs

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OM protein - protein search, using SW model

Run on: March 3, 2006, 14:10:51 / Search time 1.66667 Seconds
(without alignments)
420.009 Million cell updates/sec

Title: US-10-646-873-45

Perfect score: 175
Sequence: 1 ALPPEVSPPTDENSQSSQSGITGSYSVS 35

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA.New.*
1: /cgn2_6/pcodata/1/pubppaa/US08_NEW_PUB.pcp.*
2: /cgn2_6/pcodata/1/pubppaa/US06_NEW_PUB.pcp.*
3: /cgn2_6/pcodata/1/pubppaa/US07_NEW_PUB.pcp.*
4: /cgn2_6/pcodata/1/pubppaa/PCT_NEW_PUB.pcp.*
5: /cgn2_6/pcodata/1/pubppaa/US09_NEW_PUB.pcp.*
6: /cgn2_6/pcodata/1/pubppaa/US10_NEW_PUB.pcp.*
7: /cgn2_6/pcodata/1/pubppaa/US11_NEW_PUB.pcp.*
8: /cgn2_6/pcodata/1/pubppaa/US60_NEW_PUB.pcp.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54.5	31.1	1158	US-11-075-646-6	Sequence 6, Appl
2	52	29.7	250	US-09-978-360A-473	Sequence 473, App
3	52	29.7	339	US-11-087-099-1355	Sequence 1355, App
4	51.5	29.4	266	US-11-054-515-3229	Sequence 3229, App
5	51	29.1	227	US-10-991-285-872	Sequence 872, App
6	49.5	28.3	571	US-11-072-512-2709	Sequence 2709, App
7	49	28.0	361	US-10-995-561-612	Sequence 612, App
8	49	28.0	361	US-11-130-206-6	Sequence 6, Appl
9	49	28.0	377	US-10-517-939-274	Sequence 274, App
10	49	28.0	395	US-10-995-561-614	Sequence 614, App
11	49	28.0	425	US-10-995-561-616	Sequence 616, App
12	49	28.0	435	US-10-995-561-611	Sequence 611, App
13	49	28.0	535	US-10-995-561-610	Sequence 610, App
14	49	28.0	631	US-10-995-561-617	Sequence 617, App
15	49	28.0	699	US-11-130-206-4	Sequence 4, Appl
16	49	28.0	700	US-11-130-206-2	Sequence 2, Appl
17	49	28.0	742	US-10-995-561-615	Sequence 615, App
18	49	28.0	742	US-10-995-561-618	Sequence 618, App
19	49	28.0	742	US-11-169-041-184	Sequence 184, App
20	49	28.0	742	US-11-072-175-176	Sequence 176, App
21	48	27.4	265	US-10-799-749-78	Sequence 78, Appl
22	48	27.4	513	US-11-087-099-9245	Sequence 9245, App
23	48	27.4	594	US-10-131-826A-10	Sequence 10, Appl
24	48	27.4	594	US-10-973-115B-10	Sequence 10, Appl
25	48	27.4	743	US-10-485-517-351	Sequence 351, App

26	48	27.4	877	US-10-485-517-200	Sequence 200, App
27	47.5	27.1	1161	US-11-075-646-8	Sequence 8, Appl
28	47	26.9	133	US-10-793-626-1924	Sequence 1924, App
29	47	26.9	296	US-10-714-887-226	Sequence 226, App
30	47	26.9	380	US-11-024-959-339	Sequence 339, App
31	47	26.9	646	US-11-087-099-10725	Sequence 10725, App
32	47	26.9	698	US-11-087-099-8952	Sequence 8952, App
33	47	26.9	698	US-11-087-099-3341	Sequence 9341, App
34	47	26.9	1045	US-11-055-892-100	Sequence 100, Appl
35	47	26.9	1717	US-11-192-967-2	Sequence 2, Appl
36	47	26.9	1717	US-11-193-715-2	Sequence 2, Appl
37	46.5	26.6	159	US-11-038-676-4	Sequence 4, Appl
38	46.5	26.6	964	US-11-089-551A-30	Sequence 30, Appl
39	46	26.3	467	US-11-089-551A-304	Sequence 304, App
40	46	26.3	7102	US-11-143-980-48	Sequence 48, Appl
41	45.5	26.0	421	US-11-087-099-6078	Sequence 6078, App
42	45.5	26.0	581	US-11-072-512-2804	Sequence 2804, App
43	45.5	26.0	588	US-11-072-512-3053	Sequence 3053, App
44	45.5	26.0	769	US-11-188-743-15	Sequence 15, Appl
45	45.5	26.0	880	US-11-072-512-2834	Sequence 2834, App

ALIGNMENTS

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RESULT 1
US-11-075-646-6
; Sequence 6, Application US/11075646
; Publication No. US20050261223A1
; GENERAL INFORMATION:
; APPLICANT: Czech, Michael P.
; APPLICANT: Powell, Aimee
; APPLICANT: Guilherme, Adilson L.
; APPLICANT: Chertnick, Andrew D.
; TITLE OF INVENTION: R1P140 REGULATION OF DIABETES
; FILE REFERENCE: 17738-009001
; CURRENT APPLICATION NUMBER: US/11/075,646
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,677
; PRIOR FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-646-6

Query Match      31.1% Score 54.5; DB 7; Length 1158;
Best Local Similarity 41.2%; Pred. No. 15;
Matches 14; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY      1 ALPPEVSPPTDENSQSSQSGITGSYSVS 33
Db      403 SIFESSTPTTIDRYSDDNPFRTDSSQSDSSYSVS 436

RESULT 2
US-09-978-360A-473
; Sequence 473, Application US/09978360A
; Publication No. US20060009633A8
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclet, Aymeric
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56, US4, CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
```

```
;; PRIOR APPLICATION NUMBER: US 60/069,957
;; PRIOR FILING DATE: 1997-12-17
;; PRIOR APPLICATION NUMBER: US 60/074,121
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: US 60/081,563
;; PRIOR FILING DATE: 1998-04-13
;; PRIOR APPLICATION NUMBER: US 60/096,116
;; PRIOR FILING DATE: 1998-08-10
;; PRIOR APPLICATION NUMBER: US 60/099,273
;; PRIOR FILING DATE: -09-04
;; PRIOR APPLICATION NUMBER: US 09/191,997
;; PRIOR FILING DATE: 1998-11-13
;; PRIOR APPLICATION NUMBER: US 09/215,435
;; PRIOR FILING DATE: 1998-12-17
;; PRIOR APPLICATION NUMBER: PCT/IB98/02122
;; PRIOR FILING DATE: 1998-12-17
;; PRIOR APPLICATION NUMBER: US 09/247,155
;; PRIOR FILING DATE: 1999-02-09
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 810
;; SOFTWARE: Patent.pm
;; SEQ ID NO 473
;; LENGTH: 250
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: -85...-1
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (-30)
;; OTHER INFORMATION: unknown
US-09-978-360A-473
```

```
Query Match          29.7%; Score 52; DB 5; Length 250;
Best Local Similarity 33.3%; Pred. No. 5.5;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;
```

```
OY      5 EVFSPPTDSDNSRRSSQASGRTGSYSV 34
Db      216 ELREPAFGTNRORPSKSKAGKGLRGSAKI 245
```

```
RESULT 3
US-11-087-099-1355
; Sequence 1355, Application US/11087099
; Publication No. US20060041961A1.
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and uses for plant improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1355
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Colletotrichum gloeosporioides f. sp. malvae
US-11-087-099-1355
```

```
Query Match          29.7%; Score 52; DB 7; Length 339;
Best Local Similarity 48.0%; Pred. No. 7.9;
Matches 12; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
```

```
OY      3 FPEVFSPTDSDNSRRSSQASG 27
Db      306 FPEVVTPTPTVYSAASRSQSPQASG 330
```

```
RESULT 4
US-11-054-515-3229
; Sequence 3229, Application US/11054515
; Publication No. US20050255532A1
```

```
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
;; FILE REFERENCE: PE523P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/580,347
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: 10/293,418
;; PRIOR FILING DATE: 2002-11-14
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 3229
;; LENGTH: 266
;; TYPE: PRT
;; ORGANISM: Human sapiens
US-11-054-515-3229
```

```
Query Match          29.4%; Score 51.5; DB 7; Length 266;
Best Local Similarity 50.0%; Pred. No. 7;
Matches 14; Conservative 2; Mismatches 9; Indels 3; Gaps 2;
```

```
OY      9 PTPDE-NSDNRSSSSQASG--ITGSYS 33
Db      118 PAPGEGNSSONSRNKRAVQGPETGYSYT 145
```

```
RESULT 5
US-10-991-285-872
; Sequence 872, Application US/10991285
; Publication No. US20060041962A1
; GENERAL INFORMATION:
; APPLICANT: VIAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW
; TITLE OF INVENTION: GENES AND USES THEREOF TO MODULATE SECONDARY METABOLITE BIOSYNTHESIS
; FILE REFERENCE: DIN/SEM/V116
; CURRENT APPLICATION NUMBER: US/10/991,285
; CURRENT FILING DATE: 2004-11-16
; PRIOR APPLICATION NUMBER: EP02076973.3
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 901
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 872
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: MAP3
US-10-991-285-872
```

```
Query Match          29.1%; Score 51; DB 6; Length 227;
Best Local Similarity 50.0%; Pred. No. 6.8;
Matches 12; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
```

```
OY      3 FPEVFSPTDSDNSRRSSSSQAS 26
Db      30 FSEIFSPMSSSNLNPNSPSSSFGS 53
```



```
RESULT 6
US-11-072-512-2709
; Sequence 2709, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHITAKA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKIKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2709
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2709

Query Match      28.3%; Score 49.5; DB 7; Length 571;
Best Local Similarity 46.9%; Pred. No. 32;
Matches 15; Conservative 4; Mismatches 10; Indels 3; Gaps 2;

QY 4 PEVFSPTPDNSDONSRSQASGITGSY 35
DB 359 PE--SPSPAPSLLENHRPGSQTSHTSS--SVS 387

RESULT 7
US-10-995-561-612
; Sequence 612, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE. METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 612
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-612

Query Match      28.0%; Score 49; DB 6; Length 361;
Best Local Similarity 37.9%; Pred. No. 22;
Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 4 PEVFSPTPDNSDONSRSQASGITGSY 32
DB 165 PEDYPSNPTDDVSSGSSSERSSTSGCY 193

RESULT 8
US-11-130-206-6
; Sequence 6, Application US/11130206
; Publication No. US20060019340A1
; GENERAL INFORMATION:
; APPLICANT: Naor, David
; APPLICANT: Nedvetzki, Shlomo
; APPLICANT: Golan, Itzhak
; TITLE OF INVENTION: CD44 POLYPEPTIDES, POLYNUCLEOTIDES ENCODING SAME, ANTIBODIES
; TITLE OF INVENTION: DIRECTED THERAGAGINST AND METHOD OF USING SAME FOR DIAGNOSING AN
; FILE REFERENCE: 29306
; CURRENT APPLICATION NUMBER: US/11/130,206
; CURRENT FILING DATE: 2005-05-17
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-130-206-6

Query Match      28.0%; Score 49; DB 7; Length 361;
Best Local Similarity 37.9%; Pred. No. 22;
Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 4 PEVFSPTPDNSDONSRSQASGITGSY 32
DB 165 PEDYPSNPTDDVSSGSSSERSSTSGCY 193

RESULT 9
US-10-517-939-274
; Sequence 274, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Bateghallian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 274
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample.
; NAME/KEY: SIGNAL
; LOCATION: (1)....(74)
US-10-517-939-274

Query Match      28.0%; Score 49; DB 6; Length 377;
Best Local Similarity 44.4%; Pred. No. 23;
```

```
Matches 12; Conservative 3; Mismatches 12; Indels 0; Gaps 0;
Qy 9 PTPENDNSRRSSQASGITSYSV 35
Db 34 PPDIGSSTSSSSSSSSSSSSSS 60

RESULT 10
US-10-995-561-614
; Sequence 614, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 614
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-614

Query Match 28.0%; Score 49; DB 6; Length 395;
Best Local Similarity 37.9%; Pred. No. 24;
Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
Qy 4 PEVSPTPENDNSRRSSQASGITSY 32
Db 165 PEDIYPSNPTDDVSSGSSSRSSTSGY 193

RESULT 11
US-10-995-561-616
; Sequence 616, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 616
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-616

Query Match 28.0%; Score 49; DB 6; Length 425;
Best Local Similarity 37.9%; Pred. No. 27;
Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
Qy 4 PEVSPTPENDNSRRSSQASGITSY 32
Db 165 PEDIYPSNPTDDVSSGSSSRSSTSGY 193

RESULT 12
US-10-995-561-611
; Sequence 611, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
```

```
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 611
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-611

Query Match 28.0%; Score 49; DB 6; Length 493;
Best Local Similarity 37.9%; Pred. No. 32;
Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
Qy 4 PEVSPTPENDNSRRSSQASGITSY 32
Db 165 PEDIYPSNPTDDVSSGSSSRSSTSGY 193

RESULT 13
US-10-995-561-610
; Sequence 610, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 610
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-610

Query Match 28.0%; Score 49; DB 6; Length 535;
Best Local Similarity 37.9%; Pred. No. 35;
Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
Qy 4 PEVSPTPENDNSRRSSQASGITSY 32
Db 165 PEDIYPSNPTDDVSSGSSSRSSTSGY 193

RESULT 14
US-10-995-561-617
; Sequence 617, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 617
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-617

Query Match 28.0%; Score 49; DB 6; Length 691;
Best Local Similarity 37.9%; Pred. No. 47;
Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
```

Oy 4 PEVFSPTPDNSDNRSSSSQASGITGSY 32
 DB 165 PEDIVPSNPTDDVDVSSGSSSRSSTSGGY 193

RESULT 15

US-11-130-206-4
 ; Sequence 4, Application US/11130206
 ; Publication No. US20060019340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Naor, David
 ; APPLICANT: Nedvetzki, Shlomo
 ; APPLICANT: Golan, Itzhak
 ; TITLE OF INVENTION: CD44 POLYPEPTIDES, POLYNUCLEOTIDES ENCODING SAME, ANTIBODIES
 ; TITLE OF INVENTION: DIRECTED THERAGAINS AND METHOD OF USING SAME FOR DIAGNOSING AN
 ; TITLE OF INVENTION: TREATING INFLAMMATORY DISEASES
 ; FILE REFERENCE: 29306
 ; CURRENT APPLICATION NUMBER: US/11/130,206
 ; CURRENT FILING DATE: 2005-05-17
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 4
 ; LENGTH: 699
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-130-206-4

Query Match 28.0%; Score 49; DB 7; Length 699;
 Best Local Similarity 37.9%; Pred. No. 48;
 Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Oy 4 PEVFSPTPDNSDNRSSSSQASGITGSY 32
 DB 165 PEDIVPSNPTDDVDVSSGSSSRSSTSGGY 193

Search completed: March 3, 2006, 14:19:05
 Job time : 2.66667 secs

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OM protein - protein search, using sw model

Run on: March 3, 2006, 13:19:17 ; Search time 17.6385 Seconds
(without alignments)
822.038 Million cell updates/sec

Title: US-10-646-873-46

Perfect score: 176
Sequence: 1 EDSVDSAPPGQRKEQWYAGINPSDGINSEVLE 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003s.*
7: geneseqp2004s.*
8: geneseqp2005s.*
9: geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	100.0	33	2 AAW79680	AAW79680 Synthetic
2	176	100.0	33	2 AAE07323	AAE07323 Human CS
3	176	100.0	33	6 ADA26383	ADA26383 Synthetic
4	176	100.0	33	8 ADN17176	ADN17176 CS198 pep
5	172	97.7	172	4 AAG73987	AAG73987 Human COL
6	171	97.2	215	2 AAW79681	AAW79681 Human CS1
7	171	97.2	215	4 AAE07324	AAE07324 Human CS
8	171	97.2	215	6 ADA26384	ADA26384 Synthetic
9	171	97.2	215	8 ADN17177	ADN17177 CS198 pro
10	171	97.2	679	2 AAW79676	AAW79676 Human CS1
11	171	97.2	679	2 AAE07319	AAE07319 Human CS
12	171	97.2	679	4 AAW78590	AAW78590 Human pro
13	171	97.2	679	6 ADA26379	ADA26379 Predicted
14	171	97.2	679	8 ADN17172	ADN17172 CS198 pro
15	171	97.2	692	8 ADX97562	ADX97562 Pancreatic
16	168	95.5	679	7 AAG14341	AAG14341 Human NC2
17	166	94.3	679	7 AAM79574	AAM79574 Human pro
18	89	50.6	43	8 ABO60042	ABO60042 Human gen
19	57	32.4	124	2 AAY50146	AAY50146 Antibody
20	57	32.4	124	2 AAY50149	AAY50149 Antibody
21	57	32.4	124	2 AAY50148	AAY50148 Antibody
22	57	32.4	124	2 AAY50147	AAY50147 Antibody
23	57	32.4	124	2 AAY50150	AAY50150 Antibody
24	57	32.4	124	6 ABB98753	ABB98753 Human res

25	57	32.4	124	6 ABB98754	ABB98754 Human res
26	57	32.4	124	6 ABB98752	ABB98752 Human res
27	57	32.4	124	6 ABB98751	ABB98751 Human res
28	57	32.4	124	6 ABB98750	ABB98750 Human res
29	57	32.4	432	2 AAO17498	AAO17498 Antibody
30	57	32.4	472	2 AAY50166	AAY50166 Human res
31	57	32.4	480	5 AAO17495	AAO17495 TNF-belec
32	57	32.4	601	5 AAM49760	AAM49760 TNF-belec
33	57	32.4	614	5 AAO17494	AAO17494 Antibody
34	57	32.4	658	5 AAM49759	AAM49759 TNF-belec
35	56	31.8	142	5 ADX34147	ADX34147 Novel hum
36	56	31.8	483	9 AEB45520	AEB45520 Human Cdc
37	56	31.8	484	8 ADE28340	ADE28340 Human KPP
38	56	31.8	523	2 AAR37493	AAR37493 Cdc25A. 3
39	56	31.8	523	2 AAR66608	AAR66608 Human cdc
40	56	31.8	523	2 AAR98212	AAR98212 Human cdc
41	56	31.8	523	2 AAW59135	AAW59135 Human cdc
42	56	31.8	523	2 AAW37986	AAW37986 Amino aci
43	56	31.8	523	3 AAY54905	AAY54905 Human cdc
44	56	31.8	523	4 AAB20263	AAB20263 Human Cdc
45	56	31.8	523	4 AAB81064	AAB81064 Human Cdc

ALIGNMENTS

RESULT 1
AAW79680
AAW79680 standard; protein; 33 AA.
XX
XX AAW79680;
XX
XX 11-JAN-1999 (first entry)
XX
XX Synthetic CS198 derived peptide #4.
XX
XX Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
XX human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
XX gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
XX pancreatitis.
XX
XX Synthetic.
XX
XX OS
XX
XX EN
XX WO9844159-A1.
XX
XX 08-OCT-1998.
XX
XX 30-MAR-1998; 98WO-US006251.
XX
XX 31-MAR-1997; 97US-00828855.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Billing-Wedel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvill JD;
XX Roberts-Rapp L, Russell JC, Stroepe SD;
XX WPI; 1998-542714/46.
XX
XX New gastrointestinal polynucleotides, CS198, and their detection - used
XX for developing products for the diagnosis and treatment of
XX gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
XX
XX Claim 26; Page 103; 127pp; English.
XX
XX AAW79677-W79680 are synthetic CS198 derived peptide fragments which are
XX used in a method to detect the presence of a target human CS198
XX polynucleotide in a test sample. The CS198 gene is useful as a marker for
XX gastrointestinal (GI) tract disorders. The methods and products can be
XX used in detecting, diagnosing, staging, monitoring, prognosticating,
XX preventing or treating, or determining the predisposition to diseases and
XX conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
XX gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative

CC colitis, and pancreatitis
XX
SQ Sequence 33 AA;
Query Match 100.0%; Score 176; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EDSVDSAPPGQRKEQWYAGINPSDGINSEVLE 33
Db 1 EDSVDSAPPGQRKEQWYAGINPSDGINSEVLE 33
RESULT 2
AAE07323
ID AAE07323 standard; peptide; 33 AA.
AC AAE07323;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human CS 198 peptide #4.
XX
KM CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
KM gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
KM Barrett's oesophagus; gene therapy; drug screening; human.
OS Homo sapiens.
XX
PN US2001010904-A1.
XX
PD 02-AUG-2001.
XX
PF 30-MAR-1998; 98US-00050516.
XX
PR 31-MAR-1997; 97US-00828855.
XX
PA (BILL/) BILLINGEL P. A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T. L.
PA (FRIE/) FRIEDMAN P. N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E. N.
PA (HAYD/) HAYDEN M.
PA (HODG/) HODGES S. C.
PA (KLAS/) KLAAS M. R.
PA (KRAT/) KRATOCHVIL J. D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUS/) RUSSELL J. C.
PA (STRO/) STROUPE S. D.
XX
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
PI Granados EN, Hayden M, Hodges SC, Klaas MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
DR WPI; 2001-496163/54.
XX
PT Detecting the presence of target CS 198 polynucleotide, useful for
PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
PT contacting test sample with at least one CS 198-specific polynucleotide.
XX
PS Claim 17; Page 52; 68pp; English.
XX
CC The invention relates to a method of detecting the presence of a target
CC CS 198 polynucleotide comprising contacting the test sample with at least
CC one CS 198-specific polynucleotide. The method is useful for detecting
CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
CC treating or determining predisposition to diseases and conditions of the
CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
CC polypeptides are useful as standards or reagents in diagnostic

CC immunoassays, as components or as target sites for various therapies.
CC Antibodies directed against at least one epitope contained within these
CC polypeptides are useful as delivery agents for therapeutic agents. In
CC diagnostic tests and for screening for conditions or diseases associated
CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
CC for the generation of chimeric antibodies for therapeutic use. The CS 198
CC polynucleotide is also useful in gene therapy and drug screening. The
CC method of the invention provides an alternative, non-surgical diagnostic
CC method capable of detecting early stage GI tract disease such as cancer.
CC The present sequence is a peptide derived from human CS 198 polypeptide
CC consensus sequence
XX
SQ Sequence 33 AA;
Query Match 100.0%; Score 176; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EDSVDSAPPGQRKEQWYAGINPSDGINSEVLE 33
Db 1 EDSVDSAPPGQRKEQWYAGINPSDGINSEVLE 33
RESULT 3
ADA26383
ID ADA26383 standard; protein; 33 AA.
AC ADA26383;
XX
DT 20-NOV-2003 (first entry)
XX
DE Synthetic peptide based on CS198 protein #4.
XX
KM CS198; cancer diagnosis; cancer staging; cancer monitoring;
KM cancer prognosticating; cancer prevention; cancer;
KM gastrointestinal tract disorder; gene therapy.
XX
OS Synthetic;
XX
PN US2003082619-A1.
XX
PD 01-MAY-2003.
XX
PF 23-OCT-2002; 2002US-00278547.
XX
PR 31-MAR-1997; 97US-00828855.
PR 30-MAR-1998; 98US-00050516.
XX
PA (BILL/) BILLINGEL P. A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T. L.
PA (FRIE/) FRIEDMAN P. N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E. N.
PA (HAYD/) HAYDEN M. A.
PA (HODG/) HODGES S. C.
PA (KLAS/) KLAAS M. R.
PA (KRAT/) KRATOCHVIL J. D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUS/) RUSSELL J. C.
PA (STRO/) STROUPE S. D.
XX
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
PI Granados EN, Hayden M, Hodges SC, Klaas MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
DR WPI; 2003-596961/56.
XX
PT Detecting the presence of a target CS198 polynucleotide in a test sample
PT comprises contacting the sample with a CS198 specific polynucleotide and
PT detecting the presence of the target CS198 polynucleotide in the test
PT sample.
XX

PS Claim 17, Page 52, 67pp; English.

XX The invention describes a method of detecting the presence of a target
CC CS198 polynucleotide in a test sample. The method comprises contacting
CC the test sample with at least one CS198 specific polynucleotide or its
CC complement, and detecting the presence of the target CS198 polynucleotide
CC in the test sample, where the CS198-specific polynucleotide has at least
CC 50% identity to a polynucleotide having any of the 27 fully defined
CC sequences of 34-2894 bp (SI-27) given in the specification, or their
CC fragments or complements. The composition and methods are useful in
CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
CC or determining the predisposition of an individual to, diseases and
CC conditions of the gastrointestinal tract, e.g. cancer and in gene
CC therapy. This is the amino acid sequence of a synthetic peptide based on
CC the predicted human CS198 protein sequence derived from the CS198
CC consensus sequence shown in seq id 27.

XX Sequence 33 AA:

SO Query Match 100.0%; Score 176; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDSVDSAPPGRKKEQWYAGINPSDGINSEVLE 33
DB 1 EDSVDSAPPGRKKEQWYAGINPSDGINSEVLE 33

RESULT 4

ID ADN17176 standard; peptide, 33 AA.

XX ADN17176;

XX 17-JUN-2004 (first entry)

DE CS198 peptide #4.

XX Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.

XX Unidentified.

XX US2004043406-A1.

XX 04-MAR-2004.

XX 22-AUG-2003; 2003US-00646873.

XX 31-MAR-1997; 97US-00828855.

XX 30-MAR-1998; 98US-00050516.

XX (BILL/) BILLINGEL P A.

XX (COHE/) COHEN M.

XX (COLP/) COLPITTS T L.

XX (FRIE/) FRIEDMAN P N.

XX (GORD/) GORDON J.

XX (GRAN/) GRANADOS E N.

XX (HAYD/) HAYDEN M A.

XX (HODG/) HODGES S C.

XX (KLAS/) KLAS M R.

XX (KRAT/) KRATOCHVIL J D.

XX (ROBE/) ROBERTS-RAPP L.

XX (RUSSE/) RUSSELL J C.

XX (STRO/) STROUPE S D.

XX Billingsel P, Cohen M, Colpitts T, Friedman P, Gordon J,
PI Grandos EN, Hayden MA, Hodges SC, Kلاس MK, Kratochvil JD,
PI Roberts-Rapp L, Russell JC, Stroupe SD;
DR WPI, 2004-313754/29.

XX Diagnosing diseases such as cancer of the gastrointestinal tract, by
PT detecting aberrant expression or activity of the CS198 polypeptide, and

PT associated treatment methods.

XX Claim 17, SEQ ID NO 46; 67pp; English.

XX The invention relates to reagents and methods for detecting diseases of
CC the gastrointestinal (GI) tract. The method involves detecting the
CC presence of target CS198 polynucleotide in the test sample. The methods
CC and compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the CS198 polypeptide, such as cancer
CC of the gastrointestinal tract. These are also useful in gene therapy. The
CC present sequence is a CS198 peptide used to illustrate the method of the
CC invention.

XX Sequence 33 AA:

SO Query Match 100.0%; Score 176; DB 8; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDSVDSAPPGRKKEQWYAGINPSDGINSEVLE 33
DB 1 EDSVDSAPPGRKKEQWYAGINPSDGINSEVLE 33

RESULT 5

ID AAG73987 standard; protein, 172 AA.

XX AAG73987;

XX 03-SEP-2001 (first entry)

XX Human colon cancer antigen protein SEQ ID NO:4751.

XX Human colon cancer antigen; diagnosis; detection;

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;

XX Colorectal carcinoma.

XX Homo sapiens.

XX WO200122920-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000WO-US026524.

XX 29-SEP-1999; 99US-0157137P.

XX 03-NOV-1999; 99US-0163280P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Birse CE, Rosen CA;
PI WPI, 2001-235357/24.
DR N-PSDB; AAH33418.

XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.

XX Claim 11, Page 6550-6551, 9803pp; English.

XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patient's own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P

CC can be used in the prevention, diagnosis and treatment of colorectal
 CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
 CC sequences used in the exemplification of the present invention. N.B.
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027
 CC to 1052, 7921 and 7922

XX Sequence 172 AA;

Query Match 97.7%; Score 172; DB 4; Length 172;
 Best Local Similarity 97.0%; Pred. No. 1.2e-15;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Gy 1 EDVDSAPPGQRKKEQWYAGINPSDGINSEVLE 33
 |||
 Db 114 EDVDSAPPGQRKKEQWYAGINPSDGINSEVLE 146

RESULT 6
 AAW79681

ID AAW79681 standard; protein; 215 AA.

XX AAW79681;

DT 11-JAN-1999 (first entry)

XX Human CS198 protein C-terminal.

XX Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
 KW human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
 KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
 KW pancreatitis.

XX Homo sapiens.

XX MO9844159-A1.

XX 08-OCT-1998.

XX 30-MAR-1998; 98WO-US006251.

XX 31-MAR-1997; 97US-00828855.

XX (ABBO) ABBOTT LAB.

PI Billing-Medel PA, Cohen M, Colpitta TL, Friedman PV, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI, 1998-542714/46.

DR WPI, 1998-542714/46.

PT New gastrointestinal polynucleotides, CS198, and their detection - used
 PT for developing products for the diagnosis and treatment of
 PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.

XX Claim 26; Page 103; 127pp; English.

XX This sequence represents the C-terminal of the human CS198 protein which
 CC is used in a method to detect the presence of a target CS198
 CC polynucleotide in a test sample. The CS198 gene is useful as a marker for
 CC gastrointestinal (GI) tract disorders. The methods and products can be
 CC used in detecting, diagnosing, staging, monitoring, prognosticating,
 CC preventing or treating, or determining the predisposition to diseases and
 CC conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
 CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative
 CC colitis, and pancreatitis

XX Sequence 215 AA;

Query Match 97.2%; Score 171; DB 2; Length 215;
 Best Local Similarity 97.0%; Pred. No. 2.2e-15;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Gy 1 EDVDSAPPGQRKKEQWYAGINPSDGINSEVLE 33
 |||
 Db 157 EDPVDSAPPGQRKKEQWYAGINPSDGINSEVLE 189

RESULT 7
 AAE07324
 ID AAE07324 standard; protein; 215 AA.

XX AAE07324;

DT 06-NOV-2001 (first entry)

XX Human CS 198 protein C-terminal portion.

XX CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
 KW gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
 KW Barrett's oesophagus; gene therapy; drug screening; human.

XX Homo sapiens.

XX US2001010904-A1.

XX 02-AUG-2001.

XX 30-MAR-1998; 98US-00050516.

XX 31-MAR-1997; 97US-00828855.

XX (BILL) BILLINGEL P A.

PA (COHE) COHEN M.

PA (COLP) COLPITTS T L.

PA (FRIE) FRIEDMAN P N.

PA (GORD) GORDON J E N.

PA (GRAN) GRANADOS E N.

PA (HAYD) HAYDEN M.

PA (HODG) HODGES S C.

PA (KLAS) KLAS M R.

PA (KRAT) KRATOCHVIL J D.

PA (ROBE) ROBERTS-RAPP L.

PA (RUS) RUSSELL J C.

PA (STRO) STROUPE S D.

XX Billingel PA, Cohen M, Colpitta TL, Friedman PV, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI, 2001-496163/54.

PT Detecting the presence of target CS 198 polynucleotide, useful for
 PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
 PT contacting test sample with at least one CS 198-specific polynucleotide.

XX Claim 17; Page 52-53; 68pp; English.

XX The invention relates to a method of detecting the presence of a target
 CC CS 198 polynucleotide comprising contacting the test sample with at least
 CC one CS 198-specific polynucleotide. The method is useful for detecting
 CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
 CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
 CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
 CC treating or determining predisposition to diseases and conditions of the
 CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
 CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
 CC polypeptides are useful as standards or reagents in diagnostic
 CC immunoassays, as components or as target sites for various therapies.
 CC Antibodies directed against at least one epitope contained within these
 CC polypeptides are useful as delivery agents for therapeutic agents, in
 CC diagnostic tests and for screening for conditions or diseases associated
 CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
 CC for the generation of chimeric antibodies for therapeutic use. The CS 198
 CC polynucleotide is also useful in gene therapy and drug screening. The
 CC method of the invention provides an alternative, non-surgical diagnostic

CC aberrant expression or activity of the CS198 polypeptide, such as cancer
 CC of the gastrointestinal tract. These are also useful in gene therapy. The
 CC present sequence is a CS198 protein used to illustrate the method of the
 CC invention.

XX Sequence 215 AA;

Query Match 97.2%; Score 171; DB 8; Length 215;
 Best Local Similarity 97.0%; Pred. No. 2.2e-15;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDSVDSAPPQGRKKEQWYAGINPSDGINSEVLE 33

Db 157 EDPVDSAPPQGRKKEQWYAGINPSDGINSEVLE 189

RESULT 10
 AAW79676 standard; protein; 679 AA.

XX AAW79676;

XX 11-JAN-1999 (first entry)

XX Human CS198 protein.

XX Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
 KW human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
 KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
 KW pancreatitis.

XX Homo sapiens.

XX WO9844159-A1.

XX 08-OCT-1998.

XX 30-MAR-1998; 98WO-US006251.

XX 31-MAR-1997; 97US-00828855.

XX (ABBO) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TV, Friedman PV, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klaas MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI; 1998-542714/46.

XX New gastrointestinal polynucleotides, CS198, and their detection - used
 PT for developing products for the diagnosis and treatment of
 PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.

XX Claim 26; Page 100-102; 127pp; English.

XX This sequence represents the human CS198 protein which is used in a
 CC method to detect the presence of a target CS198 polynucleotide in a test
 CC sample. The CS198 gene is useful as a marker for gastrointestinal (GI)
 CC tract disorders. The methods and products can be used in detecting,
 CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
 CC or determining the predisposition to diseases and conditions of the GI
 CC tract, such as GI tract cancer, Barrett's oesophagus, gastric ulcer,
 CC gastritis, leiomyoma, polyps, Crohn's disease, ulcerative colitis, and
 CC pancreatitis

XX Sequence 679 AA;

Query Match 97.2%; Score 171; DB 2; Length 679;
 Best Local Similarity 97.0%; Pred. No. 7.7e-15;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDSVDSAPPQGRKKEQWYAGINPSDGINSEVLE 33

Db 621 EDPVDSAPPQGRKKEQWYAGINPSDGINSEVLE 653

RESULT 11

XX AAE07319 standard; protein; 679 AA.

XX AAE07319;

XX 06-NOV-2001 (first entry)

XX Human CS 198 protein.

XX CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
 KW gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
 KW Barrett's oesophagus; gene therapy; drug screening; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 353 /note="Encoded by CGGN"

XX US2001010904-A1.

XX 02-AUG-2001.

XX 30-MAR-1998; 98US-00050516.

XX 31-MAR-1997; 97US-00828855.

XX (BIL/) BILLINGEL P A.

XX (COHE/) COHEN M.

XX (COLP/) COLPITTS T L.

XX (FRIE/) FRIEDMAN P N.

XX (GORD/) GORDON J.

XX (GRAN/) GRANADOS E N.

XX (HAYD/) HAYDEN M.

XX (HODG/) HODGES S C.

XX (KLAAS/) KLAAS M R.

XX (KRAT/) KRATOCHVIL J D.

XX (ROBE/) ROBERTS-RAPP L.

XX (RUSS/) RUSSELL J C.

XX (STRO/) STROUPE S D.

XX Billingel PA, Cohen M, Colpitts TV, Friedman PV, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klaas MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI; 2001-496163/54.

XX N-PSDB; AAD13637.

XX Detecting the presence of target CS 198 polynucleotide, useful for
 PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
 PT contacting test sample with at least one CS 198-specific polynucleotide.

XX Claim 17; Page 49-51; 68pp; English.

XX The invention relates to a method of detecting the presence of a target
 CC CS 198 polynucleotide comprising contacting the test sample with at least
 CC one CS 198-specific polynucleotide. The method is useful for detecting
 CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
 CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
 CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
 CC treating or determining predisposition to diseases and conditions of the
 CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
 CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
 CC polypeptides are useful as standards or reagents in diagnostic
 CC immunoassays, as components or as target sites for various therapies.
 CC Antibodies directed against at least one epitope contained within these
 CC polypeptides are useful as delivery agents for therapeutic agents, in
 CC diagnostic tests and for screening for conditions or diseases associated
 CC with CS 198, particularly cancer. Monoclonal antibodies may also be used

for the generation of chimeric antibodies for therapeutic use. The CS 198 polynucleotide is also useful in gene therapy and drug screening. The method of the invention provides an alternative, non-surgical diagnostic method capable of detecting early stage GI tract disease such as cancer. The present sequence is human CS 198 polypeptide

Sequence 679 AA;

Query Match 97.2%; Score 171; DB 4; Length 679;
Best Local Similarity 97.0%; Pred. No. 7.7e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 EDSVDSAPPQKKEQWYAGINPSDGINSEVLE 33
621 EDPVDSAPPQKKEQWYAGINPSDGINSEVLE 653

RESULT 12

AA078590 standard; protein; 679 AA.

AA078590;

06-NOV-2001 (first entry)

Human protein SEQ ID NO 1252.

Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.

Home sapiens.

WO200157190-A2.

09-AUG-2001.

05-FEB-2001; 2001WO-US004098.

03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00620325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00663561.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y, Zhao Q, Wang J, Zhang J, Ren F, Chen R, Wang ZM, Xue AJ, Yang Y, Wejhrman T, Goodrich R;

WPI; 2001-476283/51.
N-PSDB; AAKS1723.

Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.

Claim 20; Page 3512-3514; 6221pp; English.

The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AA078323-AA080302) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and

inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AA080020) are omitted as the relevant pages from the sequence listing were missing at the time of publication

Sequence 679 AA;

Query Match 97.2%; Score 171; DB 4; Length 679;
Best Local Similarity 97.0%; Pred. No. 7.7e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 EDSVDSAPPQKKEQWYAGINPSDGINSEVLE 33
621 EDPVDSAPPQKKEQWYAGINPSDGINSEVLE 653

RESULT 13

ADA26379 standard; protein; 679 AA.

ADA26379;

20-NOV-2003 (first entry)

Predicted amino acid sequence of the CS198 protein.

CS198; cancer diagnosis; cancer staging; cancer monitoring; cancer prognosticating; cancer prevention; cancer; gastrointestinal tract disorder; gene therapy.

Synthetic.

US2003082619-A1.

01-MAY-2003.

23-OCT-2002; 2002US-00278547.

31-MAR-1997; 97US-00828855.
PR 30-MAR-1998; 98US-00050516.

(BILL/) BILLINGEL P A.
(COHE/) COHEN M.
(COLP/) COLPITTS T L.
(FRIE/) FRIEDMAN P N.
(GORD/) GORDON J.
(GRAN/) GRANADOS E N.
(HAYD/) HAYDEN M A.
(HODG/) HODGES S C.
(KLAS/) KLAS M R.
(KRAT/) KRATOCHVIL J D.
(ROBE/) ROBERTS-RAPP L.
(RUSSE/) RUSSELL J C.
(STRO/) STROUPE S D.

Billingel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN, Hayden MA, Hodges SC, KLAS MR, Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;

WPI; 2003-596361/56.

Detecting the presence of a target CS198 polynucleotide in a test sample comprises contacting the sample with a CS198 specific polynucleotide and detecting the presence of the target CS198 polynucleotide in the test sample.

Claim 17; Page 49-50; 67pp; English.

The invention describes a method of detecting the presence of a target CS198 polynucleotide in a test sample. The method comprises contacting the test sample with at least one CS198 specific polynucleotide or its complement, and detecting the presence of the target CS198 polynucleotide in the test sample, where the CS198-specific polynucleotide has at least 50% identity to a polynucleotide having any of the 27 fully defined

CC sequences of 34-2894 bp (SI-27) given in the specification, or their
CC fragments or complements. The composition and methods are useful in
CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
CC or determining the predisposition of an individual to, diseases and
CC conditions of the gastrointestinal tract, e.g. cancer and in gene
CC therapy. This is the predicted amino acid sequence of the human CS198
CC protein derived from the CS198 consensus sequence shown in seq id 27.

XX
SQ Sequence 679 AA;

Query Match 97.2%; Score 171; DB 6; Length 679;
Best Local Similarity 97.0%; Pred. No. 7.7e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EDSVDSAPPGQRKKEQWYAGINPSDGINSEVLE 33
Db 621 EDPVDSAPPGQRKKEQWYAGINPSDGINSEVLE 653

RESULT 14

ADN17172
ID ADN17172 standard; protein; 679 AA.

AC ADN17172;

DT 17-JUN-2004 (first entry)

DE CS198 protein #1.

KW Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.

XX Unidentified.

PN US2004043406-A1.

PD 04-MAR-2004.

PF 22-AUG-2003; 2003US-00646873.

PR 31-MAR-1997; 97US-00828855.

PR 30-MAR-1998; 98US-00050516.

PA (BILL/) BILLINGEL P A.

PA (COHE/) COHEN M.

PA (COLP/) COLPITTS T L.

PA (FRIE/) FRIEDMAN P N.

PA (GORD/) GORDON J.

PA (GRAN/) GRANADOS E N.

PA (HAYD/) HAYDEN M A.

PA (HODG/) HODGES S C.

PA (KLAS/) KLAS M R.

PA (KRAT/) KRATOCHVIL J D.

PA (ROBE/) ROBERTS-RAPP L.

PA (RUSSE/) RUSSELL J C.

PA (STRO/) STROUPE S D.

PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,

PI Granados EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;

PI Roberts-Rapp L, Russell JC, Stroupe SD;

XX MPI; 2004-313754/29.

DR GENBANK; D87440.

CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the CS198 polypeptide, such as cancer
CC of the gastrointestinal tract. These are also useful in gene therapy. The
CC present sequence is a CS198 protein used to illustrate the method of the
CC invention.

XX
SQ Sequence 679 AA;

Query Match 97.2%; Score 171; DB 8; Length 679;
Best Local Similarity 97.0%; Pred. No. 7.7e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EDSVDSAPPGQRKKEQWYAGINPSDGINSEVLE 33
Db 621 EDPVDSAPPGQRKKEQWYAGINPSDGINSEVLE 653

RESULT 15

ADX97562
ID ADX97562 standard; protein; 692 AA.

AC ADX97562;

DT 21-APR-2005 (first entry)

DE Pancreatic cancer associated human protein, SEQ ID 110.

KW pancreas tumor; cytostatic.

XX Homo sapiens.

XX EP1471075-A2.

PD 27-OCT-2004.

PF 31-MAR-2004; 2004EP-00090124.

PR 31-MAR-2003; 2003DE-01015834.

PA (HINZ/) HINZMANN B.

PA (ROSE/) ROSENTHAL A.

PA (PILA/) PILARSKY C.

PA (DAHL/) DAHL E.

PA (SPEC/) SPECHT T.

PA (LICHT/) LICHTNER R.

PI Rosenthal A, Pilarsky C, Dahl E, Specht T, Bruemendorf T,

PI Lichtner R, Staub E, Roepcke S, Li X;

XX MPI; 2004-768082/76.

XX N-PSDB; ADX97491.

DR Claim 2; SEQ ID NO 110; 28pp; German.

XX The invention relates to a novel human nucleic acid sequence of the

XX pancreas and its encoded protein. The invention further comprises:

XX proteins and peptides, preferably isolated, that contain a sequence

XX encoded by the novel nucleic acid, and methods for diagnosis and

XX treatment of pancreatic cancer, using a substance that inhibits or binds

XX to the protein or its DNA, including: an antisense oligonucleotide, short

XX interfering RNA or ribozyme directed against the pancreatic protein, an

XX organic molecule, particularly having a molecular weight below 5000,

XX especially 300, that binds to the pancreatic DNA, an aptamer or

XX (monoclonal) antibody, preferably human or humanized, that binds to the

XX monoclonal DNA, or an anti-idiotypic antibody raised against the

XX group, cytotoxic compound, immunostimulant and/or radioisotope. The novel

XX human pancreatic proteins and their encoding DNA have cytostatic

XX activity. The novel sequences are useful for inhibiting transcription

XX and/or expression of genes and proteins associated with pancreatic

CC cancer. This sequence represents one of the novel human pancreatic
 CC proteins of the invention. Note: This sequence is not shown in the
 CC specification, it has been electronically downloaded from a DVD-ROM
 CC provided with this specification by the European Patent Office.

xx
 SQ Sequence 692 AA;

Query Match 97.2%; Score 171; DB 8; Length 692;
 Best Local Similarity 97.0%; Pred. No. 7.9e-15;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDSVDSAPPQGRKKEQWYAGINPSDGINSEVLE 33
 ||||||||||||||||||||||||||||
 DB 634 EDPVDSAPPQGRKKEQWYAGINPSDGINSEVLE 666

Search completed: March 3, 2006, 13:35:25
 Job time : 19.6385 secs

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 3, 2006, 13:26:31 ; Search time 2.08455 Seconds
(without alignments)
1523.185 Million cell updates/sec

Title: US-10-646-873-46

Perfect score: 176
Sequence: 1 EDSVDSAPPGQRKKEQWYAGINPSDGINSEVLE 33

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	171	97.2	679	2	T00636	hypothetical prote
2	56	31.8	523	1	A41648	protein-tyrosine-P
3	55.5	31.5	1311	2	T08986	hypothetical prote
4	55	31.2	196	2	AH3484	2'-5' RNA ligase (
5	54.5	31.0	1775	2	A31893	collagen alpha 1(I
6	54	30.7	227	2	H69453	hypothetical prote
7	54	30.7	980	2	T49570	hypothetical prote
8	51.5	29.3	278	2	T00613	2-C-methyl-D-eryth
9	51.5	29.3	309	1	T36691	phosphoserine-re
10	51	29.0	329	2	AE1171	alcohol dehydrogen
11	51	29.0	333	2	AH0406	glycerone kinase (
12	50	28.4	695	2	A27485	Alzheimer's diseas
13	49.5	28.1	431	2	JC7330	1-aminocyclopropan
14	49	27.8	120	1	MM615	ig heavy chain V r
15	49	27.8	224	2	B87440	transcription regu
16	49	27.8	242	2	F84362	hypothetical prote
17	49	27.8	329	2	AG1528	alcohol dehydrogen
18	49	27.8	356	2	JN0041	glutamate-amonia
19	49	27.8	394	2	T34708	hypothetical prote
20	49	27.8	484	4	A32761	hypothetical Alzhe
21	49	27.8	685	1	A49795	Alzheimer's diseas
22	49	27.8	695	2	S00550	Alzheimer's diseas
23	49	27.8	770	1	GRH044	probable rRNA meth
24	48.5	27.6	259	2	G87083	hypothetical prote
25	48.5	27.6	385	2	E70910	hypothetical prote
26	48.5	27.6	419	2	T27938	glucose-1-phosphat
27	48.5	27.6	420	2	AG3057	glucose-1-phosphat
28	48.5	27.6	420	2	G98228	glucose-1-phosphat
29	48	27.3	110	2	S40503	beta-1-adrenergic

30	48	27.3	113	2	S55535	Ig heavy chain V r
31	48	27.3	290	1	B29550	hypothetical prote
32	48	27.3	315	1	AJYINB	glutamate-amonia
33	48	27.3	330	2	D95879	probable dihydroxy
34	48	27.3	408	2	SS1467	hypothetical prote
35	48	27.3	535	1	NMBEW1	U21 protein - hum
36	48	27.3	535	2	C24187	hypothetical prote
37	48	27.3	546	2	S67292	probable membrane
38	48	27.3	681	2	T01469	hypothetical prote
39	48	27.3	863	2	T49709	related to glucan
40	48	27.3	972	2	S35521	DNA topoisomerase
41	47.5	27.0	210	2	JH0794	gamma-aminobutyric
42	47.5	27.0	634	2	T27465	hypothetical prote
43	47	26.7	97	2	PH1155	Ig heavy chain V r
44	47	26.7	333	2	C37145	probable helvetic
45	47	26.7	356	1	ADNAQ	glutamate-amonia

ALIGNMENTS

RESULT 1
T00636
hypothetical protein F21856.2 - human
C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C/Species: Homo sapiens (man)
R/Accession: T00636
R/Name: J.E.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhardt-Schultz, K.;
rgescu, A.; Avila, J.; Liu, S.; Bruce, R.; Quan, G.; Montgomery, M.; Ow, D.; Nolan, M.;
submitted to the EMBL Data Library, January 1998
A/Description: Sequence analysis of a 3.5 Mb contig in 19p13.3 between CDC34 and D19S34;
A/Reference number: Z14195
A/Residues: 1-679 <LAMP>
A/Accession: T00636
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Structure: 1-679 <LAMP>
A/Cross-references: UNIPROT:Q81VT2; UNIPARC:UPI00000745CD; EMBL:AC004030; NID:G2804590;
C/Genetics:
A/Map position: 19p13.3
A/Intons: 594/1; 637/3; 650/3
A/Note: F21856_2

Query Match 97.2% Score 171; DB 2; Length 679;
Best Local Similarity 97.0%; Pred. No. 9.3e-16;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 EDSVDSAPPGQRKKEQWYAGINPSDGINSEVLE 33
621 EDPVDSAPPGQRKKEQWYAGINPSDGINSEVLE 653

RESULT 2
A41648
protein-tyrosine-phosphatase (BC 3.1.3.48) cdc25A - human
N/Alternate names: cell division cycle protein cdc25A
C/Species: Homo sapiens (man)
C/Date: 28-May-1992 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
R/Accession: A41648
R/Galaktionov, K.; Beach, D.
Cell 67, 1181-1194, 1991
A/Title: Specific activation of cdc25 tyrosine phosphatases by B-type cyclins: evidence
A/Reference number: A41648; PMID:92103683; PMID:1836978
A/Molecule type: mRNA
A/Residues: 1-523 <GALP>
A/Cross-references: UNIPROT:P30304; UNIPARC:UPI0000038993; GB:M81933; NID:G180170; PIDN
C/Comment: This protein can be activated by association with cyclin B.
C/Genetics:
A/Gene: GDB:CD25A
A/Cross-references: GDB:133773; OMIM:116947
A/Map position: 3p21.3-3p21.2
C/Function:
A/Description: catalyzes the hydrolysis of peptidyl-phosphotyrosine to release phosphat-

RESULT 6

H69453

hypothetical protein AF1633 - Archaeoglobus fulgidus

C/Species: Archaeoglobus fulgidus

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: H69453

R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirschner, E.F.

Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A/Author: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Arlisch, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A/Reference number: A69250; MUID:98049343; PMID:938475

A/Accession: H69453

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-227 <KLE>

A/Cross-references: UNIPROT:Q28640; UNIPARC:UPI000056C3B; GB:AE000989; GB:AE000782; NID

Query Match

Best Local Similarity

Matches

9; Conservative

4; Mismatches

2; Indels

0; Gaps

0; Gaps

0; Gaps

0; Gaps

0; Gaps

0; Gaps

0; Gaps

0; Gaps

0; Gaps

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A/Residues: 1-278 <ROU>

A/Cross-references: UNIPARC:UPI0000178BF; EMBL:AC004136; NID:G3184270; PID:G3184289

A/Experimental source: cultivar Columbia

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.B.; Umeyam, L.; Tallon, J.

euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A64420; MUID:20083487; PMID:10617197

A/Accession: DB4437

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-278 <STO>

A/Cross-references: UNIPARC:UPI0000178BF; GB:AE002093; NID:G3184289; PIDN:AACT18936.1; G

A/Genes: At2g02500; T8K22.20

A/Map position: 2

A/Introns: 54/1; 86/3; 91/3; 115/3; 165/3; 191/3; 214/3; 230/2; 260/3

A/Superfamily: 4-diphosphocytidyl-2-methyl-D-erythritol synthase

C/Keywords: nucleotidyltransferase

Query Match

Best Local Similarity

Matches

12; Conservative

11; Mismatches

8; Indels

5; Gaps

2; Gaps

2; Gaps

2; Gaps

2; Gaps

2; Gaps

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2; Gaps

RESULT 9

T36691

phosphoesterase-related protein SCH6.03 [similarity] - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 05-Oct-2004

C/Accession: T36691

R/Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, April 1999

A/Reference number: Z21597

A/Accession: T36691

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-309 <NR>

A/Cross-references: UNIPROT:Q9X935; UNIPARC:UPI00000DB024; EMBL:AL049731; PIDN:CAB41730

A/Experimental source: strain A3(2)

C/Comment: Although this sequence has motifs characteristic of a variety of phosphoester

C/Genes: SCOE6.03

A/Suprafamily: phosphoesterase, ykub type; phosphoesterase core homology

P/48-115/Domain: phosphoesterase core homology <PEC>

Query Match

Best Local Similarity

Matches

11; Conservative

4; Mismatches

5; Indels

3; Gaps

1; Gaps

1; Gaps

1; Gaps

1; Gaps

1; Gaps

1; Gaps

1; Gaps

1; Gaps

1; Gaps

1; Gaps

1; Gaps

1; Gaps

1; Gaps

RESULT 10

AE1171

alcohol dehydrogenase homolog lmo0773 [imported] - Listeria monocytogenes (strain EGD-e)

C/Species: Listeria monocytogenes

C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Accession: AE1171

R/Glaeser, P.; Finguel, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesunger, O.; Entian, K.D.; Feigl, H

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltournam, A.; M

ok, C.; Schluter, T.; Stines, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland

A/Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1171
A:Status: preliminary
A:Molecule type: DNA
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A:Cross-references: UNIPROT:Q8Y6W9; UNIPARC:UPI0000054D36; GB:NC_003210; PIDN:CAC98851.1
A:Experimental source: strain BGD-e
C:Genetics:
A:Gene: lmo0773
C:Superfamily: alcohol dehydrogenase, long-chain alcohol dehydrogenase homology

Query Match 29.0%; Score 51; DB 2; Length 329;
Best Local Similarity 37.0%; Pred. No. 23;
Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 1 EDSVDSAPPGQRKKEQWYAGINPSDGI 27
Db 22 ETTIDNLPENVEVTIEVHSGINXKDL 48

RESULT 11
AH0406
glycerone kinase (EC 2.7.1.29) [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH0406
R:Patkull, J.; Wren, B.W.; Thomson, N.R.; Titchall, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarrag, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0406
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333 <KUN>
A:Cross-references: UNIPROT:Q8ZBQ7; UNIPARC:UPI00000CDA05; GB:AL590842; PIDN:CAC92580.1;
C:Genetics:
A:Gene: dhxk
C:Keywords: phosphotransferase

Query Match 29.0%; Score 51; DB 2; Length 333;
Best Local Similarity 52.6%; Pred. No. 23;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DSVDSAPPGQRKKEQWYAG 20
Db 135 DSVASAPPSEREKRGVAG 153

RESULT 12
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N:Alternate names: protease nexin II
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, T.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
A:Reference number: A27485; MUID:88106489; PMID:3322280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:G191568; PIDN:
A:Experimental source: brain
R:de Strooper, B.; van Leuven, F.; van Bergh, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A:Accession: S19727
A:Reference number: S19727; MUID:92096458; PMID:1756177
A:Molecule type: mRNA
A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>

A:Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379
R:Izum, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A:Reference number: 149485; MUID:92209998; PMID:1155768
A:Accession: 149485
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:G220328; PIDN:BA01456.1; PID:
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunltz-type proteinase II
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 28.4%; Score 50; DB 2; Length 655;
Best Local Similarity 35.3%; Pred. No. 72;
Matches 12; Conservative 7; Mismatches 13; Indels 2; Gaps 1;

Qy 2 DSVDSAPPGQRKKEQWYAGINP--SDGINSEVLE 33
Db 194 DSVDSADAEEDSDVMWVGADTYADGGEKVE 227

RESULT 13
JC7730
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - Penicillium citrinum
C:Species: Penicillium citrinum
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: JC7730; PC7177
R:Kakut, Y.; Igasaki, T.; Murakami, T.; Ito, H.; Matsui, H.; Honma, M.
Biocet. Biotechnol. Biochem. 65, 1511-1518, 2001
A:Title: 1-Aminocyclopropane-1-carboxylate synthase of Penicillium citrinum: Primary str
A:Reference number: JC7730; MUID:21406359; PMID:11515533
A:Accession: JC7730
A:Molecule type: mRNA
A:Residues: 1-431 <RKA>
A:Cross-references: UNIPROT:Q9P963; UNIPARC:UPI000006C5FE; DDBJ:AB038512
A:Experimental source: strain AH06443
A:Accession: PC7177
A:Molecule type: protein
A:Residues: 28-60; 215-242; 243-273; 341-363; 391-402 <KA2>
A:Cross-references: UNIPARC:UPI000017CBAF; UNIPARC:UPI000017CBAF; UNIPARC:UPI000017CBAF;
C:Comment: This enzyme, which is related to subgroup 1 of aminotransferase, is responsi
C:Keywords: carbon-sulfur lyase

Query Match 28.1%; Score 49.5; DB 2; Length 431;
Best Local Similarity 33.3%; Pred. No. 50;
Matches 12; Conservative 6; Mismatches 15; Indels 3; Gaps 1;

Qy 1 EDSVDSAPPGQRKKEQWYAGINPSDGINSEVLE 33
Db 11 QDVVDAGSENPMDVMDKDTWASTPTGYVNVGAE 46

RESULT 14
MEMS15
Ig heavy chain V region (AC38 15.3) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A02037
R:Dildrop, R.; Boyens, J.; Stekevitz, M.; Beyreuther, K.; Rajewsky, K.
EMBO J. 3, 517-523, 1984
A:Title: A V region determinant (idiotope) expressed at high frequency in B lymphocytes
A:Reference number: A91000; MUID:84182519; PMID:6201362
A:Accession: A02037
A:Molecule type: protein
A:Residues: 1-120 <DIL>
A:Cross-references: UNIPROT:P06329; UNIPARC:UPI0000028A6B
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-98/Region: V segment
F:15-98/Domain: immunoglobulin homology <IMM>

F:99-105/Region: D segment
 F:106-120/Region: J segment
 F:22-96/Dienufide bonds: #status predicted

Query Match 27.8% Score 49; DB 1; Length 120;
 Best Local Similarity 55.6% Pred No. 14;
 Matches 10; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 9 PGQRKKEQWYAGINPSDG 26
 |||:|||||:
 Db 41 PGQGL--EWIGGINPSNG 56

RESULT 15

B87440
 transcritption regulator, Tetr family [Imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: B87440
 R:Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Kholmaveva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A>Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: B87440
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-224 <STO>
 A:Cross-References: UNIPROT:Q9A825; UNIPARC:UP100000C740A; GB:AE005673; NID:913422922; F
 C:Genetics:
 A:Gene: CC1539

Query Match 27.8% Score 49; DB 2; Length 224;
 Best Local Similarity 56.2% Pred No. 28;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 15 EQWYAGINPSDGINSE 30
 |||:|||||:
 Db 175 EAWAGIEDSDGMDDE 190

Search completed: March 3, 2006, 13:36:36
 Job time : 4.08455 secs

Page 8 of 10
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 13:19:17 ; Search time 12.6035 Seconds
(without alignment)
1847.299 Million cell updates/sec

Title: US-10-646-873-46
Perfect score: 176
Sequence: 1 EDSVDSAPPGRKKEQWYAGINPSDGINSEVLE 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_05.80: *
2: uniprot_sprot: *
3: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	171	97.2	679	1 CS021 HUMAN	Q81V22 homo sapien
2	171	97.2	685	1 CS021 HUMAN	Q51B33 pongo pygma
3	123.5	70.2	648	1 CS021 MOUSE	Q9D279 mus musculu
4	59.5	33.8	343	2 OSBAY7 BEMER	Q5B1V7 aspergillus
5	58	33.0	232	2 Q6TMR3 STRCL	Q6TMR3 streptomyc
6	56	31.8	219	2 Q9ACQ1 STRCO	Q9ACQ1 streptomyc
7	56	31.8	524	1 MIP1 HUMAN	P30304 homo sapien
8	55	31.5	1117	2 Q4W9J8 ASPFU	Q4W9J8 aspergillus
9	55.5	31.5	1311	2 Q9SZW3 ARATW	Q9SZW3 arabidopsis
10	55	31.2	196	2 Q57P75 BARUB	Q57P75 bruceella ab
11	55	31.2	196	2 Q8G3B8 BRUSU	Q8G3B8 bruceella su
12	55	31.2	196	2 Q8YEL6 BRUOM	Q8YEL6 bruceella me
13	55	31.2	794	2 Q86NA6 CIOIN	Q86NA6 cioma intes
14	55	31.2	1043	2 Q7SDZ5 ASHGO	Q7SDZ5 ashyba goss
15	54.5	31.0	115	2 Q6K9M4 ORYSA	Q6K9M4 oryza sativ
16	54.5	31.0	1775	1 C04A1 DROME	P08120 drosophila
17	54	30.7	227	1 Y1633 SWCFU	Q28640 archaeoglob
18	54	30.7	256	2 Q7NOR8 CHRYO	Q7NOR8 chromobacte
19	54	30.7	320	2 Q53MB7 ORYSA	Q53MB7 oryza sativ
20	54	30.7	375	2 Q82OP4 STRAW	Q82OP4 streptomyc
21	54	30.7	975	2 Q96UJ1 NEUCR	Q96UJ1 neurospora
22	54	30.7	980	2 Q7RU49 NEUCR	Q7RU49 neurospora
23	53.5	30.4	697	2 Q4IPV6 GIBBZ	Q4IPV6 gibberella
24	53	30.1	234	2 Q8G3B0 BRU12	Q8G3B0 bruceella
25	53	30.1	425	2 Q7S2D8 NEUCR	Q7S2D8 neurospora
26	52	29.8	250	2 Q67B42 PERFL	Q67B42 perca fluvi
27	52	29.5	202	2 Q9RNO0 BARHE	Q9RNO0 bartonella
28	52	29.5	222	2 Q6G2B4 BARHE	Q6G2B4 bartonella
29	52	29.5	236	2 Q880V5 STRIP	Q880V5 trypanosoma
30	52	29.5	319	2 Q6N2R8 RHOPA	Q6N2R8 rhodospirillum rubrum
31	52	29.5	424	1 GIGC_METCA	Q60816 methylotococc

ALIGNMENTS

32	52	29.5	575	2	Q5S323 THERM	Q5S323 thermus the
33	52	29.5	575	2	Q72J64 THER2	Q72J64 thermus the
34	52	29.5	647	2	Q63PB8 BURPS	Q63PB8 burkholderi
35	52	29.5	651	2	Q62E34 BURMA	Q62E34 burkholderi
36	52	29.5	920	2	Q53ZT3 MOUSE	Q53ZT3 mus musculu
37	52	29.5	920	2	Q87342 BRUJA	Q87342 bradyrhizob
38	52	29.5	958	2	Q5N7Y8 ORYSA	Q5N7Y8 oryza sativ
39	51.5	29.3	302	1	ISPD ARATW	Q5N7Y8 arabidopsis
40	51.5	29.3	308	2	Q82EN3 STRAW	Q82EN3 streptomyc
41	51.5	29.3	308	2	Q9X935 STRCO	Q9X935 streptomyc
42	51.5	29.3	536	2	Q4NMP1 SDELT	Q4NMP1 anaeromyxob
43	51	29.0	181	2	Q4USD8 XANCP	Q4USD8 xanthomonas
44	51	29.0	181	2	Q8PB69 XANCP	Q8PB69 xanthomonas
45	51	29.0	280	2	Q7NDY3 GLOVI	Q7NDY3 gloeobacter

RESULT 1

CS021 HUMAN	STANDARD;	PRT;	679 AA.
ID	CS021 HUMAN		
AC	Q81V22;		
DT	13-SEP-2005 (Rel. 48, Created)		
DT	13-SEP-2005 (Rel. 48, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Protein C19orf21.		
GN	Name=C19orf21;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].		
RC	TISSUE=Brain, and Colon;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Stauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,		
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Faney J., Helton E., Kettelman M., Madan A., Rodriguez Y., Bouffard G.G.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield J.S., Krzywinski M.I., Skalska U., Smallos D.E.,		
RA	Schwarz A., Schein J.E., Jones S.J.M., Marx M.A.,		
RT	Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
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CC	use as long as its content is in no way modified and this statement is not		
CC	removed.		
CC	EMBL; BC042125; AAH42125.1; -; mRNA.		
DR	EMBL; BC052236; AAH52236.1; -; mRNA.		
DR	PIR; T00636; T00636.		
DR	Ensembl; ENSG0000009812; Homo sapiens.		
DR	HGNC; HGNC:27000; C19orf21.		
KW	Coiled coil.		
FT	COILED 545 569 Potential.		
SQ	SEQUENCE 679 AA; 75357 MW; D2881CPS087E61F8 CRC64;		

Query Match 97.2%; Score 171; DB 1; Length 679;
 Best Local Similarity 97.0%; Pred. No. 6.4e-15;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDVDSAPPGRKKEQWYAGINPSDGINSEVLE 33
 |||||
 DB 621 EDVDSAPPGRKKEQWYAGINPSDGINSEVLE 653

RESULT 2
 CS021 PONPY STANDARD; PRT; 685 AA.
 AC OSRHH3;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DE Protein C19orf21 homolog.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Pongo.
 OC NCBI_TaxID=9600;
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Kidney;
 RC The German cDNA consortium;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; CR858675; CAH90887.1; -; mRNA.
 KW Coiled coil.
 FT COILED 551 575 Potential.
 SQ SEQUENCE 685 AA; 75892 MW; A3A99F4343396E81 CRC64;

Query Match 97.2%; Score 171; DB 1; Length 685;
 Best Local Similarity 97.0%; Pred. No. 6.4e-15;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDVDSAPPGRKKEQWYAGINPSDGINSEVLE 33
 |||||
 DB 627 EDVDSAPPGRKKEQWYAGINPSDGINSEVLE 659

RESULT 3
 CS021 MOUSE STANDARD; PRT; 648 AA.
 AC Q90279;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Protein C19orf21 homolog.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nakai K., Ogasawara N., Saito R., Suzuki H., Yamashita H., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balareeli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schmitt L.M., Kanapin A., Matveeva H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guetlinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie J., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pettes G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sanderlin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai K., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).

RA NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP STRAIN=FVB/N; TISSUE=Colon;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Melek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scheraga A., Schein J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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 CC -----
 DR EMBL; AK020266; BAB32049.1; -; mRNA.
 DR EMBL; BC013508; AAH13508.1; -; mRNA.
 DR Ensembl; ENSMUSG0000035852; Mus musculus.
 KW MGI; MGI:1926156; 91300170N9RLK.
 FT COILED 511 534 Potential.
 SQ SEQUENCE 648 AA; 72281 MW; 1E395B7063B3D1F CRC64;

Query Match 79.2%; Score 123.5; DB 1; Length 648;
 Best Local Similarity 79.3%; Pred. No. 2.7e-08;
 Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

OY 5 DSAPPGRKKEQWYAGINPSDGINSEVLE 32
 |||||
 DB 593 DSAPPGRKKEQWYAGINPSDGINSEVLE 621

RESULT 4
 CS017 EMENI PRELIMINARY; PRT; 343 AA.
 AC OS01Y7;
 DT 10-MAY-2005 (TREMURel. 30, Created)

Query Match 33.8%; Score 59.5; DB 2; Length 343;
 Best Local Similarity 44.8%; Pred. No. 12;
 Matches 13; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 5 DSAPPGORKKQWYAGINPSDGINSEVL 33
 DB 166 DAAAPROQKKPLW-TGVNPNKSAKSLALE 193

RESULT 5
 Q6TMR3_STRCL PRELIMINARY; PRT; 232 AA.
 AC Q6TMR3;
 DT 05-JUN-2004 (TREMBLrel. 27, Created)
 DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)
 DE Putative secreted protein.
 GN ORFName=PSCL2.6.A8.6c;
 OS Streptomyces clavuligerus.
 OC Bacteri; Actinobacteria; Actinomycetidae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OC NCBI_TaxID=1901;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Wu W., Roy K.L.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AY392416; AAC93550.1; -, Genomic_DNA.
 KW Plasmid.
 SQ SEQUENCE 232 AA; 24790 MW; 704240B23746D3F7 CRC64;

QY 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFName=ANS443.2;
 OS Aspergillus nidulans FGSC M4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; Emericella.
 OC NCBI_TaxID=27321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN-FGSC M4;
 RA Birren B., Nussbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barina N., Bastien V., Bloom T., Boguslavsky L.,
 RA Bouhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Chopel Y., Collamore A., Cook A., Cooke P., Corum B., DeArillano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
 RA Gardyna S., Gaier S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hago B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kelle C., Landers T., Levine R., Landlad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., MacDonald P., Major J., Manning J.,
 RA Matthews C., Muccelli E., McCarthy M., Meldrum J., Menus L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunthang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schaner S., Schupbach R., Seaman S., Severy P., Smitnov S.,
 RA Smith C., Spencer B., Strange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Teitel S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander B.;
 RT "Genome Sequence of Aspergillus nidulans";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC CC
 DR EMBL, AACD0100094; EAA62603.1; -, Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 343 AA; 37318 MW; 3150AB128DEBCAD7 CRC64;

Query Match 33.0%; Score 58; DB 2; Length 232;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 12; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 17 WYAGINPSDGIN--SEVL 32
 DB 71 WNAAGINPSDGCNTREVL 88

RESULT 6
 Q9ACOL1_STRCO PRELIMINARY; PRT; 219 AA.
 AC Q9ACOL1;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Putative secreted protein.
 GN OrderedLocusNames=SCP1.267;
 OS Streptomyces coelicolor.
 OC Bacteri; Actinobacteria; Actinomycetidae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OC NCBI_TaxID=1902;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN-A3(2) / M145;
 RX MEDLINE=2196410; PubMed=1200953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleeer H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinovitch B., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Barrall B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)";
 RL Nature 417:141-147(2002).
 DR EMBL, AL590464; CAC36793.1; -, Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 219 AA; 23413 MW; 417CB9C6345C9F0F CRC64;

Query Match 31.8%; Score 56; DB 2; Length 219;
 Best Local Similarity 60.0%; Pred. No. 22;
 Matches 12; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 15 EOWYAGINPSDGIN--SEVL 32
 DB 56 KHMNAGINPSDGCNTREVL 75

RESULT 7
 MPTP1_HUMAN STANDARD; PRT; 524 AA.
 ID MPTP1_HUMAN
 AC P30304; O81ZHS; Q96113; Q9H2P2;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE M-phase inducer phosphatase 1 (EC 3.1.3.48) (Dual specificity
 DE phosphatase Cdc25A).
 GN Name=CDC25A;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RX MEDLINE=92103683; PubMed=1836978; DOI=10.1016/0092-8674(91)90294-9;
 RA Galaktionov K.I., Beach D.,
 RT "Specific activation of Cdc25 tyrosine phosphatases by B-type cyclins:
 RT evidence for multiple roles of mitotic cyclins";
 RL Cell 67:1181-1194(1991).

[2]
 RN NUCLEOTIDE SEQUENCE (ISOFORM 2).
 RP Varmen-Zlate S., Manfredi U.J.
 RA Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
 RL [3]
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT PHE-88.
 RA Ridder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.,
 RA "NIHES-SNP", environmental genome project, NIHES ES15478, Department
 RT of Genome Sciences, Seattle, WA (URL: <http://esg.gs.washington.edu>).
 RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RP TISSUE-Lymph;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grove L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebli T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield V.S.N., Krzywinski M.I., Skalski U., Smallus D.E.,
 RA Schnerch A., Schain J.E., Jones S.J.W., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16839-16903(2002).
 RN [5]
 RN NUCLEOTIDE SEQUENCE OF 37-234 (ISOFORM 2).
 RP MEDLINE=21020092; PubMed=11139144;
 RA Wegener S., Hampe W., Herrmann D., Schaller H.C.,
 RT "Alternative splicing in the regulatory region of the human
 RT phosphatases CDC25A and CDC25C."
 RL Eur. J. Cell Biol. 79:810-815(2000).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 335-496.
 RX MEDLINE=98265972; PubMed=9604936; DOI=10.1016/S0092-8674(00)81190-3;
 RA Fauman E.B., Cogswell J.P., Lovejoy B., Rocque W.J., Holmes W.,
 RA Montana V.G., Plimica-Morris H., Rink M.J., Saper M.A.,
 RT "Crystal structure of the catalytic domain of the human cell cycle
 RT control phosphatase Cdc25A."
 RL Cell 93:617-625(1998).
 CC -1- FUNCTION: Functions as a dosage-dependent inducer in mitotic
 CC control. It is a tyrosine protein phosphatase required for
 CC progression of the cell cycle. It directly dephosphorylates CDK2
 CC and activate its kinase activity. It also dephosphorylates CDK2 in
 CC complex with cyclin E, in vitro.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- ENZYME REGULATION: Stimulated by cyclins B.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=CDC25A1;
 CC IsoId=P30304-1; Sequence=Displayed;
 CC Name=2; Synonyms=CDC25A2;
 CC IsoId=P30304-2; Sequence=VSP_000860;
 CC -1- SIMILARITY: Belongs to the VSP phosphatase family.
 CC -1- SIMILARITY: Contains 1 rhodanese domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 DR EMBL; M81933; AAA58415.1; -; mRNA.
 DR EMBL; AY137580; AA111305.1; -; mRNA.
 DR EMBL; AF527417; AA177917.1; -; Genomic DNA.
 DR EMBL; BC007401; AA107401.1; -; mRNA.
 DR EMBL; BC018642; AA118642.1; -; mRNA.
 DR EMBL; AF277722; AAC41884.1; -; mRNA.
 DR PIR; A41648; A41648.
 DR PDB; 1C25; X-ray; @-337-496.
 DR Ensembl; ENSG00000164045; Homo sapiens.
 DR HGNC; HGNC:1725; CDC25A.
 DR H-InvDB; HIX0003280; -.
 DR Reactome; P30304; -.
 DR MIM; 116947; -.
 DR GO; GO:0068283; P:cell proliferation; TAS.
 DR GO; GO:0000079; P:regulation of cyclin dependent protein kina. .; TAS.
 DR InterPro; IPR000751; M1 Phosphatase.
 DR InterPro; IPR001763; Rhodanese-like.
 DR PANTHER; PTHR10828; M1 Phosphatase; 1.
 DR Pfam; PF06617; M-inducer phosph; 1.
 DR Pfam; PF00581; Rhodanese; 1.
 DR PRINTS; PR00716; M1PHPHASE.
 DR SMART; SM00450; RHOD; 1.
 DR PROSITE; PS50206; RHODANES_3; 1.
 DR 3D-structure; Alternative splicing; Cell cycle; Cell division;
 KW Hydrolyase; Mitosis; Multigene family; Polymorphism;
 KW Protein phosphatase.
 KW DOMAIN 376 482
 FT ACT_SITE 431 431
 FT VASPLIC 144 183
 FT VARIANT 88 88
 FT COMPACT 6 10
 FT CONFLICT 180 182
 FT STRAND 337 337
 FT TURN 339 340
 FT STRAND 344 344
 FT STRAND 350 350
 FT TURN 355 356
 FT STRAND 359 360
 FT TURN 362 369
 FT HELIX 370 376
 FT TURN 377 384
 FT STRAND 388 392
 FT TURN 393 393
 FT STRAND 395 396
 FT TURN 397 398
 FT STRAND 400 401
 FT HELIX 405 411
 FT TURN 412 414
 FT TURN 421 422
 FT STRAND 424 430
 FT HELIX 437 451
 FT TURN 452 452
 FT TURN 455 456
 FT STRAND 463 466
 FT TURN 467 468
 FT HELIX 469 477
 FT HELIX 478 480
 FT STRAND 481 482
 SQ SEQUENCE 524 AA; 59087 MW; B2F6B792D4E6122B CRC64;

Query Match 31.8%; Score 56; DB 1; Length 524;
 Best Local Similarity 33.3%; Pred. No. 60;
 Matches 10; Conservative 7; Mismatches 13; Indels 0; Gaps 0;
 1 EDSVDSAPPGORRKEOWYAGINPSDGINSE 30
 Db 277 ERSQBSPPSTTKRKMSGASPKESTYPE 306
 RESULT 8

Q4W9J8_ASPFU
ID Q4W9J8_ASPFU PRELIMINARY; PRT; 1117 AA.
AC Q4W9J8;
DT 13-SEP-2005 (TRENBLREL. 31, Created)
DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLREL. 31, Last annotation update)
DE Calcium permease family membrane transporter.
GN ORFNames=Atu4g04670;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=330879;
OK (1)
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=AF293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H., Stanley J.,
RA Artzy J., Berriman M., Abe K., Archer D.B., Bernéjo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster G., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni L., Griffith-Jones S., Gwilliam R., Jimenez J.,
RA Haas H., Harris D., Horluchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouf H., Kiteamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Laiton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majores W.H., May G.S., Miller B.L., Mohammad Y., Molina M., Monod M.,
RA Mounya I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penava M.A., Petres M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitch B., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Romling C.M., Rutter S., Salzberg S.L., Sanchez M., Squares S.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
Aspergillus fumigatus.";
RT Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL:AAH0100016; EMBL:615.1; -; Genomic DNA.
SQ SEQUENCE 1117 AA; 123585 MW; 8A1C813C4C1A1E8B CRC64;

Query Match 31.8%; Score 56; DB 2; Length 1117;
Best Local Similarity 34.5%; Pred. No. 1.4e+02;
Matches 10; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 2 DSVDSAPPGQKKEQWYAGINPDDGINSE 30
Db 183 EAIGTRPPSQSQSEASSHHGINDGDND 211

RESULT 9
Q9SZW3_ARATH
ID Q9SZW3_ARATH PRELIMINARY; PRT; 1311 AA.
AC Q9SZW3;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 13-SEP-2005 (TRENBLREL. 31, Last annotation update)
DE Hypothetical protein F6G3.130 (Hypothetical protein ATG430100).
GN Name=F6G3.130; Synonyms=ATG430100;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosoid II; Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxID=3702;
OK (1)
RN NUCLEOTIDE SEQUENCE.
RA Bovan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Lemcke K., Scheller C.,
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RP NUCLEOTIDE SEQUENCE.

RA EU Arabidopsis sequencing project;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN (3)
RN NUCLEOTIDE SEQUENCE.
RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN (4)
RN NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL:AL078464; CAB43845.1; -; Genomic DNA.
DR EMBL:AL161576; CAB81003.1; -; Genomic DNA.
DR PIR: T08986; T08986.
KW Hypothetical protein.
SQ SEQUENCE 1311 AA; 145625 MW; 0F430B9EB3A02AA4 CRC64;

Query Match 31.5%; Score 55.5; DB 2; Length 1311;
Best Local Similarity 54.5%; Pred. No. 2e+02;
Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 1 EDSV-DSAPPGQKKEQWYAGI 21
Db 1276 EWSVDDSDPPGDRYRDWQHGI 1297

RESULT 10
ID Q57FT5_BRUB PRELIMINARY; PRT; 196 AA.
AC Q57FT5;
DT 10-MAY-2005 (TRENBLREL. 30, Created)
DT 10-MAY-2005 (TRENBLREL. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLREL. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=Brub1_0082;
OS Brucella abortus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OK NCBI_TaxID=235;
RN (1)
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=9-941 / Biovar 1;
RX PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
RA Halling S.M., Peterson-Burch B.D., Bricker B.J., Ziemer R.L.,
RA Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.,
RT "Completion of the genome sequence of Brucella abortus and comparison
RT to the highly similar genomes of Brucella melitensis and Brucella
RT suis.";
RL J. Bacteriol. 187:2715-2726(2005).
DR EMBL:AB017223; AAX73499.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 196 AA; 21701 MW; BAA4DFALFD4010FA CRC64;

Query Match 31.2%; Score 55; DB 2; Length 196;
Best Local Similarity 45.0%; Pred. No. 27;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 10 GQRKKEQWYAGINPDDGINS 29
Db 77 GSKKPSIYAGVSPGILNA 96

RESULT 11
ID Q8G368_BRUSU
AC Q8G368;
DT 01-MAR-2003 (TRENBLREL. 23, Created)
DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BR0084;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 3, 2006, 13:35:46 ; Search time 4.42566 Seconds
(without alignments)
616.473 Million cell updates/sec

Title: US-10-646-873-46

Perfect score: 176
Sequence: 1 EDVSADPPGQRKKEQWTAGINPSDGINSEVLE 33

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5-COMB.pep:.*
2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:.*
3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:.*
4: /cgn2_6/ptodata/1/1aa/RCTUS-COMB.pep:.*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:.*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	100.0	33	US-09-050-516-46	Sequence 46, Appl
2	176	100.0	33	US-10-278-547-46	Sequence 46, Appl
3	171	97.2	215	US-09-050-516-47	Sequence 47, Appl
4	171	97.2	215	US-10-278-547-47	Sequence 47, Appl
5	171	97.2	679	US-09-050-516-42	Sequence 42, Appl
6	171	97.2	679	US-10-278-547-42	Sequence 42, Appl
7	57	32.4	124	US-09-301-593-8	Sequence 8, Appl
8	57	32.4	124	US-09-301-593-10	Sequence 10, Appl
9	57	32.4	124	US-09-301-593-12	Sequence 12, Appl
10	57	32.4	124	US-09-301-593-14	Sequence 14, Appl
11	57	32.4	124	US-09-301-593-16	Sequence 16, Appl
12	57	32.4	124	US-09-301-593-38	Sequence 38, Appl
13	57	32.4	124	US-09-301-593-39	Sequence 39, Appl
14	57	32.4	124	US-09-301-593-40	Sequence 40, Appl
15	57	32.4	124	US-09-301-593-41	Sequence 41, Appl
16	57	32.4	124	US-09-301-593-108	Sequence 108, Appl
17	57	32.4	422	US-09-301-593-43	Sequence 43, Appl
18	56	31.8	523	US-08-073-183-2	Sequence 2, Appl
19	56	31.8	523	US-08-428-415-2	Sequence 2, Appl
20	56	31.8	523	US-08-379-685-2	Sequence 2, Appl
21	56	31.8	523	US-08-854-029-2	Sequence 2, Appl
22	56	31.8	523	US-08-428-762-2	Sequence 2, Appl
23	56	31.8	523	PCT-US94-06365-2	Sequence 2, Appl
24	56	31.8	560	US-09-949-016-11684	Sequence 11684, A
25	53	30.1	941	US-09-270-767-33497	Sequence 33497, A
26	53	30.1	941	US-09-270-767-48714	Sequence 48714, A
27	50.5	28.7	193	US-09-270-767-46106	Sequence 46106, A

28	50	28.4	106	2	US-09-902-540-10501	Sequence 10501, A
29	50	28.4	695	2	US-09-458-481B-4	Sequence 4, Appl
30	50	28.4	695	2	US-09-458-481B-5	Sequence 5, Appl
31	49	27.8	143	2	US-09-301-583-26	Sequence 26, Appl
32	49	27.8	284	2	US-09-141-951-1	Sequence 1, Appl
33	49	27.8	307	1	US-08-442-063A-48	Sequence 48, Appl
34	49	27.8	381	2	US-09-216-295-22	Sequence 22, Appl
35	49	27.8	381	2	US-09-632-570-22	Sequence 22, Appl
36	49	27.8	381	2	US-09-632-575-52	Sequence 16, Appl
37	49	27.8	453	2	US-09-301-583-18	Sequence 16, Appl
38	49	27.8	472	2	US-09-301-583-30	Sequence 30, Appl
39	49	27.8	487	1	US-08-462-859A-9	Sequence 9, Appl
40	49	27.8	487	1	US-08-123-659A-9	Sequence 9, Appl
41	49	27.8	487	1	US-08-123-659A-9	Sequence 9, Appl
42	49	27.8	487	1	US-08-464-247A-9	Sequence 9, Appl
43	49	27.8	492	1	US-08-462-859A-7	Sequence 7, Appl
44	49	27.8	492	1	US-08-123-659A-7	Sequence 7, Appl
45	49	27.8	492	1	US-08-464-247A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-050-516-46
Sequence 46, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TRLEX:
INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-46

Query Match 100.0%; Score 176; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.5e-18;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDSVDSAPPQGRKKQWYAGINPSDGINSEVLE 33
Db 1 EDSVDSAPPQGRKKQWYAGINPSDGINSEVLE 33

RESULT 2

US-10-278-547-46
Sequence 46, Application US/10278547
Patent No. 6660834

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>

APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids
TYPE: amino acid.
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US-10-278-547-46

Query Match 100.0%; Score 176; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.5e-18;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDSVDSAPPQGRKKQWYAGINPSDGINSEVLE 33
Db 1 EDSVDSAPPQGRKKQWYAGINPSDGINSEVLE 33

RESULT 3

US-09-050-516-47
Sequence 47, Application US/09050516
Patent No. 6627414

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPR, LISA

APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-47

Query Match 97.2%; Score 171; DB 2; Length 215;
Best Local Similarity 97.0%; Pred. No. 1.6e-16;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDVSAPPGORKEQWYAGINPSDGINSEVLE 33
DB 157 EDPVDSAPPGORKEQWYAGINPSDGINSEVLE 189

RESULT 4

US-10-278-547-47
Sequence 47, Application US/10278547
Patent No. 6660834

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547

FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065, US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6660834e

SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-278-547-47

Query Match 97.2%; Score 171; DB 2; Length 215;
Best Local Similarity 97.0%; Pred. No. 1,6e-16;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDVSAPPGORKEQWYAGINPSDGINSEVLE 33
DB 157 EDPVDSAPPGORKEQWYAGINPSDGINSEVLE 189

RESULT 5

US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. 6627414

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

APPLICANT: COHEN, MAURICE

APPLICANT: COLPITTS, TRACEY L.

APPLICANT: FRIEDMAN, PAULA N.

APPLICANT: GORDON, JULIAN

APPLICANT: GRANDOS, EDWARD N.

APPLICANT: HAYDEN, MARK

APPLICANT: HODGES, STEVEN C.

APPLICANT: KLASS, MICHAEL R.

APPLICANT: KRATOCHVIL, JON D.

APPLICANT: ROBERTS-RAPP, LISA

APPLICANT: RUSSELL, JOHN C.

APPLICANT: STROUPE, STEPHEN D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACTTITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065, US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 679 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6627414e

US-09-050-516-42

Query Match 97.2%; Score 171; DB 2; Length 679;
Best Local Similarity 97.0%; Pred. No. 5,8e-16;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDVSAPPGORKEQWYAGINPSDGINSEVLE 33
DB 621 EDPVDSAPPGORKEQWYAGINPSDGINSEVLE 653

RESULT 6

US-10-278-547-42
Sequence 42, Application US/10278547
Patent No. 6660834

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

APPLICANT: COHEN, MAURICE

COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-278-547-42
Query Match 97.2%; Score 171; DB 2; Length 679;
Best Local Similarity 97.0%; Pred. No. 5,8e-16;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 BDVSAPPGGRKKEQWYAGINPSDGINSEVLE 33
Db 621 EDPVDSAPPGGRKKEQWYAGINPSDGINSEVLE 653
RESULT 7
US-09-301-593-8
Sequence 8, Application US/09301593A
Patent No. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890001

CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 124
TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-8
Query Match 32.4%; Score 57; DB 2; Length 124;
Best Local Similarity 57.9%; Pred. No. 1.5;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
Oy 9 PGQRKEQWYAGINPSDGI 27
Db 41 PGQRLL--EWIGGINPNNGI 57
RESULT 8
US-09-301-593-10
Sequence 10, Application US/09301593A
Patent No. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 124
TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-10
Query Match 32.4%; Score 57; DB 2; Length 124;
Best Local Similarity 57.9%; Pred. No. 1.5;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
Oy 9 PGQRKEQWYAGINPSDGI 27
Db 41 PGQRLL--EWIGGINPNNGI 57
RESULT 9
US-09-301-593-12
Sequence 12, Application US/09301593A
Patent No. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301,593A


```
/ CURRENT FILING DATE: 1999-04-29
/ EARLIER APPLICATION NUMBER: EP 98107925.4
/ EARLIER FILING DATE: 1998-04-30
/ EARLIER APPLICATION NUMBER: US 60/086,049
/ EARLIER FILING DATE: 1998-05-18
/ NUMBER OF SEQ ID NOS: 108
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 12
/ LENGTH: 124
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-301-593-12
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Query Match      32.4%; Score 57; DB 2; Length 124;
Best Local Similarity 57.9%; Pred. No. 1.5;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
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```
QY      9 PGQRKEQWYAGINPSDGI 27
      ||||| : ||||| : |||||
      41 PGQRL--EWIGGINPNNGI 57
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```
RESULT 10
US-09-301-593-14
/ Sequence 14, Application US/09301593A
/ Patent No. 6455677
/ GENERAL INFORMATION:
/ APPLICANT: Park, John E.
/ APPLICANT: Garin-Chessa, Pilar
/ APPLICANT: Bamberger, Uwe
/ APPLICANT: Leger, Olivier
/ APPLICANT: Saldanha, Jose W.
/ APPLICANT: Rettig, Wolfgang J.
/ TITLE OF INVENTION: FAP-specific Antibody with Improved Productibility
/ FILE REFERENCE: 0652.1890001
/ CURRENT APPLICATION NUMBER: US/09/301,593A
/ EARLIER FILING DATE: 1999-04-29
/ EARLIER APPLICATION NUMBER: EP 98107925.4
/ EARLIER FILING DATE: 1998-04-30
/ EARLIER APPLICATION NUMBER: US 60/086,049
/ EARLIER FILING DATE: 1998-05-18
/ NUMBER OF SEQ ID NOS: 108
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 14
/ LENGTH: 124
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-301-593-14
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Query Match      32.4%; Score 57; DB 2; Length 124;
Best Local Similarity 57.9%; Pred. No. 1.5;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
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```
QY      9 PGQRKEQWYAGINPSDGI 27
      ||||| : ||||| : |||||
      41 PGQRL--EWIGGINPNNGI 57
```

```
RESULT 11
US-09-301-593-16
/ Sequence 16, Application US/09301593A
/ Patent No. 6455677
/ GENERAL INFORMATION:
/ APPLICANT: Park, John E.
/ APPLICANT: Garin-Chessa, Pilar
/ APPLICANT: Bamberger, Uwe
/ APPLICANT: Leger, Olivier
/ APPLICANT: Saldanha, Jose W.
/ APPLICANT: Rettig, Wolfgang J.
/ TITLE OF INVENTION: FAP-specific Antibody with Improved Productibility
/ FILE REFERENCE: 0652.1890001
/ CURRENT APPLICATION NUMBER: US/09/301,593A
/ CURRENT FILING DATE: 1999-04-29
```

```
/ EARLIER APPLICATION NUMBER: EP 98107925.4
/ EARLIER FILING DATE: 1998-04-30
/ EARLIER APPLICATION NUMBER: US 60/086,049
/ EARLIER FILING DATE: 1998-05-18
/ NUMBER OF SEQ ID NOS: 108
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 16
/ LENGTH: 124
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-301-593-16
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```
Query Match      32.4%; Score 57; DB 2; Length 124;
Best Local Similarity 57.9%; Pred. No. 1.5;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
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```
QY      9 PGQRKEQWYAGINPSDGI 27
      ||||| : ||||| : |||||
      41 PGQRL--EWIGGINPNNGI 57
```

```
RESULT 12
US-09-301-593-38
/ Sequence 38, Application US/09301593A
/ Patent No. 6455677
/ GENERAL INFORMATION:
/ APPLICANT: Park, John E.
/ APPLICANT: Garin-Chessa, Pilar
/ APPLICANT: Bamberger, Uwe
/ APPLICANT: Leger, Olivier
/ APPLICANT: Saldanha, Jose W.
/ APPLICANT: Rettig, Wolfgang J.
/ TITLE OF INVENTION: FAP-specific Antibody with Improved Productibility
/ FILE REFERENCE: 0652.1890001
/ CURRENT APPLICATION NUMBER: US/09/301,593A
/ EARLIER FILING DATE: 1999-04-29
/ EARLIER APPLICATION NUMBER: EP 98107925.4
/ EARLIER FILING DATE: 1998-04-30
/ EARLIER APPLICATION NUMBER: US 60/086,049
/ EARLIER FILING DATE: 1998-05-18
/ NUMBER OF SEQ ID NOS: 108
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 38
/ LENGTH: 124
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-301-593-38
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Query Match      32.4%; Score 57; DB 2; Length 124;
Best Local Similarity 57.9%; Pred. No. 1.5;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
```

```
QY      9 PGQRKEQWYAGINPSDGI 27
      ||||| : ||||| : |||||
      41 PGQRL--EWIGGINPNNGI 57
```

```
RESULT 13
US-09-301-593-39
/ Sequence 39, Application US/09301593A
/ Patent No. 6455677
/ GENERAL INFORMATION:
/ APPLICANT: Park, John E.
/ APPLICANT: Garin-Chessa, Pilar
/ APPLICANT: Bamberger, Uwe
/ APPLICANT: Leger, Olivier
/ APPLICANT: Saldanha, Jose W.
/ APPLICANT: Rettig, Wolfgang J.
/ TITLE OF INVENTION: FAP-specific Antibody with Improved Productibility
/ FILE REFERENCE: 0652.1890001
/ CURRENT APPLICATION NUMBER: US/09/301,593A
/ CURRENT FILING DATE: 1999-04-29
/ EARLIER APPLICATION NUMBER: EP 98107925.4
```

; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-39

Query Match 32.4%; Score 57; DB 2; Length 124;
Best Local Similarity 57.9%; Pred. No. 1.5;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

OY 9 PGQRKEQWYAGINPSDGI 27
||| : ||| : |||
41 PGQRL-EMIGINPNNGI 57

RESULT 14

US-09-301-593-40
; Sequence 40, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Productibility
; FILE REFERENCE: 0652.1890001
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-40

Query Match 32.4%; Score 57; DB 2; Length 124;
Best Local Similarity 57.9%; Pred. No. 1.5;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

OY 9 PGQRKEQWYAGINPSDGI 27
||| : ||| : |||
41 PGQRL-EMIGINPNNGI 57

RESULT 15

US-09-301-593-41
; Sequence 41, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Productibility
; FILE REFERENCE: 0652.1890001
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30

; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-41

Query Match 32.4%; Score 57; DB 2; Length 124;
Best Local Similarity 57.9%; Pred. No. 1.5;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

OY 9 PGQRKEQWYAGINPSDGI 27
||| : ||| : |||
41 PGQRL-EMIGINPNNGI 57

Search completed: March 3, 2006, 13:38:54
Job time : 5.59232 secs

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 3, 2006, 14:09:14 ; Search time 14.4956 Seconds
(without alignments)
951.209 Million cell updates/sec

Title: US-10-646-873-46

Perfect score: 176
Sequence: 1 EDYDSAPGQRKKEQWYAGINPDGINSEYLE 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:*

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- 2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	100.0	33	US-09-050-516-46	Sequence 46, Appl
2	176	100.0	33	US-10-278-547-46	Sequence 46, Appl
3	176	100.0	33	US-10-646-873-46	Sequence 46, Appl
4	172	97.7	172	US-10-106-698-4761	Sequence 4761, Ap
5	171	97.2	215	US-09-050-516-47	Sequence 47, Appl
6	171	97.2	215	US-10-278-547-47	Sequence 47, Appl
7	171	97.2	215	US-10-646-873-47	Sequence 47, Appl
8	171	97.2	679	US-09-050-516-42	Sequence 42, Appl
9	171	97.2	679	US-10-278-547-42	Sequence 42, Appl
10	171	97.2	679	US-10-646-873-42	Sequence 42, Appl
11	89	50.6	43	US-10-029-386-33676	Sequence 33676, A
12	60	34.1	155	US-10-425-115-244090	Sequence 244090,
13	57	32.4	124	US-09-301-593-8	Sequence 8, Appl
14	57	32.4	124	US-09-301-593-10	Sequence 10, Appl
15	57	32.4	124	US-09-301-593-12	Sequence 12, Appl
16	57	32.4	124	US-09-301-593-14	Sequence 14, Appl
17	57	32.4	124	US-09-301-593-16	Sequence 16, Appl
18	57	32.4	124	US-09-301-593-18	Sequence 18, Appl
19	57	32.4	124	US-09-301-593-39	Sequence 39, Appl
20	57	32.4	124	US-09-301-593-40	Sequence 40, Appl
21	57	32.4	124	US-09-301-593-41	Sequence 41, Appl
22	57	32.4	124	US-09-301-593-108	Sequence 108, App
23	57	32.4	124	US-10-121-464-8	Sequence 8, Appl
24	57	32.4	124	US-10-121-464-10	Sequence 10, Appl
25	57	32.4	124	US-10-121-464-12	Sequence 12, Appl
26	57	32.4	124	US-10-121-464-14	Sequence 14, Appl
27	57	32.4	124	US-10-121-464-16	Sequence 16, Appl

28	57	32.4	124	US-10-159-006-8	Sequence 8, Appl
29	57	32.4	124	US-10-159-006-10	Sequence 10, Appl
30	57	32.4	124	US-10-159-006-12	Sequence 12, Appl
31	57	32.4	124	US-10-159-006-14	Sequence 14, Appl
32	57	32.4	124	US-10-159-006-16	Sequence 16, Appl
33	57	32.4	124	US-10-159-006-38	Sequence 38, Appl
34	57	32.4	124	US-10-159-006-39	Sequence 39, Appl
35	57	32.4	124	US-10-159-006-40	Sequence 40, Appl
36	57	32.4	124	US-10-159-006-41	Sequence 41, Appl
37	57	32.4	124	US-10-159-006-108	Sequence 108, App
38	57	32.4	432	US-10-389-223A-10	Sequence 10, Appl
39	57	32.4	472	US-09-301-593-43	Sequence 43, Appl
40	57	32.4	472	US-10-159-006-43	Sequence 43, Appl
41	57	32.4	480	US-10-389-223A-4	Sequence 4, Appl
42	57	32.4	601	US-10-380-438-3	Sequence 3, Appl
43	57	32.4	614	US-10-380-438-1	Sequence 2, Appl
44	57	32.4	658	US-10-380-438-2	Sequence 1, Appl
45	56	31.8	483	US-11-022-042-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-050-516-46
Sequence 46, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KASS, MICHAEL R.
APPLICANT: KATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/938-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-46

Query Match 100.0%; Score 176; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.6e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDVSDAPPGQRKKEQWYAGINPSDGINSEVLE 33
Db 1 EDVSDAPPGQRKKEQWYAGINPSDGINSEVLE 33

RESULT 2
US-10-278-547-46
Sequence 46, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US-10-278-547-46

Query Match 100.0%; Score 176; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.6e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDVSDAPPGQRKKEQWYAGINPSDGINSEVLE 33
Db 1 EDVSDAPPGQRKKEQWYAGINPSDGINSEVLE 33

RESULT 3
US-10-646-873-46
Sequence 46, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-646-873-46

Query Match 100.0%; Score 176; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.6e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDSVDSAPPQGRKEQWYAGINPSDGINSEVLE 33
DB 1 EDSVDSAPPQGRKEQWYAGINPSDGINSEVLE 33

RESULT 4

US-10-646-873-4761
Sequence 4761, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 4761
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (35)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (116)
NAME/KEY: MISC_FEATURE
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-699-4761

Query Match 97.7%; Score 172; DB 4; Length 172;
Best Local Similarity 97.0%; Pred. No. 1.4e-14;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDSVDSAPPQGRKEQWYAGINPSDGINSEVLE 33
DB 114 EDSVDSAPPQGRKEQWYAGINPSDGINSEVLE 146

RESULT 5

US-09-050-516-47
Sequence 47, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA

ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065-US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1
US-09-050-516-47

Query Match 97.2%; Score 171; DB 3; Length 215;
Best Local Similarity 97.0%; Pred. No. 2.5e-14;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDSVDSAPPQGRKEQWYAGINPSDGINSEVLE 33
DB 157 EDPVDSAPPQGRKEQWYAGINPSDGINSEVLE 189

RESULT 6

US-10-278-547-47
Sequence 47, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-278-547-47

Query Match 97.2%; Score 171; DB 4; Length 215;
Best Local Similarity 97.0%; Pred. No. 2,5e-14;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDSVDSAPPGQRKKEQWYAGINPSDGINSEVLE 33
Db 157 EDPVDSAPPGQRKKEQWYAGINPSDGINSEVLE 189

RESULT 7
US-10-646-873-47
Sequence 47, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-AUG-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-646-873-47

Query Match 97.2%; Score 171; DB 4; Length 215;
Best Local Similarity 97.0%; Pred. No. 2,5e-14;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDSVDSAPPGQRKKEQWYAGINPSDGINSEVLE 33
Db 157 EDPVDSAPPGQRKKEQWYAGINPSDGINSEVLE 189

RESULT 8
US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-42

Query Match 97.2%; Score 171; DB 3; Length 679;
Best Local Similarity 97.0%; Pred. No. 8.2e-14;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDSVDSAPGQKKEQWYAGINPSDGINSEVLE 33
Db 621 EDPVDSAPGQKKEQWYAGINPSDGINSEVLE 653

RESULT 9
US-10-278-547-42
Sequence 42, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-278-547-42

Query Match 97.2%; Score 171; DB 4; Length 679;
Best Local Similarity 97.0%; Pred. No. 8.2e-14;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDSVDSAPGQKKEQWYAGINPSDGINSEVLE 33
Db 621 EDPVDSAPGQKKEQWYAGINPSDGINSEVLE 653

RESULT 10
US-10-646-873-42
Sequence 42, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-646-873-42

Query Match 97.2%; Score 171; DB 4; Length 679;
Best Local Similarity 97.0%; Pred. No. 8.2e-14;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EDSVDSAPPGQRKKEQWYAGINPSDGINSEYLE 33
Db 621 EDPVDSAPPGQRKKEQWYAGINPSDGINSEYLE 653

RESULT 11
US-10-029-386-33676

; Sequence 33676, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33676

; LENGTH: 43

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:
; OTHER INFORMATION: MAP TO AC004030.1

US-10-029-386-33676
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.42

Query Match 50.6%; Score 89; DB 4; Length 43;
Best Local Similarity 94.1%; Pred. No. 0.00029;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EDSVDSAPPGQRKKEQW 17
Db 27 EDPVDSAPPGQRKKEQW 43

RESULT 12
US-10-425-115-244090

; Sequence 244090, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 244090

; LENGTH: 155

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:
; NAME/KEY: unsure

; LOCATION: (1)..(155)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MWT4577_154194C.1 pep

US-10-425-115-244090

Query Match 34.1%; Score 60; DB 4; Length 155;
Best Local Similarity 61.1%; Pred. No. 7.5;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Oy 6 SAPPGQRKKEQWYAGINP 23
Db 2 SEAPGRKKHSWLAIIMP 19

RESULT 13
US-09-301-593-8

; Sequence 8, Application US/09301593A
; Publication No. US20020052480A1
; GENERAL INFORMATION:

; APPLICANT: Park, John E.
; APPLICANT: Garin-Cheesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Productibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8

; LENGTH: 124

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-301-593-8
Query Match 32.4%; Score 57; DB 3; Length 124;
Best Local Similarity 57.9%; Pred. No. 15;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

Oy 9 PGQRKKEQWYAGINPSDGI 27
Db 41 PGQRLL--EWIGGINPNNGI 57

RESULT 14
US-09-301-593-10

; Sequence 10, Application US/09301593A
; Publication No. US20020052480A1
; GENERAL INFORMATION:

; APPLICANT: Park, John E.
; APPLICANT: Garin-Cheesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Productibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10

; LENGTH: 124

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-301-593-10
Query Match 32.4%; Score 57; DB 3; Length 124;
Best Local Similarity 57.9%; Pred. No. 15;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

Oy 9 PGQRKKEQWYAGINPSDGI 27

Db 41 PGORL--EWIGGINPNNGI 57

RESULT 15
US-09-301-593-12

/ Sequence 12, Application US/09301593A
/ Publication No. US20020052480A1
/ GENERAL INFORMATION:
/ APPLICANT: Park, John B.
/ APPLICANT: Garin-Chesa, Pilar
/ APPLICANT: Bamberger, Uwe
/ APPLICANT: Leger, Olivier
/ APPLICANT: Saldanha, Jose W.
/ APPLICANT: Rettig, Wolfgang J.
/ TITLE OF INVENTION: FAP-specific Antibody with Improved Productibility
/ FILE REFERENCE: 0652.1890001
/ CURRENT APPLICATION NUMBER: US/09/301,593A
/ CURRENT FILING DATE: 1999-04-29
/ EARLIER APPLICATION NUMBER: EP 98107925.4
/ EARLIER FILING DATE: 1998-04-30
/ EARLIER APPLICATION NUMBER: US 60/086,049
/ EARLIER FILING DATE: 1998-05-18
/ NUMBER OF SEQ ID NOS: 108
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 12
/ LENGTH: 124
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-301-593-12

Query Match 32.4%; Score 57; DB 3; Length 124;
Best Local Similarity 57.9%; Pred. No. 15;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 9 PGORKEQWYAGINPSDGI 27
Db 41 PGORL--EWIGGINPNNGI 57

Search completed: March 3, 2006, 14:18:11
Job time: 15.4956 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 14:10:51 ; Search time 1.57143 Seconds
(without alignments)
420.009 Million cell updates/sec

Title: US-10-646-873-46

Perfect score: 176
Sequence: 1 EDSVDSAPPGQRKEQWTAGINPSDGINSEVLE 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.New.*
1: /cgn2_6/prodata/1/pubppaa/US08_NEW_PUB.pep.*
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3: /cgn2_6/prodata/1/pubppaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubppaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/1/pubppaa/US05_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubppaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/1/pubppaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	28.4	120	US-11-049-536-598	Sequence 598, App
2	49	27.8	356	US-11-087-099-11044	Sequence 11044, A
3	49	27.8	770	US-10-982-545-15	Sequence 15, Appl
4	49	27.8	770	US-10-789-273-38	Sequence 38, Appl
5	48	27.3	232	US-11-025-712-10	Sequence 10, Appl
6	48	27.3	315	US-11-087-099-3875	Sequence 3875, Ap
7	48	27.3	353	US-11-087-099-10589	Sequence 10589, A
8	48	27.3	356	US-11-087-099-4330	Sequence 4330, Ap
9	48	27.3	450	US-11-025-712-12	Sequence 12, Appl
10	47.5	27.0	1133	US-10-821-234-1219	Sequence 1219, Ap
11	47.5	27.0	1233	US-10-517-939-312	Sequence 312, App
12	47	26.7	186	US-10-467-657-6312	Sequence 6312, Ap
13	47	26.7	356	US-11-087-099-7589	Sequence 7589, Ap
14	46.5	26.4	375	US-10-485-517-166	Sequence 166, App
15	46.5	26.4	988	US-11-171-701-6	Sequence 6, Appl
16	46	26.1	631	US-10-510-386-4	Sequence 4, Appl
17	45.5	25.9	294	US-11-087-099-11149	Sequence 11149, A
18	45.5	25.9	348	US-11-087-099-6422	Sequence 6422, Ap
19	45.5	25.9	354	US-11-087-099-4564	Sequence 4564, Ap
20	45.5	25.9	357	US-11-087-099-3758	Sequence 3758, Ap
21	45.5	25.9	359	US-11-087-099-7895	Sequence 7895, Ap
22	45.5	25.9	1089	US-11-087-099-7653	Sequence 7653, Ap
23	45	25.6	132	US-10-993-843-12	Sequence 12, Appl
24	45	25.6	317	US-11-087-099-7583	Sequence 7583, Ap
25	45	25.6	336	US-11-087-099-1677	Sequence 1677, Ap

26	45	25.6	356	7	US-11-087-099-5793	Sequence 5793, Ap
27	45	25.6	359	6	US-10-821-234-1396	Sequence 1396, Ap
28	45	25.6	545	6	US-11-134-563-16	Sequence 16, Appl
29	45	25.6	695	6	US-10-363-924-2	Sequence 2, Appl
30	45	25.6	4913	6	US-10-453-372-1142	Sequence 1142, Ap
31	45	25.6	4961	6	US-10-453-372-1132	Sequence 1132, Ap
32	44.5	25.3	196	7	US-11-087-099-8247	Sequence 8247, Ap
33	44.5	25.3	354	7	US-11-087-099-1806	Sequence 1806, Ap
34	44.5	25.3	355	7	US-11-087-099-5542	Sequence 5542, Ap
35	44.5	25.3	356	7	US-11-087-099-846	Sequence 846, App
36	44.5	25.3	356	7	US-11-087-099-5763	Sequence 5763, Ap
37	44.5	25.3	357	7	US-11-087-099-5974	Sequence 5974, Ap
38	44.5	25.3	372	7	US-11-087-099-2822	Sequence 2822, Ap
39	44.5	25.3	378	7	US-11-087-099-11797	Sequence 11797, A
40	44.5	25.3	481	7	US-11-087-099-4975	Sequence 4975, Ap
41	44	25.0	121	7	US-11-049-536-682	Sequence 682, App
42	44	25.0	123	7	US-11-112-240-14	Sequence 14, Appl
43	44	25.0	123	7	US-11-112-304A-14	Sequence 14, Appl
44	44	25.0	363	7	US-11-087-099-9995	Sequence 9995, Ap
45	44	25.0	365	7	US-11-087-099-10907	Sequence 10907, A

ALIGNMENTS

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RESULT 1
US-11-049-536-598
; Sequence 598, Application US/11049536
; Publication No. US20060024297A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pleeter, Henk
; APPLICANT: Hufton, Rene
; APPLICANT: Hoel, Rene
; TITLE OF INVENTION: TIR COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-128001
; CURRENT APPLICATION NUMBER: US/11/049,536
; PRIOR FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 598
; LENGTH: 120
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Antibody
US-11-049-536-598

Query Match          28.4% Score 50; DB 7; Length 120;
Best Local Similarity 52.4%; Pred. No. 4;
Matches 11; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY          9 PEGQRKEQWTAGINPSDGIN 29
Db          41 PG-KGLEWVSGISPGGITS 59

RESULT 2
US-11-087-099-11044
; Sequence 11044, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Adad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
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; SEQ ID NO 11044
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Nicotiana glumbaginifolia
US-11-087-099-11044

Query Match          27.8%; Score 49; DB 7; Length 356;
Best Local Similarity 51.6%; Pred. No. 16;
Matches 16; Conservative 1; Mismatches 8; Indels 6; Gaps 2;

Qy      2 DSVDSAPPQRRKEQWYAGINPSDGINSEVL 32
Db      170 DIVDS-----HYKAYLYAGINIS-GINGEVM 194

RESULT 3
US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT FILING DATE: US/10/982,545
; PRIOR FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease
; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-N1), A-beta 1-40
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
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; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(713)
; OTHER INFORMATION: beta-amyloid protein 42
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)
; OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)
; OTHER INFORMATION: C83
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
; OTHER INFORMATION: P3(42)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(711)
; OTHER INFORMATION: P3(40)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (712)..(770)
; OTHER INFORMATION: gamma-CTF(59)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (714)..(770)
; OTHER INFORMATION: gamma-CTF(57)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (721)..(770)
; OTHER INFORMATION: gamma-CTF(50)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (740)..(770)
; OTHER INFORMATION: C31
US-10-982-545-15

Query Match          27.8%; Score 49; DB 6; Length 770;
Best Local Similarity 32.4%; Pred. No. 34;
Matches 11; Conservative 8; Mismatches 13; Indels 2; Gaps 1;

Qy      2 DSVDSAPPQRRKEQWYAGINP--SDGINSEVLE 33
Db      194 DNVDSADAEEDSDVWVGADTVYADGSEDDKYVE 227

RESULT 4
US-10-789-273-38
; Sequence 38, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Baesi, Guirig
; APPLICANT: Saidanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT FILING DATE: US/10/789,273
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
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LENGTH: 770
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-789-273-38

Query Match 27.8%; Score 49; DB 6; Length 770;
 Best Local Similarity 32.4%; Pred. No. 34;
 Matches 11; Conservative 8; Mismatches 13; Indels 2; Gaps 1;

QY 2 DSVDSAPPGQRKKEQWYAGINP-SPDGINSEVL 33
 DB 194 DAVDSADAEEDSDVWVGADVDYADGSEDKYVE 227

RESULT 5
 US-11-025-712-10
 Sequence 10, Application US/11025712
 Publication No. US20050255106A1

GENERAL INFORMATION:
 APPLICANT: Bednar, Martin M.
 Thomas, G. Roger
 Gross, Cordell E.

TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/11/025,712
 FILING DATE: 28-Dec-2004
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/10/404,286
 FILING DATE: 31-Mar-2003

APPLICATION NUMBER: 09/811384
 FILING DATE: 20-DEC-2000
 APPLICATION NUMBER: 09/251652
 FILING DATE: 17-FEB-2000
 APPLICATION NUMBER: 08/788800
 FILING DATE: 22-JAN-1997
 APPLICATION NUMBER: 60/093038
 FILING DATE: 23-JAN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Evans, David W.
 REGISTRATION NUMBER: NONE
 REFERENCE/DOCKET NUMBER: P1729C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1739
 TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 232 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-11-025-712-10

Query Match 27.3%; Score 48; DB 7; Length 232;
 Best Local Similarity 55.6%; Pred. No. 14;
 Matches 10; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 9 PGQRKKEQWYAGINPSPDG 26
 DB 41 PG--KGLEWVAGINPKNG 56

RESULT 6
 US-11-087-099-3875
 Sequence 3875, Application US/11087099
 Publication No. US20060041961A1
 GENERAL INFORMATION:
 APPLICANT: Abad, Mark S. et al.
 TITLE OF INVENTION: Genes and Uses for Plant Improvement
 FILE REFERENCE: 38-21(53450)B EP
 CURRENT APPLICATION NUMBER: US/11/087,099
 CURRENT FILING DATE: 2005-03-22
 NUMBER OF SEQ ID NOS: 12464
 SEQ ID NO 3875
 LENGTH: 315
 TYPE: PRT
 ORGANISM: Lupinus angustifolius
 US-11-087-099-3875

Query Match 27.3%; Score 48; DB 7; Length 315;
 Best Local Similarity 51.6%; Pred. No. 19;
 Matches 16; Conservative 2; Mismatches 7; Indels 6; Gaps 2;

QY 2 DSVDSAPPGQRKKEQWYAGINPSPDGINSEVL 32
 DB 170 DIVDS-----HYKACLYAGINIS-GINAEVM 194

RESULT 7
 US-11-087-099-10589
 Sequence 10589, Application US/11087099
 Publication No. US20060041961A1

GENERAL INFORMATION:
 APPLICANT: Abad, Mark S. et al.
 TITLE OF INVENTION: Genes and Uses for Plant Improvement
 FILE REFERENCE: 38-21(53450)B EP
 CURRENT APPLICATION NUMBER: US/11/087,099
 CURRENT FILING DATE: 2005-03-22
 NUMBER OF SEQ ID NOS: 12464
 SEQ ID NO 10589
 LENGTH: 353
 TYPE: PRT
 ORGANISM: Lupinus luteus
 US-11-087-099-10589

Query Match 27.3%; Score 48; DB 7; Length 353;
 Best Local Similarity 51.6%; Pred. No. 22;
 Matches 16; Conservative 2; Mismatches 7; Indels 6; Gaps 2;

QY 2 DSVDSAPPGQRKKEQWYAGINPSPDGINSEVL 32
 DB 170 DIVDS-----HYKACLYAGINIS-GINAEVM 194

RESULT 8
 US-11-087-099-4390
 Sequence 4390, Application US/11087099
 Publication No. US20060041961A1
 GENERAL INFORMATION:
 APPLICANT: Abad, Mark S. et al.
 TITLE OF INVENTION: Genes and Uses for Plant Improvement
 FILE REFERENCE: 38-21(53450)B EP
 CURRENT APPLICATION NUMBER: US/11/087,099
 CURRENT FILING DATE: 2005-03-22
 NUMBER OF SEQ ID NOS: 12464
 SEQ ID NO 4390
 LENGTH: 356
 TYPE: PRT
 ORGANISM: Hevea brasiliensis
 US-11-087-099-4390

Query Match 27.3%; Score 48; DB 7; Length 356;
 Best Local Similarity 51.6%; Pred. No. 22;

Matches 16; Conservative 1; Mismatches 8; Indels 6; Gaps 2;

Oy 2 DSVDSAPPGQRKKEQWYAGINPSDGINSEVL 32
Db 170 DVDS----HYKSCLYAGININIS-GINGEVM 194

RESULT 9

US-11-025-712-12
; Sequence 12, Application US/11025712
; Publication No. US20050255108A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; Thomas, G. Roger
; Gross, Cordell E.

; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/025,712
FILING DATE: 28-Dec-2004

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/404,286

FILING DATE: 31-Mar-2003
APPLICATION NUMBER: 09/811384
FILING DATE: 20-Dec-2000

APPLICATION NUMBER: 09/251652
FILING DATE: 17-Feb-2000
APPLICATION NUMBER: 08/788800

FILING DATE: 22-Jan-1997
APPLICATION NUMBER: 60/093038
FILING DATE: 23-Jan-1996

ATTORNEY/AGENT INFORMATION:
NAME: Evans, David W.
REGISTRATION NUMBER: NONE
REFERENCE/DOCKET NUMBER: P1729C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1739
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-11-025-712-12

Query Match 27.3%; Score 48; DB 7; Length 450;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 10; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

Oy 9 PGQRKKEQWYAGINPSDG 26
Db 41 PG--KGLEWVAGINPNKG 56

RESULT 10

US-10-821-234-1219
; Sequence 1219, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Steache-Crain, Birgit

APPLICANT: Andarmant, Susan

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: PC SEQ_genes Version 1.0

SEQ ID NO 1219

LENGTH: 1133

TYPE: PRT

ORGANISM: Homo sapiens

US-10-821-234-1219

Query Match 27.0%; Score 47.5; DB 6; Length 1133;
Best Local Similarity 35.7%; Pred. No. 79;
Matches 10; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

Oy 1 EDVDSAPPGQRKKE-QWYAGINPSDGI 27
Db 4 KSAVQAQAPGGRPSDPAMPAGLGPGL 31

RESULT 11
US-10-517-939-312
; Sequence 312, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Ertsephajan, Alireza

TITLE OF INVENTION: XYLMASES, NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 564462007901

CURRENT APPLICATION NUMBER: US/10/517,939

CURRENT FILING DATE: 2004-12-13

PRIOR APPLICATION NUMBER: PCT/US03/19153

PRIOR FILING DATE: 2003-06-16

PRIOR APPLICATION NUMBER: 60/389,299

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 380

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 312

LENGTH: 1323

TYPE: PRT

ORGANISM: Unknown

FEATURE:
OTHER INFORMATION: Obtained from an environmental sample.

NAME/KEY: SIGNAL
LOCATION: (1)...(33)
US-10-517-939-312

Query Match 27.0%; Score 47.5; DB 6; Length 1323;
Best Local Similarity 26.5%; Pred. No. 92;
Matches 9; Conservative 9; Mismatches 13; Indels 3; Gaps 1;

Oy 2 DSVDSAPPGQRKKEQWYAGINP---SDGINSEVL 32
Db 652 EALDENQPDGVRSEWRILGPTDTTIDIPXYL 685

RESULT 12

US-10-467-657-6312
; Sequence 6312, Application US/10467657

```

Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ. ID NOS: 9218
SOFTWARE: Seqwinn9, version 1.04
SEQ ID NO 6312
LENGTH: 186
TYPE: PRY
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6312

```

Query Match	26.7%	Score 47	DB 6	Length 186
Best Local Similarity	35.5%	Pred. No. 16		
Matches 11	Conservative 4	Mismatches 6	Indels 10	Gaps 1

```

Qy      12 RKCEQRYAGINP-----SDGINSEVL 32
          | : | : | | |
Db      02 RELLEEWLAGQNP LVRKAFNDALKDGTAAEVI 112

```

RESULT 13
US-11-087-099-7589
Sequence 7589, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 7589
LENGTH: 356
TYPE: prt
ORGANISM: Nicotiana tabacum
US-11-087-099-7589

Query Match	26.7%	Score 47;	DB-7;	Length 356;
Best Local Similarity	51.6%	Pred. No. 30;		
Matches 16;	Conservative 1;	Mismatches 8;	Indels 6;	Gaps 2

cy 2 DSVD SAPGQRKKKEQWYAGINPSDGINSEVL 32
 ||| | ||||| ||||| :
 Db 170 DIVDS-----HYKACL YAGINIS-GINGEWM 194

RESULT 14
 US-10-485-517-166
 , Sequence 166, Application US/10485517
 , Publication No. US20050256299A1
 , GENERAL INFORMATION:
 , APPLICANT: Universality of Shearfield
 , APPLICANT: Biosynexus Incorporated
 , APPLICANT: Foster, Simon
 , APPLICANT: Mond, James
 , TITLE OR INVENTION: Antigenic Polypeptides
 , FILE REFERENCE: P100629WO
 , CURRENT APPLICATION NUMBER: US/10/485,517
 , CURRENT FILING DATE: 2004-02-02
 , PRIOR APPLICATION NUMBER: GB 0118625.9
 , PRIOR FILING DATE: 2001-08-02
 , PRIOR APPLICATION NUMBER: GB 0200349.9
 , PRIOR FILING DATE: 2002-01-09

```

; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-166

```

Query Match	26.4%	Score 46.5;	DB 6;	Length 375;
Best Local Similarity	54.5%;	Pred. No. 37;		
Matches 12;	Conservative 4;	Mismatches 5;	Indels 1;	Gaps 1;

```

QY      13 KKEQWYAGINPS-DGINSEVLE 33
      |||:|:|:|||||||
Db      71 KDEKSGAQVGPNFEGINSEVLE 92

```

RESULT 15
US-11-171-701-6
US-11-171-701-6

```

Sequence 6 Application US/11171-01
Publication No. US20060008679A1
GENERAL INFORMATION:
APPLICANT: Ocean1, Suzanne
APPLICANT: Blinkovsky, Alexander
APPLICANT: Paul
APPLICANT: Harris, Paul
APPLICANT: Yaver, Debbie
TITLE OF INVENTION: Polypeptides Having Alpha-Glucosidase Activity And
TITLE OF INVENTION: Polynucleotides Encoding Same
FILE REFERENCE: 10655.200-US
CURRENT APPLICATION NUMBER: US/11/771,701
CURRENT FILING DATE: 2005-06-29
PRIOR APPLICATION NUMBER: 60/585,336
PRIOR FILING DATE: 2005-06-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 988
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-11-171-701-6

```

Query Match	26.4%	Score 46.5;	DB 7;	Length 988;
Best Local Similarity	28.6%	Pred. No. 95;		
Matches 10; Conservative	6;	Mismatches 14;	Indels 5;	Gaps 1

```
QY      2 DSVDSAPPGQRKKEQWT-----AGINSDGINSEV 31
          ||| | | |
DB      807 DTVGKVPFGVGSGEVMWDTMTQTAVADAKPGVNATI .641
```

Search completed: March 3, 2006, 14:19:05
Job time : 1.57143 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 13:19:17 ; Search time 114.917 Seconds
(without alignments)
822.038 Million cell updates/sec

Title: US-10-646-873-47

Perfect score: 1132
Sequence: 1 MSPRLSSSGKPKSTKQEA.....HKNAARWESRIVASEDD 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseq.21.*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*
9: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1132	100.0	215	2 AAW79681	AAW79681 Human CS1
2	1132	100.0	215	4 AAE07324	AAE07324 Human CS
3	1132	100.0	215	6 ADA26384	ADA26384 Synthetic
4	1132	100.0	215	8 ADN17177	ADN17177 CS198 pro
5	1132	100.0	679	2 AAW79676	AAW79676 Human CS1
6	1132	100.0	679	4 AAE07319	AAE07319 Human CS
7	1132	100.0	679	6 AAW78590	AAW78590 Human pro
8	1132	100.0	679	6 ADA26379	ADA26379 Predicted
9	1132	100.0	679	8 ADN17172	ADN17172 CS198 pro
10	1132	100.0	679	8 ADX97562	ADX97562 Pancreati
11	1129	99.7	679	7 ADG14341	ADG14341 Human NC2
12	1127	99.6	672	4 AAW79574	AAW79574 Human pro
13	839	74.1	172	4 AAG73987	AAG73987 Human col
14	236	20.8	43	8 ABO60042	ABO60042 Human gen
15	189	16.7	36	2 AAW79677	AAW79677 Synthetic
16	189	16.7	36	4 AAE07320	AAE07320 Human CS
17	189	16.7	36	6 ADA26380	ADA26380 Synthetic
18	189	16.7	36	8 ADN17173	ADN17173 CS198 pep
19	175	15.5	35	2 AAW79679	AAW79679 Synthetic
20	175	15.5	35	4 AAE07322	AAE07322 Human CS
21	175	15.5	35	6 ADA26382	ADA26382 Synthetic
22	175	15.5	35	8 ADN17175	ADN17175 CS198 pep
23	171	15.1	33	2 AAW79680	AAW79680 Synthetic
24	171	15.1	33	4 AAE07323	AAE07323 Human CS

25	171	15.1	33	6 ADA26383	ADA26383 Synthetic
26	171	15.1	33	8 ADN17176	ADN17176 CS198 pep
27	146	12.9	31	2 AAW79678	AAW79678 Synthetic
28	146	12.9	31	4 AAE07321	AAE07321 Human CS
29	146	12.9	31	6 ADA26381	ADA26381 Synthetic
30	146	12.9	31	8 ADN17174	ADN17174 CS198 pep
31	127.5	11.3	910	7 AAW85635	AAW85635 Human hea
32	127.5	11.3	910	7 ADJ70212	ADJ70212 Human hea
33	127.5	11.3	1103	7 ADA45973	ADA45973 Human pro
34	127.5	11.3	1103	8 ADJ75439	ADJ75439 Marker ge
35	127.5	11.3	1103	8 ADJ75439	ADJ75439 Marker ge
36	127.5	11.3	1103	8 ADP54378	ADP54378 Human PRO
37	127.5	11.3	1103	8 ADP54378	ADP54378 Human PRO
38	127.5	11.3	1103	8 ADP23410	ADP23410 PRO polyp
39	127.5	11.3	1103	8 ADP23410	ADP23410 PRO polyp
40	127.5	11.3	1103	9 ADY14898	ADY14898 PRO polyp
41	127.5	11.3	1103	9 ADY18598	ADY18598 PRO polyp
42	124	11.0	948	6 ADA55374	ADA55374 Human pro
43	118	10.4	917	6 ABP75463	ABP75463 Human sec
44	118	10.4	1090	9 ADY14900	ADY14900 PRO polyp
45	114.5	10.1	324	4 ABG06360	ABG06360 Novel hum

ALIGNMENTS

RESULT 1
AAW79681 standard; protein; 215 AA.

AAW79681;

11-JAN-1999 (first entry)

Human CS198 protein C-terminal.

Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;

human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;

gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;

pancreatitis.

Homo sapiens.

WO9844159-A1.

08-OCT-1998.

30-MAR-1998; 98WO-US006251.

31-MAR-1997; 97US-00828855.

(ABBO) ABBOTT LAB.

Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

Grandeos EN, Hayden M, Hodges SC, Klaes MR, Kratochvil JD,

Roberts-Rapp L, Russell JC, Scroupe SD;

WPI; 1998-542714/46.

New gastrointestinal polynucleotides, CS198, and their detection - used

for developing products for the diagnosis and treatment of

gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.

Claim 26; Page 103; 127pp; English.

This sequence represents the C-terminal of the human CS198 protein which is used in a method to detect the presence of a target CS198 polynucleotide in a test sample. The CS198 gene is useful as a marker for gastrointestinal (GI) tract disorders. The methods and products can be used in detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition to diseases and conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus, gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative

CC colitis, and pancreaticitis
XX
SQ Sequence 215 AA;
Query Match 100.0%; Score 1132; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.8e-108;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPRLSSSGKPLSTQKASKEPPGCGPOANRGVWMEYFRLRLRPRADEPQOAVPH 60
DB 1 MSPRLSSSGKPLSTQKASKEPPGCGPOANRGVWMEYFRLRLRPRADEPQOAVPH 60
QY 61 VMGWEVAGAPALRLQKQSSDLERERESVLRREQVEAERRNALFPEVFSPTDENSQ 120
DB 61 VMGWEVAGAPALRLQKQSSDLERERESVLRREQVEAERRNALFPEVFSPTDENSQ 120
QY 121 NSRSSSQASGITGSYSVESPPFSPILHNSNVMTVEDPVD SAPPGQRKKEQWYAGINPS 180
DB 121 NSRSSSQASGITGSYSVESPPFSPILHNSNVMTVEDPVD SAPPGQRKKEQWYAGINPS 180
QY 181 DGINSEVLEAIRVTRHKNAEAERWESRIYASEED 215
DB 181 DGINSEVLEAIRVTRHKNAEAERWESRIYASEED 215
RESULT 2
AAE07324
ID AAE07324 standard; protein; 215 AA.
XX
AC AAE07324;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human CS 198 protein C-terminal portion.
XX
KM CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
KW gastritis; Crohn's disease; ulcerative colitis; pancreaticitis;
KM Barrett's oesophagus; gene therapy; drug screening; human.
OS Homo sapiens.
XX
PN US2001010904-A1.
XX
PD 02-AUG-2001.
XX
PF 30-MAR-1998; 98US-00050516.
XX
PR 31-MAR-1997; 97US-00828855.
XX
PA (BILL/) BILLINGEL P A.
XX
PA (COHE/) COHEN M.
XX
PA (COLP/) COLPITTS T L.
XX
PA (FRIE/) FRIEDMAN P N.
XX
PA (GORD/) GORDON J.
XX
PA (GRAN/) GRANADOS E N.
XX
PA (HAYD/) HAYDEN M.
XX
PA (HODG/) HODGES S C.
XX
PA (KLAS/) KLAS M R.
XX
PA (KRAT/) KRATOCHVIL J D.
XX
PA (ROBE/) ROBERTS-RAPP L.
XX
PA (RUSSE/) RUSSELL J C.
XX
PA (STRO/) STROUBE S D.
XX
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden M, Hodges SC, KLAS MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
DR MPI; 2001-496163/54.
XX
PT Detecting the presence of target CS 198 polynucleotide, useful for
PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
PT contacting test sample with at least one CS 198-specific polynucleotide.
XX

PS Claim 17; Page 52-53; 68pp; English.
XX
CC The invention relates to a method of detecting the presence of a target
CC CS 198 polynucleotide comprising contacting the test sample with at least
CC one CS 198-specific polynucleotide. The method is useful for detecting
CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
CC The CS 198 polynucleotide, polypeptides and antibodies are useful for
CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
CC treating or determining predisposition to diseases and conditions of the
CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
CC ulcerative colitis, pancreaticitis and Barrett's oesophagus. The CS 198
CC polypeptides are useful as standards or reagents in diagnostic
CC immunoassays, as components or as target sites for various therapies.
CC Antibodies directed against at least one epitope contained within these
CC polypeptides are useful as delivery agents for therapeutic agents, in
CC diagnostic tests and for screening for conditions or diseases associated
CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
CC for the generation of chimeric antibodies for therapeutic use. The CS 198
CC polynucleotide is also useful in gene therapy and drug screening. The
CC method of the invention provides an alternative, non-surgical diagnostic
CC method capable of detecting early stage GI tract disease such as cancer.
CC The present sequence is C-terminal portion of human CS 198 polypeptide
XX
SQ Sequence 215 AA;
Query Match 100.0%; Score 1132; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.8e-108;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPRLSSSGKPLSTQKASKEPPGCGPOANRGVWMEYFRLRLRPRADEPQOAVPH 60
DB 1 MSPRLSSSGKPLSTQKASKEPPGCGPOANRGVWMEYFRLRLRPRADEPQOAVPH 60
QY 61 VMGWEVAGAPALRLQKQSSDLERERESVLRREQVEAERRNALFPEVFSPTDENSQ 120
DB 61 VMGWEVAGAPALRLQKQSSDLERERESVLRREQVEAERRNALFPEVFSPTDENSQ 120
QY 121 NSRSSSQASGITGSYSVESPPFSPILHNSNVMTVEDPVD SAPPGQRKKEQWYAGINPS 180
DB 121 NSRSSSQASGITGSYSVESPPFSPILHNSNVMTVEDPVD SAPPGQRKKEQWYAGINPS 180
QY 181 DGINSEVLEAIRVTRHKNAEAERWESRIYASEED 215
DB 181 DGINSEVLEAIRVTRHKNAEAERWESRIYASEED 215
RESULT 3
ADA26384
ID ADA26384 standard; protein; 215 AA.
XX
AC ADA26384;
XX
DT 20-NOV-2003 (first entry)
XX
DE Synthetic peptide based on CS198 protein #5.
XX
KM CS198; cancer diagnosis; cancer staging; cancer monitoring;
KW cancer prognosticating; cancer prevention; cancer;
KM gastrointestinal tract disorder; gene therapy.
OS Synthetic.
XX
PN US2003082619-A1.
XX
PD 01-MAY-2003.
XX
PF 23-OCT-2002; 2002US-00278547.
XX
PR 31-MAR-1997; 97US-00828855.
XX
PR 30-MAR-1998; 98US-00050516.
XX
PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.

PA (COLP/) COLPITS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HAYD/) HAYDEN M A.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUSSE/) RUSSELL J C.
 PA (STRO/) STROUPE S D.
 XX
 PI Billingsel PA, Cohen M, Colpits TL, Friedman PN, Gordon J,
 PI Granados EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD,
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI; 2003-596961/56.
 XX
 PT Detecting the presence of a target CS198 polynucleotide in a test sample
 PT comprises contacting the sample with a CS198 specific polynucleotide and
 PT detecting the presence of the target CS198 polynucleotide in the test
 PT sample.
 XX
 PS Claim 52; Page 52; 67pp; English.
 XX
 CC The invention describes a method of detecting the presence of a target
 CC CS198 polynucleotide in a test sample. The method comprises contacting
 CC the test sample with at least one CS198 specific polynucleotide or its
 CC complement, and detecting the presence of the target CS198 polynucleotide
 CC in the test sample, where the CS198-specific polynucleotide has at least
 CC 50% identity to a polynucleotide having any of the 27 fully defined
 CC sequences of 34-2894 bp (S1-27) given in the specification, or their
 CC fragments or complements. The composition and methods are useful in
 CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
 CC or determining the predisposition of an individual to, diseases and
 CC conditions of the gastrointestinal tract, e.g. cancer and in gene
 CC therapy. This is the amino acid sequence of a synthetic peptide based on
 CC the predicted human CS198 protein sequence derived from the CS198
 CC consensus sequence shown in seq id 27.
 CC
 XX
 SQ Sequence 215 AA;
 60
 Query Match 100.0%; Score 1132; DB 6; Length 215;
 Best Local Similarity 100.0%; Pred. No. 2.8e-108;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRRHLSSESGKPLSTQKASKPPRCGPQANRGVWMEYFRLPLFRAPDEPQQAQVPH 60
 DB 1 MSRRHLSSESGKPLSTQKASKPPRCGPQANRGVWMEYFRLPLFRAPDEPQQAQVPH 60
 QY 61 VMGMEVAGAPALRLQKSSDDLREERESVLRREQVAEERRNALPPEVSPPTDENSQ 120
 DB 61 VMGMEVAGAPALRLQKSSDDLREERESVLRREQVAEERRNALPPEVSPPTDENSQ 120
 QY 121 NSRSSQASGITGSYSVSESPFPIHLHSNVMTVEDPVDSAPPGQRKKEQWYAGINPS 180
 DB 121 NSRSSQASGITGSYSVSESPFPIHLHSNVMTVEDPVDSAPPGQRKKEQWYAGINPS 180
 QY 181 DGINSEVLEAIRVTRHKNMAERWESRIYASEED 215
 DB 181 DGINSEVLEAIRVTRHKNMAERWESRIYASEED 215

KW Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.
 XX
 OS Unidentified.
 XX
 PN US2004043406-A1.
 XX
 PD 04-MAR-2004.
 XX
 PF 22-AUG-2003; 2003US-00646873.
 XX
 PR 31-MAR-1997; 97US-00828855.
 PR 30-MAR-1998; 98US-00050516.
 XX
 PA (BILL/) BILLINGEL P A.
 PA (COHE/) COHEN M.
 PA (COLP/) COLPITS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HAYD/) HAYDEN M A.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUSSE/) RUSSELL J C.
 PA (STRO/) STROUPE S D.
 XX
 XX Billingsel PA, Cohen M, Colpits TL, Friedman PN, Gordon J,
 PI Granados EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD,
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI; 2004-313754/29.
 XX
 PT Diagnosing diseases such as cancer of the gastrointestinal tract, by
 PT detecting aberrant expression or activity of the CS198 polypeptide, and
 PT associated treatment methods.
 XX
 PS Claim 17; SEQ ID NO 47; 67pp; English.
 XX
 CC The invention relates to reagents and methods for detecting diseases of
 CC the gastrointestinal (GI) tract. The method involves detecting the
 CC presence of target CS198 polynucleotide in the test sample. The methods
 CC and compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of diseases or conditions associated with
 CC aberrant expression or activity of the CS198 polypeptide, such as cancer
 CC of the gastrointestinal tract. These are also useful in gene therapy. The
 CC present sequence is a CS198 protein used to illustrate the method of the
 CC invention.
 CC
 XX
 SQ Sequence 215 AA;
 60
 Query Match 100.0%; Score 1132; DB 8; Length 215;
 Best Local Similarity 100.0%; Pred. No. 2.8e-108;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRRHLSSESGKPLSTQKASKPPRCGPQANRGVWMEYFRLPLFRAPDEPQQAQVPH 60
 DB 1 MSRRHLSSESGKPLSTQKASKPPRCGPQANRGVWMEYFRLPLFRAPDEPQQAQVPH 60
 QY 61 VMGMEVAGAPALRLQKSSDDLREERESVLRREQVAEERRNALPPEVSPPTDENSQ 120
 DB 61 VMGMEVAGAPALRLQKSSDDLREERESVLRREQVAEERRNALPPEVSPPTDENSQ 120
 QY 121 NSRSSQASGITGSYSVSESPFPIHLHSNVMTVEDPVDSAPPGQRKKEQWYAGINPS 180
 DB 121 NSRSSQASGITGSYSVSESPFPIHLHSNVMTVEDPVDSAPPGQRKKEQWYAGINPS 180
 QY 181 DGINSEVLEAIRVTRHKNMAERWESRIYASEED 215
 DB 181 DGINSEVLEAIRVTRHKNMAERWESRIYASEED 215

RESULT 5

AAW79676
ID AAW79676 standard; protein; 679 AA.
XX
AC AAW79676;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human CS198 protein.
XX
KW Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
KW human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
KW pancreatitis.
XX
OS Homo sapiens.
XX
PN W09844159-A1.
XX
PD 08-OCT-1998.
XX
PF 30-MAR-1998; 98MO-US006251.
XX
PR 31-MAR-1997; 97US-00828855.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden M, Hodges SC, Klaas MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
DR WPI, 1998-542714/46.
XX
PT New gastrointestinal polynucleotides, CS198, and their detection - used
PT for developing products for the diagnosis and treatment of
PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
XX
PS Claim 26; Page 100-102; 127pp; English.
XX
CC This sequence represents the human CS198 protein which is used in a
CC method to detect the presence of a target CS198 polynucleotide in a test
CC sample. The CS198 gene is useful as a marker for gastrointestinal (GI)
CC tract disorders. The methods and products can be used in detecting,
CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
CC or determining the predisposition to diseases and conditions of the GI
CC tract, such as GI tract cancer, Barrett's oesophagus, gastric ulcer,
CC gastritis, leiomyoma, polyps, Crohn's disease, ulcerative colitis, and
CC pancreatitis
XX
SQ Sequence 679 AA;
XX
Query Match 100.0%; Score 1132; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.4e-107;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSRRHSSSGKPLSTKQKASRPPGCGPOANGVVRWMEFRRLRPFRAPDEPOAOYPH 60
DB 465 MSRRHSSSGKPLSTKQKASRPPGCGPOANGVVRWMEFRRLRPFRAPDEPOAOYPH 524
QY 61 VWGWEVAGAPALRLQKSSDLEBRRESVLRDEQVAEERNALPFEVFSPTPDNSDQ 120
DB 525 VWGWEVAGAPALRLQKSSDLEBRRESVLRDEQVAEERNALPFEVFSPTPDNSDQ 584
QY 121 NSRSSQASGTCGTSVSSPFPPIHLHSNVAWTVEDPVDASAPFGQKKEQWYGINPS 180
DB 585 NSRSSQASGTCGTSVSSPFPPIHLHSNVAWTVEDPVDASAPFGQKKEQWYGINPS 644
QY 181 DGINSEVLEAIRVTRHKNAAMERWSRIYASEDD 215
DB 645 DGINSEVLEAIRVTRHKNAAMERWSRIYASEDD 679

AAE07319 standard; protein; 679 AA.
XX
AC AAE07319;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human CS 198 protein.
XX
KW CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
KW gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
KW Barrett's oesophagus; gene therapy; drug screening; human.
XX
OS Homo sapiens.
XX
FT Key Location/Qualifiers
FT Misc-difference 353 /note="Encoded by CGGN"
XX
XX US2001010904-A1.
XX
XX 02-AUG-2001.
XX
XX 30-MAR-1998; 98US-00050516.
XX
XX 31-MAR-1997; 97US-00828855;
XX
PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M.
PA (HODG/) HODGES S C.
PA (KLAAS/) KLAAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUSSE/) RUSSELL J C.
PA (STRO/) STROUPE S D.
XX
PI Billingel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden M, Hodges SC, Klaas MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
DR WPI; 2001-496163/54.
DR N-PSDB; AAD13637.
XX
PT Detecting the presence of target CS 198 polynucleotide, useful for
PT detecting or diagnosing diseases of the gastrointestinal tract, comprises
PT contacting test sample with at least one CS 198-specific polynucleotide.
XX
PS Claim 17; Page 49-51; 68pp; English.
XX
CC The invention relates to a method of detecting the presence of a target
CC CS 198 polynucleotide comprising contacting the test sample with at least
CC one CS 198-specific polynucleotide. The method is useful for detecting
CC diseases of the gastrointestinal (GI) tract organs, particularly cancer.
CC The CS 198 polynucleotides, polypeptides and antibodies are useful for
CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
CC treating or determining predisposition to diseases and conditions of the
CC GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
CC ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
CC polypeptides are useful as standards or reagents in diagnostic
CC immunoassays, as components or as target sites for various therapies.
CC Antibodies directed against at least one epitope contained within these
CC polypeptides are useful as delivery agents for therapeutic agents, in
CC diagnostic tests and for screening for conditions or diseases associated
CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
CC for the generation of chimeric antibodies for therapeutic use. The CS 198
CC polynucleotide is also useful in gene therapy and drug screening. The
CC method of the invention provides an alternative, non-surgical diagnostic
CC method capable of detecting early stage GI tract disease such as cancer.
CC The present sequence is human CS 198 polypeptide

XX SQ Sequence 679 AA;
 Query Match 100.0%; Score 1132; DB 4; Length 679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-107;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQKASRPGCCPOANRGVWMEYFRLRPLRFAPDEPQQAQVPH 60
 DB 465 MSPRLSSSGKPLSTKQKASRPGCCPOANRGVWMEYFRLRPLRFAPDEPQQAQVPH 524

QY 61 VWGWEVAGAPALRLQKSSDILERRRSVLRREQVAEERNALPPEVFSPTPENSQ 120
 DB 525 VWGWEVAGAPALRLQKSSDILERRRSVLRREQVAEERNALPPEVFSPTPENSQ 584

QY 121 NSRSSSQASGITGSYSVSESPFSPHLSNVAMTVEDVPDSAPPGQRKQGMVAGINPS 180
 DB 585 NSRSSSQASGITGSYSVSESPFSPHLSNVAMTVEDVPDSAPPGQRKQGMVAGINPS 644

QY 181 DGINSEVLEAIRVTRHKNAERWESRIYASEED 215
 DB 645 DGINSEVLEAIRVTRHKNAERWESRIYASEED 679

RESULT 7
 AAM78590
 ID AAM78590 standard; protein; 679 AA.
 XX AAM78590;
 XX 06-NOV-2001 (first entry)
 XX Human protein SEQ ID NO 1252.
 DE Human, cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX Homo sapiens.
 OS
 XX WO200157190-A2.
 XX 09-AUG-2001.
 PD
 XX 05-FEB-2001; 2001MO-US004098.
 PF
 XX 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Dymnac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhtman T, Goodrich R;
 XX WPI; 2001-476283/51.
 DR N-PSDB; AAKS1723.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX
 PS Claim 20; Page 3512-3514; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAKS1456-AAK51435) and the
 CC encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 210 (AAK52581), 211
 CC (AAK52582) and 366 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX

QY Sequence 679 AA;
 Query Match 100.0%; Score 1132; DB 4; Length 679;
 Best Local Similarity 100.0%; Pred. No. 1.4e-107;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQKASRPGCCPOANRGVWMEYFRLRPLRFAPDEPQQAQVPH 60
 DB 465 MSPRLSSSGKPLSTKQKASRPGCCPOANRGVWMEYFRLRPLRFAPDEPQQAQVPH 524

QY 61 VWGWEVAGAPALRLQKSSDILERRRSVLRREQVAEERNALPPEVFSPTPENSQ 120
 DB 525 VWGWEVAGAPALRLQKSSDILERRRSVLRREQVAEERNALPPEVFSPTPENSQ 584

QY 121 NSRSSSQASGITGSYSVSESPFSPHLSNVAMTVEDVPDSAPPGQRKQGMVAGINPS 180
 DB 585 NSRSSSQASGITGSYSVSESPFSPHLSNVAMTVEDVPDSAPPGQRKQGMVAGINPS 644

QY 181 DGINSEVLEAIRVTRHKNAERWESRIYASEED 215
 DB 645 DGINSEVLEAIRVTRHKNAERWESRIYASEED 679

RESULT 8
 ADA26379
 ID ADA26379 standard; protein; 679 AA.
 XX ADA26379;
 XX 20-NOV-2003 (first entry)
 DT
 XX Predicted amino acid sequence of the CS198 protein.
 DE
 XX CS198; cancer diagnosis; cancer staging; cancer monitoring;
 KW cancer prognosticating; cancer prevention; cancer;
 KW gastrointestinal tract disorder; gene therapy.
 XX
 XX Synthetic;
 OS
 XX US2003082619-A1.
 XX
 XX 01-MAY-2003.
 PD
 XX 23-OCT-2002; 2002US-00278547.
 PF
 XX 31-MAR-1997; 97US-00828855.
 PR 30-MAR-1998; 98US-00050516.
 XX
 XX (BILL/) BILLINGEL P A.
 PA (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS B N.
 PA (HAYD/) HAYDEN M A.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAP L.
 PA (RUSSE/) RUSSELL J C.
 PA (STRO/) STROUPE S D.
 XX

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PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden MA, Hodges SC, Klass MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
DR WPI; 2003-596961/56.
XX
XX
XX PS Claim 17; Page 48-50; 67pp; English.
XX
XX CC The invention describes a method of detecting the presence of a target
XX CC CS198 polynucleotide in a test sample. The method comprises contacting
XX CC the test sample with at least one CS198 specific polynucleotide or its
XX CC complement, and detecting the presence of the target CS198 polynucleotide
XX CC in the test sample, where the CS198-specific polynucleotide has at least
XX CC 50% identity to a polynucleotide having any of the 27 fully defined
XX CC sequences of 34-2894 bp (51-27) given in the specification, or their
XX CC fragments or complements. The composition and methods are useful in
XX CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
XX CC or determining the predisposition of an individual to, diseases and
XX CC conditions of the gastrointestinal tract, e.g. cancer and in gene
XX CC therapy. This is the predicted amino acid sequence of the human CS198
XX CC protein derived from the CS198 consensus sequence shown in seq id 27.
XX
XX SQ Sequence 679 AA;
XX
XX Query Match 100.0%; Score 1132; DB 6; Length 679;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-107;
XX Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MSPRHLSSSGKPLSTKQEQASKPPGCGQANNGVYRWKXFPRLRPRFAPDEPQOAYPH 60
Dd 465 MSPRHLSSSGKPLSTKQEQASKPPGCGQANNGVYRWKXFPRLRPRFAPDEPQOAYPH 524
QY 61 VWGWEVAGAPALRLQKQSSDLERERESVLRREQEVAEERNALPFEVFSPTDENSQ 120
Dd 525 VWGWEVAGAPALRLQKQSSDLERERESVLRREQEVAEERNALPFEVFSPTDENSQ 584
QY 121 NSRSSQASGRTGSYSVSESPFFSTIHLHSNVAWTVEDPVDASAPGCKQKQWYAGINPS 180
Dd 585 NSRSSQASGRTGSYSVSESPFFSTIHLHSNVAWTVEDPVDASAPGCKQKQWYAGINPS 644
QY 181 DGINSEVLEAIRVTRHKNAAMERWESRTIYASEDD 215
Dd 645 DGINSEVLEAIRVTRHKNAAMERWESRTIYASEDD 679
XX
XX RESULT 9
XX ADN17172
XX ID ADN17172 standard; protein; 679 AA.
XX
XX AC ADN17172;
XX
XX DT 17-JUN-2004 (first entry)
XX
XX DE CS198 protein #1.
XX
XX KW Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.
XX
XX OS Unidentified.
XX
XX PN US2004043406-A1.
XX
XX PD 04-MAR-2004.
XX
XX PF 22-AUG-2003; 2003US-00646873.
XX
XX PR 31-MAR-1997; 97US-00828855.
XX PR 30-MAR-1998; 98US-00050516.
XX

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PA (BILL//) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M A.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUSSEL/) RUSSELL J C.
PA (STROU/) STROUPE S D.
XX
XX Billingel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden MA, Hodges SC, Klas MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 2004-313754/29.
DR GENBANK; D87440.
XX
XX Diagnosing diseases such as cancer of the gastrointestinal tract, by
PT detecting aberrant expression or activity of the CS198 polypeptide, and
PR associated treatment methods.
XX
XX Claim 17; SEQ ID NO 42; 67bp; English.
XX
XX The invention relates to reagents and methods for detecting diseases of
CC the gastrointestinal (GI) tract. The method involves detecting the
CC presence of target CS198 polynucleotide in the test sample. The methods
CC and compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the CS198 polypeptide, such as cancer
CC of the gastrointestinal tract. These are also useful in gene therapy. The
CC present sequence is a CS198 protein used to illustrate the method of the
CC invention.
XX
XX SQ Sequence 679 AA;
XX
Query Match 100.0%; Score 1132; DB 8; Length 679;
Beat Local Similarity 100.0%; Pred. No. 1.4e-107;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 MSPRHLSSESGKPLSTKQEASKPPRGCPQANRGVVVRWMEYFLRLPFRAPADEPQAQVPH 60
DB 46S MSPRHLSSESGKPLSTKQEASKPPRGCPQANRGVVVRWMEYFLRLPFRAPADEPQAQVPH 524
QY 61 VMGWGVAAQAPALRLQKSSSDLLERERSVYLRRGEVAEERNALPFVEFSSTPPENSNO 120
DB 52S VMGWGVAAQAPALRLQKSSSDLLERERSVYLRRGEVAEERNALPFVEFSSTPPENSNO 584
QY 121 NSRSSSQASGITGSYSVESPPFSFIHLHSNVAMTWVPVD SAPPGORKKEQMYAGINPS 180
DB 56S NSRSSSQASGITGSYSVESPPFSFIHLHSNVAMTWVPVD SAPPGORKKEQMYAGINPS 644
QY 181 DGINSEVLEAIRVTFRKNMAERMESRTIYASEDD 215
DB 64S DGINSEVLEAIRVTFRKNMAERMESRTIYASEDD 679
XX
RESULT 10
ID ADX97562
XX ADX97562 standard; protein; 692 AA.
AC ADX97562;
DT 21-APR-2005 (first entry)
XX
DE Pancreatic cancer associated human protein, SEQ ID 110.
XX pancreas tumor; cytoablastic.
OS Homo sapiens

```

XX EPI471075-A2.
XX 27-OCT-2004.
XX 31-MAR-2004; 2004EP-00090124.
XX 31-MAR-2003; 2003DE-01015834.
XX (HINZ/) HINZMANN B.
XX (ROSE/) ROSENTHAL A.
XX (PILAI/) PILARSKY C.
XX (DAHL/) DAHL E.
XX (SPEC/) SPECHT T.
XX (LICHTNER R.)
XX Rosenthal A., Pilarczyk C., Dahl E., Specht T., Bruemendorf T.,
XX Lichtner R., Staud E., Roepecke S., Li X;
XX WPI; 2004-768082/76.
XX N-PSDB; ADX97491.
XX New nucleic acid differentially expressed in pancreatic tumor tissue, for
XX use as diagnostic agents and in screening for therapeutic agents.
XX Claim 2; SEQ ID NO 110; 28bp; German.
XX The invention relates to a novel human nucleic acid sequence of the
XX pancreas and its encoded protein. The invention further comprises:
XX protein and peptides, preferably isolated, that contain a sequence
XX encoded by the novel nucleic acid; and methods for diagnosis and
XX treatment of pancreatic cancer, using a substance that inhibits or binds
XX to the protein or its DNA, including: an antisense oligonucleotide, short
XX interfering RNA or ribozyme directed against the pancreatic protein, an
XX organic molecule, particularly having a molecular weight below 5000,
XX especially 300, that binds to the pancreatic DNA, an aptamer or
XX (monoclonal) antibody, preferably human or humanized, that binds to the
XX pancreatic DNA, or an anti-idiotypic antibody raised against the
XX monoclonal antibody, any of which may be derivatized with a reporter
XX group, cytotoxic compound, immunostimulant and/or radiolabeled. The novel
XX human pancreatic protein and their encoding DNA have cytostatic
XX activity. The novel sequences are useful for inhibiting transcription
XX and/or expression of genes and proteins associated with pancreatic
XX cancer. This sequence represents one of the novel human pancreatic
XX proteins of the invention. Note: This sequence is not shown in the
XX specification, it has been electronically downloaded from a DVD-ROM
XX provided with this specification by the European Patent Office.
XX SQ Sequence 692 AA;
XX
XX Query Match 100.0%; Score 1132; DB 8; Length 692;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-107;
XX Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MSPRHLSESSGKPLSTKQASKPPRCGPOANRGVMEYFRLPLFRAPDEPQQAQVPH 60
XX DB MSRRLHSESSGKPLSTKQASKPPRCGPOANRGVMEYFRLPLFRAPDEPQQAQVPH 537
XX 478 MSRRLHSESSGKPLSTKQASKPPRCGPOANRGVMEYFRLPLFRAPDEPQQAQVPH 537
XX
XX 61 VMGMEVAGAPALRLQKSSQSDLLERRESEVLRBOEVAERERNAALPEVFSPTPDENSQ 120
XX DB VMGMEVAGAPALRLQKSSQSDLLERRESEVLRBOEVAERERNAALPEVFSPTPDENSQ 597
XX 538 VMGMEVAGAPALRLQKSSQSDLLERRESEVLRBOEVAERERNAALPEVFSPTPDENSQ 597
XX
XX 121 NSRSSHQAAGITGSYSVSSPPSPHLSNVAWTVEDPVDASAPPGQRKKEQWYAGINPS 180
XX DB NSRSSHQAAGITGSYSVSSPPSPHLSNVAWTVEDPVDASAPPGQRKKEQWYAGINPS 657
XX 598 NSRSSHQAAGITGSYSVSSPPSPHLSNVAWTVEDPVDASAPPGQRKKEQWYAGINPS 657
XX
XX 181 DGINSEVLEAIRVTRHKNMAAERMSRIYASEED 215
XX DB DGINSEVLEAIRVTRHKNMAAERMSRIYASEED 692

RESULT 11
ADG14341

ID ADG14341 standard; protein; 679 AA.
XX AC ADG14341;
XX 26-FEB-2004 (first entry)
XX Human NC2.
XX Human, NC1; NC2; NC3; PHH1; pancreas beta-cell; insulin; antidiabetic;
XX neuroprotective.
XX Homo sapiens.
XX WO2003078631-A1.
XX 25-SEP-2003.
XX 06-MAR-2003; 2003WO-JP002620.
XX 15-MAR-2002; 2002JP-00071592.
XX (KANF) KANEKA CORP.
XX Niwa H, Yamashita K;
XX WPI; 2003-767524/72.
XX N-PSDB; ADG14344.
XX Familial persistent hyperinsulinemic hypoglycemia of infancy (PHH1)
XX patient-expressed genes for detecting and screening e.g. proliferative
XX insulin-producing cells in treatment of PHH1.
XX Claim 1; SEQ ID NO 2; 34bp; Japanese.
XX The present invention relates to human NC1, NC2 and NC3 proteins and
XX coding sequences (ADG14340-ADG14345). The coding sequences are useful for
XX detecting and screening proliferative insulin-producing cells as well as
XX differentiation and proliferation of such cells and their precursors as
XX analogous cells in treatment of e.g. PHH1 and diseases due to
XX differentiation/proliferation abnormality, diseases of the nervous system
XX and pancreas. The coding sequences are also useful as spontaneous
XX and proliferation models of pancreas beta-cells. The novel genes NC1, NC2 and
XX NC3 were isolated from the pancreas of PHH1 patients, which were used in
XX testing for the detection of proliferative insulin-producing cells or
XX pancreas beta-cells by Northern analysis.
XX SQ Sequence 679 AA;
XX
XX Query Match 99.7%; Score 1129; DB 7; Length 679;
XX Best Local Similarity 99.5%; Pred. No. 2.9e-107;
XX Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MSPRHLSESSGKPLSTKQASKPPRCGPOANRGVMEYFRLPLFRAPDEPQQAQVPH 60
XX DB MSRRLHSESSGKPLSTKQASKPPRCGPOANRGVMEYFRLPLFRAPDEPQQAQVPH 524
XX 465 MSRRLHSESSGKPLSTKQASKPPRCGPOANRGVMEYFRLPLFRAPDEPQQAQVPH 524
XX
XX 61 VMGMEVAGAPALRLQKSSQSDLLERRESEVLRBOEVAERERNAALPEVFSPTPDENSQ 120
XX DB VMGMEVAGAPALRLQKSSQSDLLERRESEVLRBOEVAERERNAALPEVFSPTPDENSQ 584
XX 525 VMGMEVAGAPALRLQKSSQSDLLERRESEVLRBOEVAERERNAALPEVFSPTPDENSQ 584
XX
XX 121 NSRSSHQAAGITGSYSVSSPPSPHLSNVAWTVEDPVDASAPPGQRKKEQWYAGINPS 180
XX DB NSRSSHQAAGITGSYSVSSPPSPHLSNVAWTVEDPVDASAPPGQRKKEQWYAGINPS 644
XX 585 NSRSSHQAAGITGSYSVSSPPSPHLSNVAWTVEDPVDASAPPGQRKKEQWYAGINPS 644
XX
XX 181 DGINSEVLEAIRVTRHKNMAAERMSRIYASEED 215
XX DB DGINSEVLEAIRVTRHKNMAAERMSRIYASEED 679

RESULT 12
AAM79574
ID AAM79574 standard; protein; 672 AA.
XX


```
AC AAM79574;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human protein SEQ ID NO 3220.
DE
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
OS
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX 20-JUN-2000; 2000US-00598075.
XX 19-JUL-2000; 2000US-00620325.
XX 01-SEP-2000; 2000US-00654936.
XX 15-SEP-2000; 2000US-00663561.
XX 20-OCT-2000; 2000US-00693325.
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Dramanac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao QH, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wehrman T, Goodrich K;
XX
XX WPI; 2001-476283/51.
XX
XX N-PSDB; AAK52707.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX
XX Claim 20; Page 288; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activity/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
XX (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
XX sequence listing were missing at the time of publication
XX
XX Sequence 672 AA;
SQ
Query Match 99.6%; Score 1127; DB 4; Length 672;
Best Local Similarity 99.5%; Pred. No. 4,6e-107;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPRLSSSGKPLSTTKQEAASPPRGCPQANRGVVRWEYFRLRLRFRAPDPEDQAVPH 60
DB 458 MSPRLSSSGKPLSTTKQEAASPPRGCPQANRGVVRWEYFRLRLRFRAPDPEDQAVPH 517
QY 61 VMGWVAGAPALRLQKSSDLEERESVLRBOEVAEERNALFPEVFSPTPENSDQ 120
DB 518 VMGWVAGAPALRLQKSSDLEERESVLRBOEVAEERNALFPEVFSPTPENSDQ 577
QY 121 NSRSSQASGITGYSVSESPFPIHLHSNVAMVVEDPVD SAPGQRKKEQWYAGINPS 180
DB 578 NSRSSQASGITGYSVSESPFPIHLHSNVAMVVEDPVD SAPGQRKKEQWYAGINPS 637
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QY 181 DGINSEVLEAIRVTRHKNAMAEKRESRIYASEEDD 215
DB 638 DGINSEVLEAIRVTRHKNAMAEKRESRIYASEEDD 672
RESULT 13
AAG73987
ID AAG73987 standard; protein; 172 AA.
XX
XX AAG73987;
XX
XX 03-SEP-2001 (first entry)
XX
XX Human colon cancer antigen protein SEQ ID NO:4751.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma.
XX
XX Homo sapiens.
OS
XX WO200122920-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000WO-US026524.
XX
XX 29-SEP-1999; 99US-0157137P.
XX 03-NOV-1999; 99US-0163280P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruden SM, Barash SC, Birse CE, Rosen CA;
XX
XX WPI; 2001-235357/24.
XX
XX N-PSDB; AAH33418.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.
XX
XX Claim 11; Page 6550-6551; 9803pp; English.
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where the
XX proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytotoxic activity and can be used in gene therapy
XX and vaccine production. N and P may be used in the prevention, diagnosis
XX and treatment of diseases associated with inappropriate P expression. For
XX example, N and P may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of P by expressing inactive proteins or to
XX supplement the patients own production of P. Additionally, N may be used
XX to produce the colon cancer-associated Ps, by inserting the nucleic acids
XX into a host cell and culturing the cell to express the proteins. N and P
XX can be used in the prevention, diagnosis and treatment of colorectal
XX carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent
XX sequences used in the exemplification of the present invention. N.B.
XX Pages 666 to 682 and page 7053 of the sequence listing were missing at
XX time of publication, meaning no sequences are present for SEQ ID NO:1027
XX to 1052, 7921 and 7922
XX
XX Sequence 172 AA;
SQ
Query Match 74.1%; Score 839; DB 4; Length 172;
Best Local Similarity 87.0%; Pred. No. 3.9e-78;
Matches 167; Conservative 0; Mismatches 5; Indels 20; Gaps 1;
QY 24 PRGQPOANRGVVRWEYFRLRLRFRAPDPEDQAVPHVMGWVAGAPALRLQKSSDLE 83
DB 1 PTRPPOANRGVVRWEYFRLRLRFR-----APALRLQKSSDLE 40
QY 84 EREKESVLRBOEVAEERNALFPEVFSPTPENSDQNSRSSQASGITGYSVSESPF 143
```


DB 41 ERESVLRREQVXERRNNLFPVEVSPTPDENSDONSSQASGITGSVSESPFF 100
 QY 144 SIPIHLSNVAMTWEDPVDSAPPGORKKEGWYAGINPSDQINSEVLEATRWTHKRAMER 203
 DB 101 SIPIHLSNVAMTWEDPVDSAPPGORKKEGWYAGINPSDQINSEVLEATRWTHKRAMER 160
 QY 204 WESRIYASEDD 215
 DB 161 WESRIYASEDD 172

RESULT 14

ABO60042
 ID ABO60042 standard; protein; 43 AA.
 AC ABO60042;
 XX
 XX
 DT 29-JUL-2004 (first entry)
 XX
 XX
 DE Human genome derived single exon protein #6276.
 XX
 XX
 KW Human; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 XX
 OS Homo sapiens.
 XX
 XX
 PN US2003194704-A1.
 XX
 PD 16-OCT-2003.
 XX
 PF 03-APR-2002; 2002US-00029386.
 XX
 PR 03-APR-2002; 2002US-00029386.
 XX
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 XX
 PI Penn SG, Rank DR, Hanzel DK;
 XX
 DR MPI; 2004-119264/12.

PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 XX
 PS Claim 45; SEQ ID NO 33676; 80bp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressed set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying

CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 CC
 XX
 SQ Sequence 43 AA;

Query Match 20.8%; Score 236; DB 8; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.2e-16;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 ITGSYSVESSEPPFSPIHLSNVAMTWEDPVDSAPPGORKKEGW 173
 DB 1 ITGSYSVESSEPPFSPIHLSNVAMTWEDPVDSAPPGORKKEGW 43

RESULT 15

AAW79677
 ID AAW79677 standard; protein; 36 AA.
 AC AAW79677;
 XX
 XX
 DT 11-JAN-1999 (first entry)
 XX
 XX
 DE Synthetic CS198 derived peptide #1.
 XX
 XX
 KW Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
 KW human; predilection; treatment; Barrett's oesophagus; gastric ulcer;
 KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
 KW pancreatitis.
 XX
 OS Synthetic.
 XX
 XX
 PN WO9844159-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98WO-US006251.
 XX
 PR 31-MAR-1997; 97US-00828855.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitta TL, Friedman PV, Gordon J;
 PI Grandoe EN, Hayden M, Hodges SC, Klaas WR, Kralovich JJ;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR MPI; 1998-542714/46.

PT New gastrointestinal polynucleotides, CS198, and their detection - used
 PT for developing products for the diagnosis and treatment of
 PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
 XX
 PS Claim 26; Page 102; 127bp; English.

XX AAW79677-W79680 are synthetic CS198 derived peptide fragments which are
 CC used in a method to detect the presence of a target human CS198
 CC polynucleotide in a test sample. The CS198 gene is useful as a marker for
 CC gastrointestinal (GI) tract disorders. The methods and products can be
 CC used in detecting, diagnosing, staging, monitoring, prognosticating,
 CC preventing or treating, or determining the predisposition to diseases and
 CC conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
 CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative
 CC colitis, and pancreatitis

XX Sequence 36 AA;

Query Match 16.7%; Score 189; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 6.5e-12;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSPRLSSSGKPLSTKQASKPPRGCPQANRGVVR 36
 |||||
 Db 1 MSPRLSSSGKPLSTKQASKPPRGCPQANRGVVR 36
 |||||

Search completed: March 3, 2006, 13:35:25
 Job time : 114.917 secs

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 3, 2006, 13:26:31 / Search time 13.5811 Seconds
(without alignments)
1523.185 Million cell updates/sec

Title: US-10-646-873-47

Perfect score: 1132

Sequence: 1 MSPRHLSGSGKPLSTKQEA.....HKMAERWESRIVASEDD 215

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1132	100.0	679	2 T00636	hypothetical prote
2	118	10.4	321	2 T14787	hypothetical prote
3	101.5	9.0	1048	2 T23764	hypothetical prote
4	101	8.9	1145	2 A59251	myosin - Acetabula
5	96	8.5	1446	1 A45344	immediate-early pr
6	94.5	8.3	862	2 T46389	hypothetical prote
7	93.5	8.3	699	2 A43734	probable protein k
8	93	8.2	329	2 G83744	uricase BH0759 (lm
9	93	8.2	490	2 S67581	STP4 protein - yea
10	92.5	8.2	7962	2 T38346	elastic titin - hu
11	92	8.1	638	2 D85435	BE1-like homeobox
12	90	8.0	783	2 T00354	hypothetical prote
13	89.5	7.9	564	2 S37241	legumin B - fava b
14	88	7.8	1390	2 T14004	trif protein - all
15	87	7.7	814	2 T02195	hypothetical prote
16	86.5	7.6	872	2 S62061	SCDS protein - yea
17	86.5	7.6	969	2 A70912	probable leus prot
18	86.5	7.6	1872	2 T30888	vitellogenin - Ath
19	86	7.6	1486	2 B85618	hypothetical prote
20	86	7.6	1486	2 G90754	kinasin-like cell
21	86	7.6	1486	2 C64832	cell division prot
22	86	7.6	1534	2 JH0228	cell division prot
23	85	7.5	564	2 T53106	gene g11 protein -
24	85	7.5	1071	2 B85343	hypothetical prote
25	85	7.5	1488	2 AH0615	cell division prot
26	84.5	7.5	398	2 S35264	cell division prot
27	84.5	7.5	1033	2 T33470	hypothetical prote
28	84.5	7.5	1051	1 JH0051	serine/threonine-S
29	84	7.4	723	2 A48217	single-strand DNA/

30	84	7.4	884	2 S66308	nitrate reductase
31	84	7.4	1378	2 G86837	protein F53H1.4 [i
32	84	7.4	5327	2 T13564	microtubule-associ
33	83.5	7.4	489	2 B69680	para-nitrobenzyl e
34	83.5	7.4	581	2 T22455	hypothetical prote
35	83.5	7.4	611	2 T22456	hypothetical prote
36	83.5	7.4	881	2 S25445	nitrate reductase
37	83.5	7.4	1230	2 T22458	hypothetical prote
38	83	7.3	275	1 TYRTR	transforming prote
39	83	7.3	686	2 T20898	hypothetical prote
40	83	7.3	1435	2 A37793	erythrocyte-bindin
41	82.5	7.3	210	2 F69983	hypothetical prote
42	82.5	7.3	261	1 WMBEX	infected cell prot
43	82.5	7.3	386	2 A41950	retrovirus-related
44	82.5	7.3	450	2 T21931	hypothetical prote
45	82.5	7.3	1196	2 T23832	protein-tyrosine k

ALIGNMENTS

RESULT 1

T00636 hypothetical protein F21856.2 - human

C:Species: Homo sapiens (man)

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C:Accession: T00636

R:Amesdin, J.E.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhart-Schultz, K.; C

rgescu, A.; Avila, J.; Liu, S.; Bruce, R.; Quan, G.; Montgomery, M.; Ow, D.; Nolan, M.;

submitted to the EMBL Data Library, January 1998

A:Description: Sequence analysis of a 3.5 Mb contig in 19p13.3 between CDC34 and D19S342

A:Reference number: Z14195

A:Accession: T00636

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-679 <1AM>

A:Cross-references: UNIPROT:Q8IVT2; UNIPARC:UPI00000745CD; EMBL:AC004030; NID:G2804590;

C:Genetic8:

A:Map position: 19p13.3

A:Introns: 594/1; 637/3; 650/3

A>Note: F21856_2

Query Match	Score	DB 2:	Length	679:
Best Local Similarity	100.0%	Pred. No. 8.5e-84:		
Matches 215;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps 0;				
QY	1	MSPRHLSGSGKPLSTKQEA	60	
DB	465	MSPRHLSGSGKPLSTKQEA	524	
QY	61	VWGMEVAGAPALRLQKSGSSDLLE	120	
DB	525	VWGMEVAGAPALRLQKSGSSDLLE	584	
QY	121	NRSSSQASGIGTGSVSSPFP	180	
DB	585	NRSSSQASGIGTGSVSSPFP	644	
QY	181	DGINSFVLEAIRVTRHKNA	215	
DB	645	DGINSFVLEAIRVTRHKNA	679	

RESULT 2

T14787 hypothetical protein DKFZP564L0716.1 - human (fragments)

C:Species: Homo sapiens (man)

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T14787

R:Diesterhoef, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, August 1999

A:Reference number: Z18178

A:Accession: T14787

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119;120-321 <DUE>
A:Cross-references: UNIPARC:UP1000017C19B; UNIPARC:UP1000017C19C; EMBL:AL110268
A:Experimental source: fetal brain; clone DKFZps64L0716
A>Note: the cDNA sequence contains a +1 frameshift near codon 119
C:Genetics:
A>Note: DKFZps64L0716.1

Query Match
Best Local Similarity 23.3%; Score 118; DB 2; Length 321;
Matches 42; Conservative 34; Mismatches 46; Indels 58; Gaps 6;

Qy 66 VAGAPALLOKSSQSDLLERERESTLRREQVAER-----RNALPEPV----- 109
Db 167 MVGPPLKLSRKQRTLSMIEBIRAAQEREBELKRGVLTQSPRTNA--PSLPSFTC 224
Qy 110 -----PSPFPDENSDNSRSSQASGITGSYSVESPPSPFIHLHSNVAMT 155
Db 225 YKTAPGKLEKVPSPSPFTTEGSLQPDLAPEBAAG-----TQNP-----KNLMQT 269
Qy 156 VEDPVSAPPGQKKKQWYAGINPSDGINSEVLEIRVTRHKNAVERMESRIYASEED 215
Db 270 LMEDVETHKSKRREMD-----DSSVLEATRVNRKRSALALRWEGVYANGEEB 318

RESULT 3
T23764
hypothetical protein M142.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A:Accession: T23764; T27112
R:McMurray, A.
A:Reference number: 219795
A:Submitted to the EMBL Data Library, May 1996
A:Accession: T23764
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1048 <WIL>
A:Cross-references: UNIPROT:O45962; UNIPARC:UP1000082454; EMBL:Z73428; PIDN:CAA97810.1;
A:Experimental source: clone M142
R:Steward, C.
A:Submitted to the EMBL Data Library, September 1997
A:Reference number: Z20313
A:Accession: T27112
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1048 <WT2>
A:Cross-references: UNIPARC:UP1000082454; EMBL:Z99276; PIDN:CA16481.1; GSPDB:GN00021;
A:Experimental source: clone Y52D3
C:Genetics:
A:Gene: CESP:M142.6
A:Map position: 3
A:Introns: 21/3; 122/3; 381/3; 579/3; 647/2; 683/1; 783/2; 855/1; 871/2; 909/1; 993/1

Query Match
Best Local Similarity 9.0%; Score 101.5; DB 2; Length 1048;
Matches 49; Conservative 26; Mismatches 83; Indels 59; Gaps 11;

Qy 3 PHLTESSGKPLSTQKASKPPRGCPQANRGVVRWEYFLR--PLRFR-----APDBQ 54
Db 478 PRRMGVSDAPPFRTSHQQPP--PQ-----FRNSCHLPFRFGKRGKAPPPPP 525
Qy 55 QAQVHWGWEVAGAPALRLQKSSDLLERERESTLRREQVAERBNALFPEVFSPT- 113
Db 526 PQPMWMLTGYDMPGAPBM-----QATEVLTADGGVNVNGTPQGVVIMQ-----SPTH 571
Qy 114 -----PDENSQNSRSSQASGITGSYSVESPPSPFIHLHSNVAMTYEDVD-- 162
Db 572 LPGGVWVMIPOQGVVPPQSMTPVGGPMGPMGPMTPSI--PVQVDPNMTMTATSPGTVI 629
Qy 163 ----APGQKKKQWYAGINPSDGI--NSEVLEAIR 192

Db 630 YPASPSPGPPHRTWIOSI-----GVFKRSNFKLIVR 662

RESULT 4
A59251
myosin - Acetabularia cliftonii
C:Species: Acetabularia cliftonii
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
A:Accession: A59251
R:Vugrek, O.; Menzel, D.
A:Submitted to GenBank, March 1997
A:Description: Molecular analysis of the cDNA coding for an unconventional myosin from *A. cliftonii*
A:Reference number: A59251
A:Accession: A59251
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1145 <VUG>
A:Cross-references: UNIPROT:O04146; UNIPARC:UP10000A9550; GB:U94398; NID:G2051982; PIDN
C:Genetics:
A:Gene: myo2
A:Genetic code: SGC5
A:97-799/Domain: myosin motor domain homology <MMO>

Query Match
Best Local Similarity 8.9%; Score 101; DB 2; Length 1145;
Matches 40; Conservative 21; Mismatches 62; Indels 22; Gaps 6;

Qy 6 LSSESGK-----PLSTQKASKPPRGCPQANRGVVRWEYFLRPLRFPAP--DEPOAQ 57
Db 542 LLEGCGKAKKAGLPPLI--DEACKMPVTVYQNLANSLRTQLAGIE--RFEAPKQDPNAFT 597
Qy 58 VPHWGWGWEVAGAPALRLQKSSDLLERERESTLRREQVAERBNALFPEVFSPTDEN 117
Db 598 VDHVAG--EVT-----YQTQQLMDKRDVYASEHQAALMASNDVLVSLFEESDDQN 647

Qy 118 SDQNSRSSQASGITGSYSVESPF 142
Db 648 SDSNSSENSNANVRNARNNGQSSF 672

RESULT 5
A45344
immediate-early protein - suid herpesvirus 1 (strain Kaplan)
C:Species: suid herpesvirus 1
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
A:Accession: A45344
R:Vilecek, C.; Kozmik, Z.; Paces, V.; Schlim, S.; Schwyzler, M.
A:Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented op
A:Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented op
A:Reference number: A45344; MUID:91021039; PMID:2171211
A:Accession: A45344
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1446 <VLC>
A:Cross-references: UNIPROT:P33479; UNIPARC:UP1000120219; GB:M34651; NID:G334070; PIDN:;
C:Keywords: DNA binding; early protein; transcription regulation

Query Match
Best Local Similarity 8.5%; Score 96; DB 1; Length 1446;
Matches 60; Conservative 23; Mismatches 82; Indels 114; Gaps 9;

Qy 20 ASKPPR-----GCPQANRGVVRWEYFLRPLRFPAPDEPQAOQVHWG----WEVAG 68
Db 676 AAQGRVPRRLADACVACGVLE---RLIPCPLRL---PAPARAPALGPACTLEVTY 728
Qy 69 A-----PALRLQKSSDLLERERESTLRREQVAERBNALFPEVFSPTDEN 104
Db 729 ALTALRLALPAGFAERRQADSVALTAKTYAPLVRIISVDARAKKAAWYAAALFAPAN 788
Qy 105 -----LFPF-----VSPPTDE 116
Db 789 VAAARLAAAPAPAPAPAGLPFLWPEQPGELVVPAPAPAAAGAPSGLPSSPSSASTK 848

A:Experimental source: strain S288C
A>Note: this sequence has been revised in reference S76573
R.Urretazarazu, L.A.; Andre, B.; Vissers, S.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67535
A:Accession: S67582
A:Molecule type: DNA
A:Residues: 1-490 <UBR>
A:Cross-references: UNIPARC:UPI000006A7F5; EMBL:Z74096; MIPS:YDL048C
A:Experimental source: strain S288C
A:Genetics:
A:Gene: SGD:STP4
A:Cross-references: SGD:S0002206; MIPS:YDL048C
A:Map position: 4L
A:Function:
A:Description: involved in pre-rRNA splicing and in uptake of branched-chain amino acids
A:Keywords: zinc finger
F:306-326/Region: zinc finger CCHH motif

Query Match 8.2%; Score 93; DB 2; Length 490;
Best Local Similarity 23.2%; Pred. No. 6.1;
Matches 43; Conservative 23; Mismatches 65; Indels 54; Gaps 8;

QY 50 PDEPOAO-----VPH---VWGWVAGAPALRLQKSSDILERESEVLRQEV 97
DB 192 PSPPTQHOSILPTAVDNPFRKSVSLPVSGFPPLIVQOOOOLNSSSASAL----- 245

QY 98 ABERNALPPEVSPPTPDNSDSSSSQASGITGSVSESP---PSPHILHNSVA 153
DB 246 -----PSIHSLPTLHNTSRYSLSLKDKKCKEPCFCHNFYANLSTHKSTH 296

QY 154 WTVEPVASAPPGCKKQKQWYGINPSGINSVEVLAIRVTHKAMAEKES---RIVA 210
DB 297 LTPEORPHKCPICQKGFAR-----NNDLI-----RHKK---RHWKDEPMQIYA 336

QY 211 SEEDD 215
DB 337 RESDN 341

RESULT 10
138346
elastic titin - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: 138346
R:Label: S.; Kolmerer, B.
Science 270, 293-296, 1995
A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A:Reference number: A57430; MUID:96026330; PMID:7569978
A:Accession: 138346
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-7962 <RES>
A:Cross-references: UNIPROT:Q10465; UNIPARC:UPI000011010C; EMBL:X90569; NID:g1017426; PI
A:Genetics:
A:Gene: GDB:TTN
A:Cross-references: GDB:127867; OMIM:188840
A:Map position: 2q31-2q31

Query Match 8.2%; Score 92.5; DB 2; Length 7962;
Best Local Similarity 20.5%; Pred. No. 2.2e+02;
Matches 43; Conservative 30; Mismatches 62; Indels 75; Gaps 9;

QY 13 PLSTQKASKPPRGCPQANRGVVRWEYFRLRLFRAPDEPOAOVPHVWGVEVAGAPAL 72
DB 6025 PVAKKKA--PPAKVPEVQKGVTEKTIIVQRESF--PPAVPEIP----- 6068

QY 73 RLQKSSDILERESEVLRQEVAEERRNALPPEVSPPTPDNSDSSSSQASGIT 132
DB 6069 -----KKVPEEKPPVRKEEVPVPPKVPALPK--KPVPEEKV----- 6105

QY 133 GSYVSSESPFPPIHLHNSVAVTVDPV--DSAPQQRK-----KEQWYGINPSDGIN 184

DB 6106 -----AVPVPVAKKAPPPRAVSVSKTVVEKRFVA-----EKLIS 6140
QY 185 SEVLEAIRVTRHKAMAEKESRIYASEED 214
DB 6141 FAVPQVAVTRHVEVSAEEWS---YSEEE 6167

RESULT 11
DB5435
BEL1-like homeobox 2 protein (BLH2) [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
A:Accession: DB5435
R:Anonymous; The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: DB5435
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-638 <STO>
A:Cross-references: UNIPROT:O23196; UNIPARC:UPI00000AA90A; GB:NC_001268; NID:97270636; PI
A:Genetics:
A:Gene: AT4G36870
A:Map position: 4

Query Match 8.1%; Score 92; DB 2; Length 638;
Best Local Similarity 25.0%; Pred. No. 10;
Matches 35; Conservative 24; Mismatches 53; Indels 28; Gaps 6;

QY 14 LSTQKASKPPRGCPQANRGVVR--WEYFRLRLFRAPDEPOAOV---PHVWGVEV 66
DB 491 KGWQZAMRPQKGLPENSUNILKWLFEHR-LHPYSDADKHLARQTGLSRNOVSNWFI 549

QY 67 AGAPALRLQKSSDIL-----ERERSEVLRQEVAEERRNALPPEVSPPTPDNSD 121
DB 550 NA--RVRLKPMVEMWQSSKERERELEENEDQ-----TKSNDSKS 594

QY 122 SRSSSQASGITGSVSESP 141
DB 595 TKSNNESNFTAVVTTTQTP 614

RESULT 12
T00354
hypothetical protein KIAA0692 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00354
R:Ikishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res. 5, 169-176, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A:Reference number: Z14142; MUID:98403880; PMID:9744811
A:Accession: T00354
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-783 <ISH>
A:Cross-references: UNIPROT:O75176; UNIPARC:UPI000006F01B; EMBL:AB014592; NID:g3327197;
A:Experimental source: brain
A:Genetics:
A>Note: KIAA0692

Query Match 8.0%; Score 90; DB 2; Length 783;
Best Local Similarity 24.0%; Pred. No. 19;
Matches 49; Conservative 38; Mismatches 89; Indels 28; Gaps 11;

QY 19 EASKPPRGCPQANRGVVRWEYFRLRLFRAPDEP--QQAQVPHVWGVEVAGAPALRLQK 76
DB 532 EAAPR--GGPHSSNGLCHPLNHSRTLAGKKPKAPHGEGALPVSVDITVE--FDKLANQN 588

QY 77 SQSSDILERESEVLRQEVAEERRNALPPEVSPPTPDNSDSSSSQASGITGSY 135

DB 589 TGRS--VSKTPPESTTKQOILSRINAVERDLLESPADQLNGHRTSEMSARIAC 646
 QY 136 SVSESPFPPIHLNSVANTVEDPDV-SAPPCQKKEQWYAGINSGINSEVLEAIR-- 192
 DB 647 SLSPS---SPRH-----EDQLEVTREPAR--LFLPGSEPSK-LDQVLAALBCA 690
 QY 193 -VTRHKNMAAERWESRIYASEED 215
 DB 691 DVDPHQFPAVHRKWSAVLCYSPSD 714

RESULT 13

337241
 Legumin B - fava bean
 C/Species: Vicia faba (fava bean)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Oct-2004
 C/Accession: S46503; S37241
 R/Helm, U.; Baumlein, H.; Wobus, U.
 Plant Mol. Biol. 25, 131-135, 1994
 A/Title: The legumin gene family: a reconstructed Vicia faba legumin gene encoding a hig
 A/Reference number: S46503; PMID:94272010; PMID:8003694
 A/Accession: S46503
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-564 <HE2>
 A/Cross-references: UNIPROT:Q43673; UNIPARC:UPI00000AC87A; EMBL:Z26489; NID:9403335; PII
 C/Genetics:
 A/Introns: 178/3; 439/3

Query Match 7.9%; Score 89.5; DB 2; Length 564;
 Best Local Similarity 22.9%; Pred. No. 14;
 Matches 39; Conservative 27; Mismatches 61; Indels 43; Gaps 6;

QY 7 SSSSGPLSTKQASPPRCQPOANGVWMEYFRLPLFRAPDEPQQAQVPHWV--GWE 65
 DB 233 AEPLGSLNTEKENTAK-----RLRSPRD-QRQIVKENGDL 268
 QY 66 VAGAPALRLQKSSDLEERESVLRQGEVAERNNALFPVFPPTPDNSQSRSS 125
 DB 269 II-----SALQEEQOSHSGEEEBERQQRHRRYSKEDDEDEKEQE 317
 QY 126 SQASGITGSVSESPFPPIHLNSVAV--TVEDPVDASPPCQKKEQ 172
 DB 318 QR---HGKSKKEEDEDDEPRSYESRKWKTKTEKKRGESHGGEKQEQ 363

RESULT 14

T14004
 trfA protein - slime mold (Dictyostelium discoideum)
 C/Species: Dictyostelium discoideum
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T14004
 R/Saito, J.; Adachi, H.; Sutoh, K.
 J. Biol. Chem. 273, 24654-24659, 1998
 A/Title: Dictyostelium TRPA homologs to yeast Sam6 is required for normal growth and e
 A/Reference number: Z17852; PMID:98406112; PMID:9733762
 A/Accession: T14004
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1390 <SAI>
 A/Cross-references: UNIPROT:O77033; UNIPARC:UPI000007B414; EMBL:AB009080; NID:dl228566;
 C/Genetics:
 A/Gene: trfA
 A/Introns: 333/3; 364/3; 637/1

Query Match 7.8%; Score 88; DB 2; Length 1390;
 Best Local Similarity 23.5%; Pred. No. 57;
 Matches 36; Conservative 27; Mismatches 58; Indels 32; Gaps 6;

QY 1 MSPRHLSESGK-----PLSTQKQASKPPRCQPOANGVWMEYFRLPLFRAPDEP 53
 DB 1204 VEPHKKKESKNDTTTTTTTTTKSKSKSPNSPTRSDEV-----EPHQDASQBEI 1256

QY 54 QOAGVPHWGWVAGAPALRLQ-----KQSSDLEERESVLRQGEVAERNNALFP 107
 DB 1257 NKRKLED-----DITSPKRLKPDTPSSATTAISPPSQPSPLKKENPVGE---TISP 1308
 QY 108 EVFSPPTPDNSQSRSSQASGITGSVSEBS 140
 DB 1309 EI-----KQSKSSSSSSSSSSSTNTGSSSTNMS 1337

RESULT 15

T02195
 hypothetical protein At2g46920 [imported] - Arabidopsis thaliana
 N/Alternate names: hypothetical protein F14M4.25
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
 C/Accession: T02195; H84908
 R/Rounsaey, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ron
 submitted to the EMBL Data Library, September 1998
 A/Description: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.
 A/Reference number: Z14609
 A/Accession: T02195
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-814 <ROU>

A/Cross-references: UNIPROT:O80732; UNIPARC:UPI000009E59E; EMBL:AC004411; NID:93522932;
 A/Experimental source: cultivar Columbia
 R/Lin, X.; Kaul, S.; Rounsaey, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.B.; Umayam, L.; Taiton, L.
 enes, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A/Reference number: A84420; PMID:120083487; PMID:1061197
 A/Accession: H84908
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-814 <STO>
 A/Cross-references: UNIPARC:UPI000009E59E; GB:AE002093; NID:93522937; PIDN:AA34239.1;

C/Genetics:
 A/Gene: F14M4.25; At2g46920
 A/Map position: 2
 A/Introns: 680/3; 718/3
 C/Superfamily: Arabidopsis thaliana hypothetical protein At2g46920

Query Match 7.7%; Score 87; DB 2; Length 814;
 Best Local Similarity 22.8%; Pred. No. 35;
 Matches 38; Conservative 25; Mismatches 74; Indels 30; Gaps 7;

QY 24 PRGCPQANGVWMEYFRLPLFRAPDEPQQAQVPHWGW-----EVAGAPALRLQK 76
 DB 268 PESCLSSNNR-LQMAH-----GKAGEBRHVAVLSEEGMLPFIGIDGFGPDADPVM 319
 QY 77 SQSSDLEERESVLRQGEVAERNNALFPVFPPTPDNSQSRSSQASGITGSYS 136
 DB 320 SHIYKXIDELBELWDYEPSED--NQAPDEPTENMCDPESISQHSKSVAR-- 375
 QY 137 VSSSPFPPIHLNSVAVTVD--PYDASPPGQR-----KKEW 173
 DB 376 -SEEWIMIDISSIGNDTQIADGPPDSAGPGKSKWELVQLQLEW 421

Search completed: March 3, 2006, 13:36:37
 Job time: 14.5811 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 13:19:17 ; Search time 82.1137 Seconds
(without alignment(s))
1847.299 Million cell updates/sec

Title: US-10-646-873-47

Sequence: 1 MSPRLSSSSGKPLSTKQEA.....HKNAARWESRIYASEDD 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1132	100.0	679	1 CS021_HUMAN	Q81V22 homo sapien
2	1060	93.6	685	1 CS021_PONPY	Q5Tbh3 pongo pygma
3	786.5	69.5	648	1 CS021_MOUSE	Q9d279 mus musculi
4	127.5	11.3	1103	1 AKAP2_HUMAN	Q9T721 homo sapien
5	127.5	11.3	1103	2 Q5T721_HUMAN	Q5T721 homo sapien
6	120.5	10.6	848	2 Q5XG09_XENLA	Q5XG09 xenopus lae
7	118.5	10.5	870	2 Q5U301_RAT	Q5U301 rattus norv
8	118	10.4	949	2 Q5J724_HUMAN	Q5J724 homo sapien
9	117.5	10.4	880	2 Q8CSW1_MOUSE	Q8CSW1 mus musculi
10	114.5	10.1	1493	2 Q9H4G2_HUMAN	Q9H4G2 homo sapien
11	114	10.1	1502	2 Q9ULI8_HUMAN	Q9ULI8 homo sapien
12	108.5	9.6	1518	1 HR4_DROME	Q9W539 drosophila
13	108.5	9.6	1518	2 Q56AW0_DROME	Q56AW0 drosophila
14	105.5	9.3	793	2 Q4PBW3_USTMA	Q4PBW3 usiliago ma
15	105	9.3	1066	2 Q5STP8_CRYNE	Q5STP8 crypococcu
16	105	9.3	1066	2 Q5KIN7_CRYNE	Q5KIN7 crypococcu
17	104.5	9.2	1006	2 Q4Q354_LEIMA	Q4Q354 leishmania
18	103	9.1	1395	2 Q69ZNV_MOUSE	Q69ZNV mus musculi
19	102	9.0	355	1 SURF6_MOUSE	P70279 mus musculi
20	101.5	9.0	686	2 Q9V550_DROME	Q9V550 drosophila
21	101.5	9.0	1014	2 Q45962_CABEL	Q45962 caenorhabdi
22	101	8.9	1145	2 Q04146_ACECI	Q04146 acetabulari
23	100.5	8.9	465	2 Q8W846_PUROC	Q8W846 olkopleura
24	99	8.7	731	1 DAXX_RAT	Q8V142 rattus norv
25	99	8.7	1100	2 Q7RMM0_NEUCR	Q7RMM0 neurospora
26	98	8.7	757	2 Q7RX41_NEUCR	Q7RX41 neurospora
27	97.5	8.6	373	2 Q4RLM2_TETNG	Q4RLM2 tetraodon n
28	97	8.6	543	2 Q652N7_ORYSA	Q652N7 oryza sativ
29	96	8.5	517	2 Q4PES3_USTMA	Q4PES3 usiliago ma
30	96	8.5	1200	2 Q4IYV6_GIBZE	Q4IYV6 gibberella
31	96	8.5	1271	2 Q7S817_NEUCR	Q7S817 neurospora

32	96	8.5	1446	1 IE18_PRYKA	P33479 pseudorabie
33	96	8.5	1446	2 Q5PP75_9ALPH	Q5PP75 suid herpes
34	95.5	8.4	239	2 Q4Q1H8_LEIMA	Q4Q1H8 leishmania
35	95.5	8.4	414	2 Q7XIE4_ORYSA	Q7XIE4 oryza sativ
36	95.5	8.4	771	2 Q52GSI_MAGOR	Q52GSI magnaporthe
37	95.5	8.4	917	2 Q5H144_XANOR	Q5H144 xanthomonas
38	94.5	8.3	1287	1 TCGAP_HUMAN	O14559 homo sapien
39	94.5	8.3	1781	2 Q6QW45_CABER	O6QW49 caenorhabdi
40	94	8.3	309	2 Q9H7C7_HUMAN	Q9H7C7 homo sapien
41	93.5	8.3	500	2 Q4SSP6_TETNG	Q4SSP6 tetraodon n
42	93.5	8.3	699	1 NIMA_EMENT	P11837 emeticicella
43	93.5	8.3	699	2 Q5AQC6_EMENT	Q5AQC6 aspergillus
44	93	8.2	329	2 Q9XKUD_BACHD	Q9XKUD bacillus ha
45	93	8.2	490	2 Q07351_YEAST	Q07351 saccharomyc

ALIGNMENTS

RESULT 1
ID CS021_HUMAN STANDARD; PRT; 679 AA.
AC Q81V22;
DT 13-SRP-2005 (Rel. 48, Created)
DT 13-SRP-2005 (Rel. 48, Last sequence update)
DT 13-SRP-2005 (Rel. 48, Last annotation update)
DE Protein Clp9orf21.
GN Name=Clp9orf21;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain and Colon;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Yoshizuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millar S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalak U., Smalleg D.E.,
RA Schurch A., Schein J.E., Jones S.J.M., Merra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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CC removed.
CC EMBL: BC042125; AAH42125.1; -; mRNA.
CC EMBL: BC052236; AAH52236.1; -; mRNA.
CC PIR: T00636; T00636.
CC DR HGNemb1; ENSG0000009812; Homo sapiens.
CC DR HGNemb1; HGNc:27000; Clp9orf21.
CC Colled coll.
CC COLLED 545 569 Potential.
CC FT SEQUENCE 679 AA; 75357 MW; D2881CF5087E61F8 CRC64;

```

Query Match      100.0%; Score 1132; DB 1; Length 679;
Best Local Similarity 100.0%; Pred. No. 1e-77;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRHSSSGKPLSTKQKASRPKPGCCPOANGVVRWEXFRLRPFRAPDEPQQAQVPH 60
DB MSPRHSSSGKPLSTKQKASRPKPGCCPOANGVVRWEXFRLRPFRAPDEPQQAQVPH 524
QY 61 VGMGVVAGAPALRLQKSSDILLERERESVLRREQVAAERNNALFPEVFSTPTDENSDQ 120
DB VGMGVVAGAPALRLQKSSDILLERERESVLRREQVAAERNNALFPEVFSTPTDENSDQ 584
QY 121 NSRSSSQASGRTGSYSVSESPFPIHLHSNVAWTVEDPVDSPAPGQRKKEQWYAGINPS 180
DB NSRSSSQASGRTGSYSVSESPFPIHLHSNVAWTVEDPVDSPAPGQRKKEQWYAGINPS 644
QY 181 DGINSEVLEAIRVTRHKNAAMRWESRRIYASEDD 215
DB DGINSEVLEAIRVTRHKNAAMRWESRRIYASEDD 679

RESULT 2
CS021 PONPY STANDARD; PRT; 685 AA.
ID CS021 PONPY
AC 05REH3;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DE Protein C19orf21 homolog.
OS Pongo pygmaeus (orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Pongo.
OX NCBI_TaxID=9600;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP TISSUE=Kidney;
RC The German cDNA consortium;
RG Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC removed.
CC -----
CC EMBL; CR858675; CAH90887.1; -; mRNA.
CC -----
CC COLLED 551 575 Potential.
CC FT COILED 551 575
CC SQ SEQUENCE 685 AA, 75892 MW, A3A99F4343396B81 CRC64;

Query Match      93.6%; Score 1060; DB 1; Length 685;
Best Local Similarity 94.0%; Pred. No. 3.1e-72;
Matches 202; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSPRHSSSGKPLSTKQKASRPKPGCCPOANGVVRWEXFRLRPFRAPDEPQQAQVPH 60
DB MSPRHSSSGKPLSTKQKASRPKPGCCPOANGVVRWEXFRLRPFRAPDEPQQAQVPH 530
QY 61 VGMGVVAGAPALRLQKSSDILLERERESVLRREQVAAERNNALFPEVFSTPTDENSDQ 120
DB VGMGVVAGAPALRLQKSSDILLERERESVLRREQVAAERNNALFPEVFSTPTDENSDQ 590
QY 121 NSRSSSQASGRTGSYSVSESPFPIHLHSNVAWTVEDPVDSPAPGQRKKEQWYAGINPS 180
DB NSRSSSQASGRTGSYSVSESPFPIHLHSNVAWTVEDPVDSPAPGQRKKEQWYAGINPS 650
QY 181 DGINSEVLEAIRVTRHKNAAMRWESRRIYASEDD 215
DB DGINSEVLEAIRVTRHKNAAMRWESRRIYASEDD 685

RESULT 3

```

```

CS021 MOUSE
ID CS021 MOUSE STANDARD; PRT; 648 AA.
AC Q9D275;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DE Protein C19orf21 homolog.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamana A., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirni L.M., Kanapin A., Matsuda H., Batalov S., Beisler K.W.,
RA Blake J.A., Bradt D., Brusic V., Choitha C., Corbani L.E., Cousins S.,
RA Daila E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petca G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Warande Y., Wells C.,
RA Wilming L.G., Wynnshaw-Boris A., Yangisawa M., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaunushli A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP STRAIN=FVB/N; TISSUE=Colon;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldi M.F., Casavant T.P., Scheetz T.B.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguailano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heltan E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywnicki M.I., Skalska V., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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CC removed. -----
CC DR EMBL, AK020266; BAB32049.1; -, mRNA.
CC DR EMBL, BC013508; AAH13508.1; -, mRNA.
CC DR Ensembl, ENSMUSG00000035852; Mus musculus.
CC DR MGI, MGI:1926156; 913001.7N09RLK.
CC DR KW Coiled coil.
CC FT COILED 511 534 Potential.
CC SEQUENCE 648 AA; 72281 MW; 1E395B0763B3D1F CRC64;
CC
CC Query Match 69.5%; Score 786.5; DB 1; Length 648;
CC Best Local Similarity 71.0%; Pred. No. 2e-51;
CC Matches 154; Conservative 22; Mismatches 36; Indels 5; Gaps 3
CC
CC Oy 2 SPRHSESSGKPLSTKQESKSPKRCPPQANRQVWVWVRYRLPLFRAPDSEQAOVPHV 61
CC Db SPRHSESSGRLSKQESKPPG--KATNVVVKLGKHLPLRKVDVPOGTETPT 491
CC Oy 62 MGWEVAGPAPALPLQKSSDDLERRERESVLRREOVAERRRNALPPEVSPPT--DENSD 119
CC Db MGWEVAGGPILALQKSSDDLERRMESVLRREVAERRRNALPPEVSPPADSESH 551
CC Oy 120 QNSRSSSQASGITGSYSVSESPFSEIHLSNVAMTVEDPVDAPPGQR-KKEQVYAGIN 178
CC Db QDSRSSSRASGITGSYSVESPLFVHLNLSGLVWKEVAPEDSAPPGQTRKEMVYAGIN 611
CC Oy 179 PSDGINSVLEAIRVTRHKMAAERNEKSIYASEED 215
CC Db PSDSVNSEVLTGATRVGRHKLALERWEAHIVASEDEN 648
CC
CC RESULT 4
CC AAAP2_HUMAN STANDARD; PRT; 1103 AA.
CC ID AKAP2_HUMAN
CC AC Q9Y2D5; Q9UG26;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 13-SEP-2005 (Rel. 48, Last annotation update)
CC DE A-kinase anchor protein 2 (Protein kinase A anchoring protein 2)
CC DE (PRAK2) (AKAP-2).
CC GN Name=AKAP2; Synonyms=KIAA0920;
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homnidae;
CC OC Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP NUCLEOTIDE SEQUENCE (mRNA) (ISOFORM A).
CC RA Schuetz N., Reichel S., Ruecker N., Lechner A., Eulert J., Jakob F.,
CC RT "Homo sapiens AKAP-2 complete cDNA sequence."
CC RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC RN [2]
CC RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM A).
CC RC TISSUE=Brain;
CC RX MEDLINE=99246063; PubMed=10231032;
CC RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirotsawa M.,
CC RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,
CC RT "Prediction of the coding sequences of unidentified human genes. XIII.
CC RT The complete sequences of 100 new cDNA clones from brain which code
CC RT for large proteins in vitro."
CC RL DNA Res. 6:63-70(1999).
CC RN [3]
CC RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 770-1103 (ISOFORM B).
CC RC TISSUE=Brain;
CC RG The German cDNA consortium;
CC RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC CC -1- FUNCTION: Binds to regulatory subunit (RII) of protein kinase A.
CC CC May be involved in establishing polarity in signaling systems or
CC CC in integrating PKA-RII isoforms with downstream effectors to
CC CC capture, amplify and focus diffuse, trans-cellular signals carried
CC CC by cAMP (by similarity).
CC CC -1- ALTERNATIVE PRODUCTS:
CC CC Event=Alternative splicing; Named isoforms=2;

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CC Name=A;
CC Isoid=Q9Y2D5-1; Sequence=Displayed;
CC Name=B;
CC Isoid=Q9Y2D5-2; Sequence=VSP_004096;
CC Note=No experimental confirmation available;
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AJ303079; CAC38839.1; -, mRNA.
DR EMBL; AB023137; BAA6764.2; ALT INTR, mRNA.
DR EMBL; AL110268; CAB53707.1; -, mRNA.
DR Ensembl; ENSG00000157654; Homo sapiens.
DR HGNC; HGNC:372; AKAP2.
DR MIM; 604582; -.
DR GO; GO:0019899; P:enzyme binding; NAS.
DR KW Alternative splicing; Coiled coil.
FT REGION 797 810 PKA-R11 subunit binding domain.
FT COILED 3 117 Potential.
FT COILED 483 521 Potential.
FT COILED 940 980 Potential.
FT COMBINS 512 521 Poly-Gln.
FT VASAPLIC 1059 1071 Missing (in isoform B).
FT FT /Frtid=VSP_004096.
FT FT E -> G (in Ref. 3).
SQ SEQUENCE 1103 AA; 122071 MW; B501182135112PE5 CRC64;
Query Match 11.3%; Score 127.5; DB 1; Length 1103;
Beet Local Similarity 24.7%; Pred. No. 0.58;
Matches 45; Conservative 35; Mismatches 53; Indels 49; Gaps 6;
QY 66 VAGAPALRLQKSGSGLLRERRESEVLRREGEVAER-----RNALPPEV----- 109
DQ 936 MVGPPLKRSRQRTLSMIEEIRAAQERHEBLKQRYLQSTGSPRTGNA--PSLPSRTC 993
QY 110 -----PSPTDENSDONSRSSQASGITGSYSVSSPFSPTHLHSNVAMT 155
DB 994 YKTAAGKLEKYPSPPTGEPSPLOPDAPPEAAG-----TGRP-----KNLMQT 1038
QY 156 VEDPPLDASAPQQRKK--EQWYAGINPSDGINSEVLEAIRVTRHKNAMERWESRYASEE 213
DB 1039 LMEDEVTHKSKRRERMDSDSYTSKLSCKTVSEVLEAIRVTRHKNRSALALRWEGAGIYANQE 1098
QY 214 DD 215
DB 1099 EE 1100
RESULT 5
Q5T721_HUMAN PRELIMINARY; PRT; 1103 AA.
ID Q5T721_HUMAN PRELIMINARY;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE A kinase (PKA) anchor protein 2.
GN Name=AKAP2; ORFNames=Rp11-47020.3-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lawlor S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pandian R.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

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NCBI EOTIDE SEQUENCE.

Tissue-Spleen:

MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

R Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

R Richardson P.;

R "Genetic and genomic tools for Xenopus research: The NIH Xenopus

R initiative."

R Dev. Dyn. 225:384-391(2002).

RN [2].

NCBI EOTIDE SEQUENCE.

Tissue-Spleen:

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

R Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

R Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

R Altschul S.F., Zeeberg B., Blueton K.H., Schaefer C.F., Bhat N.K.,

R Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Helen F.,

R Dickenson L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,

R Stadlton M., Soares M.B., Bonaldo M.F., Cassatini P., Prange C.,

R Brownstein M.J., Udell T.B., Toshitsugu S., Cantinici P., Mullaly S.J.,

R Rana S.S., Loguano N.A., Peters G.J., Abramson R.D., Mulvey S.J.,

R Bosak S.A., McKernan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

R Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

R Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R Butcherfield Y.S.N., Krzywinski W.T., Skalka U., Smallie D.E.,

R Scheraga A., Schein J.B., Jones S.J.M., Maier M.A.,

R "Generation and initial analysis of more than 15,000 full-length human

R and mouse cDNA sequences."

R Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [3].

RP NCBI EOTIDE SEQUENCE.

RC Tissue-Spleen;

RC Klein S., Gerhard D.S.;

RL Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.

DR EMBL, BC084662; AAH84662.1; -, mRNA

SQ SEQUENCE 848 AA; 94904 MW; DF7CA5F63828D8B CRC64;

Query Match 10.6%; Score 120.5; DB 2; Length 848;

Best Local Similarity 23.1%; Pred. No. 1.4;

Matches 53; Conservative 40; Mismatches 83; Indels 53; Gaps 8;

OY 13 PLSTKQASKEPPRCPPANGNVW-EYFLRPLRFAPDEPQAQVPHWGWEVACAP-70
||| ||| : : : : :
Db 645 PLSTK-SLSPTEONCTEHEKHQSXYFSKCSASAEIR-----STASILATQETISVGPF 696
OY 71 ALRIQKSQSSDLERESVLRQGEVAEEERRNLPEFVSPTPDENSDONSRSQASG 130
||| : : : : :
Db 697 KLRRKKOKTSMIEELRAAOERODKKPKEROISQSHSP-----SNKSAPVLPT 748
OY 131 ITGSYSVS-----ESPFPSPHL-----HSNVATVEDPVDSAPPG 166
||| | : : : : :
Db 749 RTVSYTKAPAKIKLRNPSPRGSPFIQDILLLEATGSRPNKLMTLLMDPESHKTK 808
OY 167 QRKKEQWYAGINPSDGINSVEYLAIKRVTRHKNAEAERESRIYASEDD 215
::: | : : : : :
Db 809 RRDMWD-----DATVLDAVRVNRKRSLALTKKEAGIYANRDD 846

RESULT 7

OSU301 RAT PRELIMINARY; PART; 870 AA.

OSU301 RAT

AC OSU301

DT 01-FEB-2005 (TREMBLrel_29, Created)

DT 01-FEB-2005 (TREMBLrel_29, Last sequence update)

DT 01-FEB-2005 (TREMBLrel_29, Last annotation update)

DE A kinase (PRKA) anchor protein 2 (Predicted).

GN Name=Akap2 predicted;

OS Rattus norvegicus (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeebner B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stjepicon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney.
 RG NIH MGC Project;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC085790; AAH85790.1; mRNA.
 DR EMBL; EMBRN00000011504; Rattus norvegicus.
 DR GO; GO:0016301; P:kinase activity; IEA.
 KM Kinase.
 SQ SEQUENCE 870 AA; 95941 MW; 516C22A6D7A2DD2 CRC64;
 Query Match 10.5%; Score 118.5; DB 2; Length 870;
 Best Local Similarity 24.1%; Pred. No. 2.1;
 Matches 42; Conservative 30; Mismatches 57; Indels 45; Gaps 6;
 QY 66 VAGAPALRLQKSSGDLEREREVLRQGEVAERNNLFPYVSPPTDENSQNSRS 125
 DB 715 WVGPPKLRKORLTSMIEEIRAAQEREELKRCR-----QVROSTSPRA-QVAPSL 767
 QY 126 SGASGITSYS-----VSBSPPFSP-----IHHSNVAMTVDPD 161
 DB 768 PSR---TTCYKAPGKIEKYKPPSPPTTGPSPLOPLAPEBAAGQRPQVLMQTLMEDE 824
 QY 162 SAPPGORKKEQWYAGINPSDGINSEVLEAIRVTRHKNAAERESRIYASEBD 215
 DB 825 THKSRRERMD-----DSSVLEKTRVNRKRSALALRREAGIYANQEE 867

RP NUCLEOTIDE SEQUENCE.
 RA Kimberley A.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL353598; CAI40818.1; -; Genomic_DNA.
 DR EMBL; AL158823; CAI19562.1; -; Genomic_DNA.
 DR EMBL; AL158823; CAI19562.1; JOINED; Genomic_DNA.
 DR EMBL; AL353598; CAI19562.1; JOINED; Genomic_DNA.
 DR GO; GO:0016301; P:kinase activity; IEA.
 KM Kinase.
 FT NON TER
 SQ SEQUENCE 949 AA; 104234 MW; 4E6ACAFCA2A6F2EBD CRC64;
 Query Match 10.4%; Score 118; DB 2; Length 949;
 Best Local Similarity 23.3%; Pred. No. 2.6;
 Matches 42; Conservative 34; Mismatches 46; Indels 58; Gaps 6;
 QY 66 VAGAPALRLQKSSGDLEREREVLRQGEVAER-----RNALFPEV----- 109
 DB 795 WVGPPKLRKORLTSMIEEIRAAQEREELKRCRQVLAGSTQSPRTGNA--PSIPRRC 852
 QY 110 -----PSPPDENSQNSSSQASGITSYSVSBSPPFPHHSNVAMT 155
 DB 853 YKTAAPGKIEKYKPPSPPTTGPSPLOPLAPEBAAG-----TORP----- 897
 QY 156 VEDPDSAPPGORKKEQWYAGINPSDGINSEVLEAIRVTRHKNAAERESRIYASEBD 215
 DB 898 LMEDEYTHKSRRERMD-----DSSVLEKTRVNRKRSALALRREAGIYANQEE 946

RESULT 9
 Q8CSW1_MOUSE PRELIMINARY; PRT; 880 AA.
 ID Q8CSW1;
 AC Q8CSW1;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 DE library, clone:4932411M01 product:A kinase anchor protein 2, full
 DE insert sequence.
 DE Name=Akap2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saico T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saico R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Holtman M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata J., Storch K.-F.,
 RA Suzuki H., Toyono K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,

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RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RT The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci F., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci F.,
RA Kono H., Akiyama Y., Nishi K., Kitasuna T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwa K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Aichi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci F.,
RA Fukuda S., Futano M., Hasegaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hoti F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaubukwa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsumoto T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohmoto N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saeki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK077020; BAC36571.1; -, mRNA.
DR MGI; MGI:1306795; Akap2.
DR GO; GO:0051018; F:protein kinase A binding; IPI.
DR GO; GO:0007015; P:actin filament organization; IDA.
DR GO; GO:0008104; P:protein localization; IPI.
DR GO; GO:0001178; P:transmembrane receptor protein serine/threo. .; IPI.
KW kinase.
SQ SEQUENCE 880 AA, 97137 MW, 1CD1888BA92C55D CRC64;

Query Match 10.4%; Score 117.5; DB 2; Length 880;
Best Local Similarity 23.2%; Pred. No. 2.5;
Matches 42; Conservative 34; Mismatches 46; Indels 59; Gaps 6;

QY 66 VAGAPALRLQKSSDRLERERESVLRROEVAERER-----RNALPFEV----- 109
DB 725 MVGPFLKSRKQRTLSMIEELRAQOEERBELKROVROSTPSPRANA--PSLPSTT 782
QY 110 -----FSPTDENSQNSRSSQASGITSYSVSESPFPIHLSNVAM 154
DB 783 CYKTAFGKLEKYPPTTEBPSLQPDLPAPBAAG-----TQRP-----KNLMQ 827
QY 155 TVEEDVDSAPPGQKKEQWYAGINSDGINSFVLAIRVTRHKNAARWESRIYASEED 214
DB 828 TLMEDEYTHKSKRRERMD-----DSSVLEATRVNRRKSKALRLMEAGIYANOE 876
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QY 215 D 215
DB 877 E 877

RESULT 10
Q9HAG2 HUMAN PRELIMINARY; PRT; 1493 AA.
AC Q9HAG2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Novel protein.
GN Name=RP11-119E20.1; ORFNames=RP11-119E20.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleia; Euarctonoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Whitehead S.;
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Bird C.;
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 PDZ (DHR) domain.
DR EMBL; AL121865; CAC08472.2; -, Genomic DNA.
DR EMBL; AL359272; CA195315.1; -, Genomic DNA.
DR EMBL; AL359272; CAC08472.2; JOINED; Genomic DNA.
DR EMBL; AL121865; CA195315.1; JOINED; Genomic DNA.
DR Ensembl; ENSG00000158352; Homo sapiens.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF00595; PDZ; 1.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS50106; PDZ; 1.
SQ SEQUENCE 1493 AA; 164857 MW; 40260DC12A24ANF CRC64;

Query Match 10.1%; Score 114.5; DB 2; Length 1493;
Best Local Similarity 25.2%; Pred. No. 8.3;
Matches 53; Conservative 20; Mismatches 72; Indels 65; Gaps 10;

QY 8 ESSGKPLSTQKQAKPRGCPQANKGVWYFPLRLPRAPDPQQAQVPHWGWV 67
DB 1086 ETQGDLLGARKKAPPPRPPPP-----NMKKYL-----FRLAQKQKQKQ 1125
QY 68 GAPALRLQKSSDRLERERESVLRROEVAERERNAALPFEVSP-----TPDENS 118
DB 1126 -----QQKQOEERERERERERERERERERERERERERERERERER 1180
QY 119 DQ-----NSRSSQA-SGITGSYSVSESPFPIHLSNVAMTVEEDVDSAPP- 165
DB 1181 EQPPLPSFGLGSRQSSQVPAEQESFALHSDFLPPIRHLG-----SQPEQAQPCY 1235
QY 166 -----GQRKKE---QWYAGINPSDG 182
DB 1236 YGIGLWRTSQEATBSAKQEFQHFSPSG 1265

RESULT 11
Q9ULI8 HUMAN
ID Q9ULI8 HUMAN PRELIMINARY; PRT; 1502 AA.
AC Q9ULI8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE KIAA1202 protein (Fragment).
GN Name=KIAA1202;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```


	induced regulatory genes and an inducer of the <i>ftr</i> - <i>fl</i> midgut prepupal competence factor.
CC	-1- SUBCELLULAR LOCATION: Nuclear.
CC	-1- TISSUE SPECIFICITY: During L2 and L3 stages, strong constitutive expression is seen in the ring gland. Lower expression is detected in specific neurons of the central nervous system (CNS) (at protein level).
CC	-1- MISCELLANEOUS: Flies lacking Hrt4 exhibit larvae that precociously leave the food to form premature prepupae, resulting in abbreviated larval development that translates directly into smaller and lighter animals.
CC	-1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1 subfamily.
CC	-1- SIMILARITY: Contains 1 nuclear receptor DNA-binding domain.
CC	-1- CAUTION: Ref.2 and Ref.3 sequences differ from that shown due to erroneous gene model prediction.
CC	-----
CC	This Swiss-Prot entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC	-----
DR	EMBL; AL035245; CAA32836.1; ALT_SRO; Genomic_DNA.
DR	EMBL; AE003422; AAP45702.3; ALT_SEQ; Genomic_DNA.
DR	HSSP; P19793; ZNLU.
DR	Ensembl; CG16902; Drosophila melanogaster.
DR	FLYbase; FBgn0023546; Hrt4.
DR	GO; GO:0005634; C:nucleus; IDA.
DR	GO; GO:0040879; F:lignand-dependent nuclear receptor activity; IMP.
DR	GO; GO:0040007; P:growth; IMP.
DR	GO; GO:0030518; P:steroid hormone receptor signaling pathway; IMP.
DR	InterPro; IPR001628; Hrmn_rcpt_bd.
DR	InterPro; IPR000536; Hrmn_rcpt_lig_bd.
DR	InterPro; IPR000354; Involucrin_rpt.
DR	InterPro; IPR001723; Stchrmn_receptor.
DR	InterPro; IPR000324; Vtld_receptor.
DR	Pfam; PF00104; Hormone_recip_1.
DR	Pfam; PF00904; Involucrin; 1.
DR	Pfam; PF00105; ze-C4; 1.
DR	PRINTS; PR00398; STRDHOMONER.
DR	PRINTS; PR00047; STROIDRINGER.
DR	PRINTS; PR00350; VTDMINDR.
DR	SMART; SMO0399; ZNF_C4; 1.
DR	PROSITE; PS00031; NUCLEAR_REC_DBD_1; 1.
DR	PROSITE; PS01030; NUCLEAR_REC_DBD_2; 1.
KW	DNA-binding; Metal-binding; Nuclear protein; Transcription;
KW	Transcription regulation; Zinc; Zinc-finger.
FT	DNA_BIND 918..993 Nuclear receptor.
FT	ZN_FING 921..941 NR_C4-type 1.
FT	ZN_FING 957..976 NR_C4-type 2.
FT	COMBIAS 94..144 Ala-rich.
FT	COMBIAS 135..223 Ser-rich.
FT	COMBIAS 229..277 Gly-rich.
FT	COMBIAS 401..427 Arg-rich.
FT	COMBIAS 460..1194 Gln-rich.
FT	CONFLICT 140..140 A -> R (in Ref. 1).
FT	CONFLICT 144..144 A -> R (in Ref. 1).
FT	CONFLICT 213..213 I -> V (in Ref. 1).
FT	CONFLICT 1452..1452 K -> KA (in Ref. 1).
SO	SEQUENCE 1518 AA; 162655 MW; DDDBFEBA416D1A CRC64;
	Query Match 9.6%; Score 108.5; DB 1; Length 1518;
	Best Local Similarity 20.8%; Pred. No. 24;
	Matches 48; Conservative 30; Mismatches 80; Indels 73; Gaps 9;
OY	2 SPRHLSSSGKPLSTKQBSKPPRCGPQANRG-----VTRWEYFRLRLPRPADDE- 53
Db	687 SPHPSSSSSSQLSPQTSPQRPTPIYMIGSCGVATWWGX-----EPPPSA 737
Oy	54 -----GQAQVHWGWGEVAGAPALRLQKSQSDDLRRERSVLRRQVAERRNA 104
Db	738 GASHQHDPQQDDQSH-----HQPQQQQQQQQQQQQSQQQQQQQQSLGGQCCHL 786

QY	105	LEPVEVSTPTDENS-----DONSRSSQAGITGSYSVSE-----	133
DB	787	SSPSAGSLTPSSSSGCGGVSQGGVCGPLTPSSVADQNNEEAAQLLISLQITRIQDWRSRP	846
QY	140	SPFSPSPHSHSNVATVEDPVDSPAPGQ-----RKTEQWYAGINPSDGI	183
DB	847	HPFRPHALNNERLWAGD--YSQLPFGQLQALNTLSAQGGQW--GSSNSITGL	893
RESULT 13			
ID	Q56AM0	DROME PRELIMINARY; PRT; 1518 AA.	
AC	Q56AM0-		
DT	10-MAY-2005	(TREMBLrel. 30, Created)	
DT	10-MAY-2005	(TREMBLrel. 30, Last sequence update)	
DT	10-MAY-2005	(TREMBLrel. 30, Last annotation update)	
DE		Hormone receptor 4.	
GN		Name=Hr4; ORFNames=CG16902;	
OS		Drosophila melanogaster (Fruit fly).	
OC		Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,	
OC		Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,	
OC		Ephydroidea, Drosophilidae, Drosophila.	
OX		NCBI_TaxID=7227;	
RN		[1]	
RP		NUCLEOTIDE SEQUENCE.	
RX		PubMed=15935763; DOI=10.1016/j.cell.2005.03.030.	
RA		King-Jones K., Charles J.P., Lam G., Thummel C.S.;	
RT		"The ecdysone-induced DHR4 orphan nuclear receptor coordinates growth	
RT		and maturation in Drosophila."	
RL		Cell 121:773-784(2005).	
CC		-1- SUBCELLULAR LOCATION: Nuclear (By similarity).	
CC		-1- SIMILARITY: Belongs to the nuclear hormone receptor family.	
DR		EMBL; AY971884; AAX7335.1 -; mRNA.	
DR		GO; GO:0005634; C:nucleus; IEA.	
DR		GO; GO:0046872; F:metal ion binding; IEA.	
DR		GO; GO:0003707; F:steroid hormone receptor activity; IEA.	
DR		GO; GO:0003700; F:transcription factor activity; IEA.	
DR		GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.	
DR		GO; GO:0006350; P:transcription; IEA.	
DR		InterPro; IPR001628; Hrmu_rcp1_DNA_bd.	
DR		InterPro; IPR000536; Hrmu_rcp1_11g_bd.	
DR		InterPro; IPR000354; Involucrin_fpl.	
DR		InterPro; IPR001723; Stchrmu_receptor.	
DR		InterPro; IPR000324; Vldt_receptor.	
DR		Pfam; PF00104; Hormone_recep. 1.	
DR		Pfam; PF00904; Involucrin; 1.	
DR		Pfam; PF00105; zf-C4; 1.	
DR		PRINTS; PR00398; STRDHOMOMER.	
DR		PRINTS; PR00047; STEROIDINGER.	
DR		PRINTS; PR00350; VITAMINDR.	
DR		SMART; SM00430; HOL1; 1.	
DR		SMART; SM00399; ZNF_C4; 1.	
DR		PROSITE; PS00031; NUCLEAR_REC_DBD_1; 1.	
DR		PROSITE; PS51030; NUCLEAR_REC_DBD_2; 1.	
KW		DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;	
KW		Transcription regulation; Zinc; Zinc-finger.	
SEQ		SEQUENCE 1518 AA; 16265 MW; DDDBFEDRA41SD17AA CRC64;	
QY		Query Match 9.6%; Score 108.5; DB 2; Length 1518;	
DB		Best Local Similarity 20.8%; Pred. No. 24;	
DB		Matches 48; Conservative 30; Mismatches 80; Indels 73; Gaps 9	
QY	2	SPRHSSSGRLSTKQKASRPKPCQPAANG-----VVRVEYRLRLRRAAPER--	53
DB	687	SPHSPSSSSSSQLSPQTSPTPTPTFVINGESGCVRTMWGY-----EPPPSA	737
QY	54	-----QQAQVPHVWGWGVEAGAPALRLQKSSSDLLERRESVLRRQGEVAERRNA	104
DB	738	GSHGQHQQQQQQQSH-----HQPQQQQQQQQQQQQQQQQQQQQQSLGQQQHCL	786
QY	105	LPEVVFSTPTDENS-----DONSRSSQAGITGSYSVSE-----	139

DB 787 SPSGSLTPSSSGGSGVGGVGPPLTPSSVAQNNNEAQLLSLQRTIOMRBRP 846

QY 140 SPSGSLTPSSSGGSGVGGVGPPLTPSSVAQNNNEAQLLSLQRTIOMRBRP 183

DB 847 HFFRRPHALNMRWAGD--YSLPPGQALNTLSAQQQW--GSSNSTGL 893

RESULT 14

Q4PBW3 USTMA PRELIMINARY; PRT; 793 AA.

AC 04PBW3-

DT 13-SEP-2005 (TRENBLrel. 31, Created)

DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)

DE 13-SEP-2005 (TRENBLrel. 31, Last annotation update)

GN Hypothetical protein.

ORFNames=U002400.1;

US11ago maydis 521.

US11agocota; Basidiomycota; Ustilaginomycetes;

US11aginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

NCBI_TaxId=237631;

NCBI_TaxId=237631;

NUCLEOTIDE SEQUENCE.

RC STRAIN=521.

RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,

RA Alt-Zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,

RA Arachchi H., Armbruster J., Bachantang P., Baldwin J., Barry A.,

RA Bayl T., Blitshstein B., Bloom T., Biye J., Boguslavsky L.,

RA Borowsky M., Boukhalter B., Brunache A., Butler J., Callicote N.,

RA Calvo S., Camarero J., Campo K., Chang J., Chesnang V., Citroen M.,

RA Collymore A., Conditine T., Cook A., Cooke P., Corum B., Cuomo C.,

RA David R., Dawe T., Degray S., Dodge S., Dooley K., Dojle P.,

RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,

RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,

RA Fitzgerald M., Foley K., Gage D., Galagan J., Geahrin G., Gnerre S.,

RA Guitke A., Goyette A., Graham J., Grandbois B., Gyaltsen K., Hafez N.,

RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,

RA Homan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,

RA Jaffe D., Jones C., Kamal M., Kamat A., Kamyssele M., Karlsson E.,

RA Jelle C., Kleu A., Kliner P., Kodira C., Kulbokas E., Labutti K.,

RA Lema D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,

RA Lindblad-toh K., Liu X., Lokytang T., Lokytang Y., Lucien O.,

RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,

RA Manning J., Marabelli R., Maru K., Matthews C., Maucelli E.,

RA Mccarthy M., McDonough S., Moghee T., Mordim J., Meneis L.,

RA Mestrov J., Mhalay A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,

RA Mozes J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C.,

RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,

RA Norbu N., O'donnell P., Okawa O., O'leary S., Omotosho B.,

RA O'Neill K., Osman S., Parker S., Perrin D., Phunthang P., Pignani B.,

RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,

RA Retta R., Rodriguez S., Rise C., Rodriguez J., Rogers J., Rogov P.,

RA Rutman M., Schupbach R., Seaman C., Settippalli S., Shapre T.,

RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougenec C.,

RA Spencer B., Stalker J., Stange-Chomann N., Stavropoulos S.,

RA Steaton K., Steady S., Stone S., Stubbs M., Talamas J., Tchinga P.,

RA Tenzing P., Teffaye S., Theodore J., Thoultsang Y., Toham K.,

RA Towey S., Tzamba T., Tsomo N., Vallée D., Vassiliev H.,

RA Venkatarman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,

RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,

RA Zammer A., Zody M., Zander E.,

RT "The genome sequence of Ustilago maydis".

CC Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).

CC EMBL; AACPO1000083; EAK83438.1; -; Genomic_DNA.

DR InterPro: IPR006565; BTP.

DR InterPro: IPR007124; Hic_TAP.

DR Pfam: PF07524; Bromo_TP; I.

DR SMART: SM00576; BTP; I.

KM DNA-binding; Hypothetical protein; Nuclear protein.

SQ SEQUENCE 793 AA; 84916 MW; 8627A3C45F71ACE2 CRC64;

Query Match 9.3%; Score 105.5; DB 2; Length 793;

Best Local Similarity 26.9%; Pred. No. 18;

Matches 36; Conservative 26; Mismatches 41; Indels 31; Gaps 6;

QY 72 LRLQSGSDLLERESVLRQEVAEERNNALFPEVFSPTPDNSDNRSSQASG- 130

DB 669 LQREKKEHLEPHEKELQROQELQLOAL-----ASENSGGSDSAVLSGL 720

QY 131 ITGSYSVSESPFSPHLSNVA-----WTVEDPVDSAPPQQRKEQWYAGINP- 179

DB 721 IADSYA-----SRIR-NGNITWHTWDTMPBDYDMLPGKKVKTGSRGVGVALEK 772

QY 180 ---SDGINSVLEA 190

DB 773 RMRSESTSDLDLA 786

RESULT 15

Q5STP8-CRYNE PRELIMINARY; PRT; 1066 AA.

AC 05STP8;

DT 13-SEP-2005 (TRENBLrel. 31, Created)

DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)

DE 13-SEP-2005 (TRENBLrel. 31, Last annotation update)

GN Hypothetical protein.

ORFNames=CMBD4050;

OS Cryptococcus neoformans var. neoformans B-3501A.

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;

OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.

NCBI_TaxId=283643;

NCBI_TaxId=283643;

NUCLEOTIDE SEQUENCE.

RC STRAIN=B-3501A.

RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,

RA Mikes B.L., Fu J., Davis R.W.;

RT "Cryptococcus neoformans serotype D sequencing."

CC Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC EMBL; AAEY01000021; EAL21029.1; -; Genomic_DNA.

KM Hypothetical protein.

SQ SEQUENCE 1066 AA; 114328 MW; B00601SD4771A5AF CRC64;

Query Match 9.3%; Score 105; DB 2; Length 1066;

Best Local Similarity 24.3%; Pred. No. 29;

Matches 60; Conservative 25; Mismatches 78; Indels 84; Gaps 12;

QY 2 SPRHLSSESGKPLS-----TKQBASKPPPGC-----PQNRGVNRWEYR----- 41

DB 188 SPRRSNTSSRPPLSLARPSPNALSPPSAAGSPSPQATKKKSHSTRNSISLPIK 247

QY 42 -----LRPLRR-----ADPEQQAQVPHVWGVEVAGAPALRLQKSSDLR 85

DB 248 LQMAASRPSPFVHLSPSVGSVPSPSPGSKSPS-----RLAGLSQRLKFPSPGGA 303

QY 86 ERESVLRQEVAEERNNAL-----PPEVSPPT-----PDNSDNRSSS 126

DB 304 EREK-----EESRRRLKELTSGESRSTPFPVSPVAELISLPDDESSSVASNR 355

QY 127 QASGTTG--SYSVSESPFS--PIHLSNVAMTVEDPVDSAPPQQRKEQWYAGINSPG 182

DB 356 PLSGARGQPTFGWSNPGSPSFLPLPGS-----SSPFLASAP-----FSGASPADG 402

QY 183 INSEVLE 189

DB 403 QSDATPE 409

Search completed: March 3, 2006, 13:26:17

Job time : 84.1137 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 13:35:46 ; Search time 28.8338 Seconds
(without alignments)
616.473 Million cell updates/sec

Title: US-10-646-873-47

Perfect score: 1132
Sequence: 1 MSPRLSSSGKPLSTKQEA.....HKNAERWESRIYASEDD 215

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents, AA:
1: /cgn2_6/prodata/1/1aa/5-COMB.pep.*
2: /cgn2_6/prodata/1/1aa/6-COMB.pep.*
3: /cgn2_6/prodata/1/1aa/H-COMB.pep.*
4: /cgn2_6/prodata/1/1aa/ECTUS-COMB.pep.*
5: /cgn2_6/prodata/1/1aa/RE-COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1132	100.0	215	2	US-09-050-516-47
2	1132	100.0	215	2	US-10-278-547-47
3	1132	100.0	679	2	US-09-050-516-42
4	1132	100.0	679	2	US-10-278-547-42
5	189	16.7	36	2	US-09-050-516-43
6	189	16.7	36	2	US-10-278-547-43
7	175	15.5	35	2	US-09-050-516-45
8	175	15.5	35	2	US-10-278-547-45
9	171	15.1	33	2	US-09-050-516-46
10	171	15.1	33	2	US-10-278-547-46
11	146	12.9	31	2	US-09-050-516-44
12	146	12.9	31	2	US-10-278-547-44
13	101.5	9.0	1048	2	US-09-921-099A-11
14	93.5	8.3	699	2	US-09-457-040B-18
15	90	8.0	876	2	US-09-294-531B-2
16	88.5	7.8	371	2	US-10-104-047-3421
17	87.5	7.7	249	2	US-09-248-796A-15373
18	86.5	7.6	1158	2	US-09-060-482-2
19	85.5	7.6	342	2	US-09-252-911A-27223
20	84.5	7.5	1051	2	US-09-428-711A-14
21	83.5	7.4	489	1	US-08-124-674-2
22	83.5	7.4	933	2	US-09-248-796A-20513
23	83.5	7.4	1172	2	US-09-949-016-8593
24	83	7.3	1182	2	US-09-041-886-21
25	83	7.3	1435	1	US-08-568-459A-4
26	83	7.3	1435	1	US-08-467-826B-4
27	83	7.3	1435	2	US-09-210-288-4

28	83	7.3	1435	2	US-10-153-273-4	Sequence 4, Appli
29	82.5	7.3	489	1	US-08-589-893-10	Sequence 10, Appl
30	82.5	7.3	489	1	US-08-589-893-22	Sequence 22, Appl
31	82.5	7.3	489	1	US-09-020-991-10	Sequence 10, Appl
32	82.5	7.3	489	1	US-09-020-991-22	Sequence 22, Appl
33	82.5	7.3	489	1	US-09-062-890-10	Sequence 10, Appl
34	82.5	7.3	489	1	US-09-062-890-22	Sequence 22, Appl
35	82.5	7.3	489	1	US-09-062-890-38	Sequence 38, Appl
36	82.5	7.3	489	1	US-09-062-890-30	Sequence 30, Appl
37	82.5	7.3	489	1	US-09-062-890-32	Sequence 32, Appl
38	82.5	7.3	489	1	US-09-062-890-34	Sequence 34, Appl
39	82.5	7.3	489	1	US-09-062-890-36	Sequence 36, Appl
40	82.5	7.3	489	1	US-09-062-890-38	Sequence 38, Appl
41	82.5	7.3	489	1	US-08-635-121-2	Sequence 2, Appli
42	82.5	7.3	1346	2	US-08-978-277A-2	Sequence 2, Appli
43	82.5	7.3	1346	2	US-08-978-277A-2	Sequence 2, Appli
44	82	7.2	281	2	US-09-252-991A-17976	Sequence 17976, A
45	82	7.2	470	2	US-10-104-047-2022	Sequence 2022, Ap

ALIGNMENTS

RESULT 1
US-09-050-516-47
Sequence 47, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-BAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-47

Query Match 100.0%; Score 1132; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.9e-113;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQKASKPPRGCPQANRGVVRWEYFRLRLPRAPDEPQOAVPH 60
DB 1 MSPRLSSSGKPLSTKQKASKPPRGCPQANRGVVRWEYFRLRLPRAPDEPQOAVPH 60
QY 61 VWGMEVAGAPALRLQKSSDILLERERESVLRREQVAEERRNALPPEVFSPTPDENSQ 120
DB 61 VWGMEVAGAPALRLQKSSDILLERERESVLRREQVAEERRNALPPEVFSPTPDENSQ 120
QY 121 NSRSSQASGIGTSYSVSESPFSPITLHNSVAMTVDPVDSAPPGQKKQWYAGINPS 180
DB 121 NSRSSQASGIGTSYSVSESPFSPITLHNSVAMTVDPVDSAPPGQKKQWYAGINPS 180
QY 181 DGINSEVLEAIRVTRHKNMAERWESRIYASEDD 215
DB 181 DGINSEVLEAIRVTRHKNMAERWESRIYASEDD 215

RESULT 2

US-10-278-547-47
Sequence 47, Application US/10278547
Patent No. 6660834
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLAAS, MICHAEL R.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-10-278-547-47

Query Match 100.0%; Score 1132; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.9e-113;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQKASKPPRGCPQANRGVVRWEYFRLRLPRAPDEPQOAVPH 60
DB 1 MSPRLSSSGKPLSTKQKASKPPRGCPQANRGVVRWEYFRLRLPRAPDEPQOAVPH 60
QY 61 VWGMEVAGAPALRLQKSSDILLERERESVLRREQVAEERRNALPPEVFSPTPDENSQ 120
DB 61 VWGMEVAGAPALRLQKSSDILLERERESVLRREQVAEERRNALPPEVFSPTPDENSQ 120
QY 121 NSRSSQASGIGTSYSVSESPFSPITLHNSVAMTVDPVDSAPPGQKKQWYAGINPS 180
DB 121 NSRSSQASGIGTSYSVSESPFSPITLHNSVAMTVDPVDSAPPGQKKQWYAGINPS 180
QY 181 DGINSEVLEAIRVTRHKNMAERWESRIYASEDD 215
DB 181 DGINSEVLEAIRVTRHKNMAERWESRIYASEDD 215

RESULT 3

US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLAAS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-42

Query Match 100.0%; Score 1132; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 5e-112;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQASKPPGCCPOANGVWMEYFRLRPLRFRAPDEPQQAQVPH 60
DB 465 MSPRLSSSGKPLSTKQASKPPGCCPOANGVWMEYFRLRPLRFRAPDEPQQAQVPH 524

QY 61 VNGWEVAGAPALRLQKSSDILLERRESVLRREQVAEERNALPPEVFSPTPDNSQ 120
DB 525 VNGWEVAGAPALRLQKSSDILLERRESVLRREQVAEERNALPPEVFSPTPDNSQ 584

QY 121 NSRSSQASGITGSYSVSESPFSPILHNSNVAWTEVPDAPPGQRKKEQWYAGINS 180
DB 585 NSRSSQASGITGSYSVSESPFSPILHNSNVAWTEVPDAPPGQRKKEQWYAGINS 644

QY 181 DGINSEVLEAIRVTRHKNAERWESRIYASEED 215
DB 645 DGINSEVLEAIRVTRHKNAERWESRIYASEED 679

RESULT 4
US-10-278-547-42
Sequence 42, Application US/10278547
Patent No. 6660834
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLETTIS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASCSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-278-547-42

Query Match 100.0%; Score 1132; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 5e-112;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQASKPPGCCPOANGVWMEYFRLRPLRFRAPDEPQQAQVPH 60
DB 465 MSPRLSSSGKPLSTKQASKPPGCCPOANGVWMEYFRLRPLRFRAPDEPQQAQVPH 524

QY 61 VNGWEVAGAPALRLQKSSDILLERRESVLRREQVAEERNALPPEVFSPTPDNSQ 120
DB 525 VNGWEVAGAPALRLQKSSDILLERRESVLRREQVAEERNALPPEVFSPTPDNSQ 584

QY 121 NSRSSQASGITGSYSVSESPFSPILHNSNVAWTEVPDAPPGQRKKEQWYAGINS 180
DB 585 NSRSSQASGITGSYSVSESPFSPILHNSNVAWTEVPDAPPGQRKKEQWYAGINS 644

QY 181 DGINSEVLEAIRVTRHKNAERWESRIYASEED 215
DB 645 DGINSEVLEAIRVTRHKNAERWESRIYASEED 679

RESULT 5
US-09-050-516-43
Sequence 43, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLETTIS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park

STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FaastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050.516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828.855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-43

Query Match 16.7%; Score 189; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQASKEPPRCGPOANGVVR 36
Db 1 MSPRLSSSGKPLSTKQASKEPPRCGPOANGVVR 36

RESULT 6
US-10-278-547-43
Sequence 43, Application US/10278547
Patent No. 6660834
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLAAS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FaastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
CLASSIFICATION:

APPLICATION NUMBER: US/10/278.547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050.516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828.855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-278-547-43

Query Match 16.7%; Score 189; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQASKEPPRCGPOANGVVR 36
Db 1 MSPRLSSSGKPLSTKQASKEPPRCGPOANGVVR 36

RESULT 7
US-09-050-516-45
Sequence 45, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLAAS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FaastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050.516
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6627414e
US-09-050-516-45

Query Match 15.5%; Score 175; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.le-11;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 ALPEVFSPTPENSQNSRSSQASGITGSYSVS 138
DB 1 ALPEVFSPTPENSQNSRSSQASGITGSYSVS 35

RESULT 8
US-10-278-547-45
Sequence 45, Application US/10278547
Patent No. 6660834
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-OCT-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-278-547-45

Query Match 15.5%; Score 175; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.le-11;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 ALPEVFSPTPENSQNSRSSQASGITGSYSVS 138
DB 1 ALPEVFSPTPENSQNSRSSQASGITGSYSVS 35

RESULT 9
US-09-050-516-46
Sequence 46, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAFF, LISA
APPLICANT: ROBERTS-RAFF, LISA
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-46

Query Match 15.1%; Score 171; DB 2; Length 33;
Best Local Similarity 97.0%; Pred. No. 2.8e-11;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 157 EDPVDSAPPGORKKEQWYAGINPSDGINSEVLE 189
Db 1 EDSVDSAPPGORKKEQWYAGINPSDGINSEVLE 33

RESULT 10
US-10-278-547-46
Sequence 46, Application US/10278547
Patent No. 6660834
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US-10-278-547-46

Query Match 15.1%; Score 171; DB 2; Length 33;
Best Local Similarity 97.0%; Pred. No. 2.8e-11;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 157 EDPVDSAPPGORKKEQWYAGINPSDGINSEVLE 189
Db 1 EDSVDSAPPGORKKEQWYAGINPSDGINSEVLE 33

RESULT 11
US-09-050-516-44
Sequence 44, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-44

Query Match 12.9%; Score 146; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using SW model

Run on: March 3, 2006, 14:09:14 / Search time 94.4412 Seconds
(without alignments)
951.209 Million cell updates/sec

Title: US-10-646-873-47

Sequence: 1 MSPRLSSSSGKPLSTKQEA.....HKNAWERESRIYASEDD 215

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications AA Main:*

1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubppaa/US12_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1132	100.0	215	US-09-050-516-47	Sequence 47, App1
2	1132	100.0	215	US-10-278-547-47	Sequence 47, App1
3	1132	100.0	215	US-10-646-873-47	Sequence 42, App1
4	1132	100.0	679	US-09-050-516-42	Sequence 42, App1
5	1132	100.0	679	US-10-278-547-42	Sequence 42, App1
6	1132	100.0	679	US-10-646-873-42	Sequence 42, App1
7	839	74.1	172	US-10-106-698-4761	Sequence 4761, App
8	236	20.8	43	US-10-029-386-33676	Sequence 33676, A
9	189	16.7	36	US-10-278-547-43	Sequence 43, App1
10	189	16.7	36	US-10-646-873-43	Sequence 43, App1
11	175	15.5	35	US-09-050-516-45	Sequence 45, App1
12	175	15.5	35	US-10-278-547-45	Sequence 45, App1
13	175	15.5	35	US-10-646-873-45	Sequence 45, App1
14	175	15.5	35	US-09-050-516-46	Sequence 46, App1
15	171	15.1	33	US-10-278-547-46	Sequence 46, App1
16	171	15.1	33	US-10-646-873-46	Sequence 46, App1
17	171	15.1	33	US-09-050-516-44	Sequence 44, App1
18	146	12.9	31	US-10-278-547-44	Sequence 44, App1
19	146	12.9	31	US-10-646-873-44	Sequence 44, App1
20	127.5	11.3	910	US-10-087-192-1320	Sequence 1320, App
21	127.5	11.3	913	US-10-408-765A-2018	Sequence 2018, App
22	127.5	11.3	923	US-10-719-993-748	Sequence 748, App
23	127.5	11.3	923	US-10-719-993-749	Sequence 749, App
24	127.5	11.3	1103	US-10-719-993-745	Sequence 745, App
25	127.5	11.3	1103	US-10-756-149-4788	Sequence 4788, App
26	127.5	11.3	1103	US-10-631-467-604	Sequence 604, App
27	127.5	11.3	1103	US-10-631-467-604	Sequence 604, App

28	127.5	11.3	1103	US-10-631-467-691	Sequence 691, App
29	127.5	11.3	1335	US-10-719-993-742	Sequence 742, App
30	127.5	11.3	1337	US-10-719-993-743	Sequence 743, App
31	127.5	11.3	1337	US-10-719-993-747	Sequence 747, App
32	124	11.0	948	US-10-094-749-2942	Sequence 2942, App
33	118	10.4	1092	US-10-719-993-744	Sequence 744, App
34	114.5	10.1	324	US-10-450-763-36719	Sequence 36719, A
35	114.5	10.1	1454	US-10-408-765A-1328	Sequence 1328, App
36	114.5	10.1	1493	US-10-211-462-59	Sequence 59, App1
37	111	9.8	1520	US-10-467-555-14	Sequence 14, App1
38	102	9.0	956	US-10-437-963-167398	Sequence 167398, App
39	101.5	9.0	686	US-11-097-143-768	Sequence 768, App
40	101.5	9.0	1048	US-10-619-992-12	Sequence 11, App1
41	99	8.7	629	US-10-384-919-2	Sequence 2, App1
42	98	8.7	869	US-10-437-963-204823	Sequence 204823, App
43	96	8.5	851	US-10-437-963-204825	Sequence 204825, App
44	94.5	8.3	1071	US-10-188-248-24	Sequence 24, App1
45	94.5	8.3	1121	US-10-437-963-152820	Sequence 152820, App

ALIGNMENTS

RESULT 1
US-09-050-516-47
Sequence 47, Application US/09050516
Patent No. US200100109041
GENERAL INFORMATION:
APPLICANT: BILLING-MEDTEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL TRACT
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET INFORMATION: 6065:US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/938-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-47

Query Match 100.0%; Score 1132; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 6e-94;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQKASKEPPGCPQANRGVWMEYFLRLPRLFRAPDEPOQAVPH 60
Db 1 MSPRLSSSGKPLSTKQKASKEPPGCPQANRGVWMEYFLRLPRLFRAPDEPOQAVPH 60
Qy 61 VMGEVAGAPALRLQKSSDLLEERESVLRREQEVAEERRNALPPEVFSPTDENSDQ 120
Db 61 VMGEVAGAPALRLQKSSDLLEERESVLRREQEVAEERRNALPPEVFSPTDENSDQ 120
Qy 121 NSRSSQASGTTGSYSVSESPFPIHLHSNVAMTVEDPDVAPGQKKQWYAGINPS 180
Db 121 NSRSSQASGTTGSYSVSESPFPIHLHSNVAMTVEDPDVAPGQKKQWYAGINPS 180
Qy 181 DGINSEVLEAIRVTRHKNAMAEWRWESRIYASEDD 215
Db 181 DGINSEVLEAIRVTRHKNAMAEWRWESRIYASEDD 215

RESULT 2

US-10-278-547-47
Sequence 47, Application US/10278547
Publication No. US20030082619A1

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.

HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547

FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065.US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. US20030082619A1e

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-10-278-547-47

Query Match 100.0%; Score 1132; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 6e-94;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQKASKEPPGCPQANRGVWMEYFLRLPRLFRAPDEPOQAVPH 60
Db 1 MSPRLSSSGKPLSTKQKASKEPPGCPQANRGVWMEYFLRLPRLFRAPDEPOQAVPH 60
Qy 61 VMGEVAGAPALRLQKSSDLLEERESVLRREQEVAEERRNALPPEVFSPTDENSDQ 120
Db 61 VMGEVAGAPALRLQKSSDLLEERESVLRREQEVAEERRNALPPEVFSPTDENSDQ 120
Qy 121 NSRSSQASGTTGSYSVSESPFPIHLHSNVAMTVEDPDVAPGQKKQWYAGINPS 180
Db 121 NSRSSQASGTTGSYSVSESPFPIHLHSNVAMTVEDPDVAPGQKKQWYAGINPS 180
Qy 181 DGINSEVLEAIRVTRHKNAMAEWRWESRIYASEDD 215
Db 181 DGINSEVLEAIRVTRHKNAMAEWRWESRIYASEDD 215

RESULT 3

US-10-646-873-47

Sequence 47, Application US/10646873

Publication No. US20040043406A1

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.

HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/646,873

FILING DATE: 22-Aug-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: 30-MAR-1998

APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-646-873-47

Query Match 100.0%; Score 1132; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 6e-94;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQASKPPGCCPOANGVWMEYFRLPRLFRAPDDEPQQAQVPH 60
DB 1 MSPRLSSSGKPLSTKQASKPPGCCPOANGVWMEYFRLPRLFRAPDDEPQQAQVPH 60
QY 61 VWGWEVAGAPALRLQKSSDILLERRESVLRREQEVAERNNALPPEVFSPTPDNSDQ 120
DB 61 VWGWEVAGAPALRLQKSSDILLERRESVLRREQEVAERNNALPPEVFSPTPDNSDQ 120
QY 121 NSRSSSQASGITGSYSVSESPFSPHLSNVAWTEDEVDPSAPPGQRKKEQWYAGINS 180
DB 121 NSRSSSQASGITGSYSVSESPFSPHLSNVAWTEDEVDPSAPPGQRKKEQWYAGINS 180
QY 181 DGINSEVLEAIRVTRHKNAERWESRIYASEDD 215
DB 181 DGINSEVLEAIRVTRHKNAERWESRIYASEDD 215

RESULT 4
US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUBE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-42

Query Match 100.0%; Score 1132; DB 3; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.7e-93;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQASKPPGCCPOANGVWMEYFRLPRLFRAPDDEPQQAQVPH 60
DB 465 MSPRLSSSGKPLSTKQASKPPGCCPOANGVWMEYFRLPRLFRAPDDEPQQAQVPH 524
QY 61 VWGWEVAGAPALRLQKSSDILLERRESVLRREQEVAERNNALPPEVFSPTPDNSDQ 120
DB 525 VWGWEVAGAPALRLQKSSDILLERRESVLRREQEVAERNNALPPEVFSPTPDNSDQ 584
QY 121 NSRSSSQASGITGSYSVSESPFSPHLSNVAWTEDEVDPSAPPGQRKKEQWYAGINS 180
DB 585 NSRSSSQASGITGSYSVSESPFSPHLSNVAWTEDEVDPSAPPGQRKKEQWYAGINS 644
QY 181 DGINSEVLEAIRVTRHKNAERWESRIYASEDD 215
DB 645 DGINSEVLEAIRVTRHKNAERWESRIYASEDD 679

RESULT 5
US-10-278-547-42
Sequence 42, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-278-547-42

Query Match 100.0%; Score 1132; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.7e-93;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQASKPPRGCPQANRGVVRWEYFLRLPFRAPDEPQOAVPH 60
DB 465 MSPRLSSSGKPLSTKQASKPPRGCPQANRGVVRWEYFLRLPFRAPDEPQOAVPH 524
QY 61 VMGWEVAGAPALRLQKSSDILLERERESVLRREQEVAEERRNALFPEVFSPTPDENSQ 120
DB 525 VMGWEVAGAPALRLQKSSDILLERERESVLRREQEVAEERRNALFPEVFSPTPDENSQ 584
QY 121 NSRSSQASGITGYSYSESPFPIHLHSNVAVTVEPVDASAPPGQKKQWYAGINPS 180
DB 585 NSRSSQASGITGYSYSESPFPIHLHSNVAVTVEPVDASAPPGQKKQWYAGINPS 644
QY 181 DGINSEVLEAIRVTRHKNAEMERWESRIYASEDD 215
DB 645 DGINSEVLEAIRVTRHKNAEMERWESRIYASEDD 679

RESULT 6
US-10-646-873-42
Sequence 42, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-646-873-42

Query Match 100.0%; Score 1132; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.7e-93;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQASKPPRGCPQANRGVVRWEYFLRLPFRAPDEPQOAVPH 60
DB 465 MSPRLSSSGKPLSTKQASKPPRGCPQANRGVVRWEYFLRLPFRAPDEPQOAVPH 524
QY 61 VMGWEVAGAPALRLQKSSDILLERERESVLRREQEVAEERRNALFPEVFSPTPDENSQ 120
DB 525 VMGWEVAGAPALRLQKSSDILLERERESVLRREQEVAEERRNALFPEVFSPTPDENSQ 584
QY 121 NSRSSQASGITGYSYSESPFPIHLHSNVAVTVEPVDASAPPGQKKQWYAGINPS 180
DB 585 NSRSSQASGITGYSYSESPFPIHLHSNVAVTVEPVDASAPPGQKKQWYAGINPS 644
QY 181 DGINSEVLEAIRVTRHKNAEMERWESRIYASEDD 215
DB 645 DGINSEVLEAIRVTRHKNAEMERWESRIYASEDD 679

RESULT 7
US-10-106-698-4761
Sequence 4761, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patent In Ver. 3.0
SEQ ID NO 4761
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (55)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC FEATURE
LOCATION: (116)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-4761

Query Match 74.1%; Score 839; DB 4; Length 172;
Best Local Similarity 87.0%; Pred. No. 1,3e-67;
Matches 167; Conservative 0; Mismatches 5; Indels 20; Gaps 1;

QY 24 PRGPOANGVVMWYFRLPLFRAPDEPOQAQVPHWGWVAGAPALRLQKSSDDL 83
1 PRRPOANGVVMWYFRLPLFR-----APALRLQKSSDDL 40
DB 84 EERESVLRREQEVAERENALPPEVFSPTPDENSQNSRSSQASGITGSYSVSESPPF 143
41 EERESVLRREQEVAERENALPPEVFSPTPDENSQNSRSSQASGITGSYSVSESPPF 100
QY 144 SPHLHSNVAWTVEDVDAPPGQRKKEQWYAGINSDDGINSRVLAIVTRHKMAAR 203
DB 101 SPHLHSNVAWTVEDVDAPPGQRKKEQWYAGINSDDGINSRVLAIVTRHKMAAR 160
QY 204 MESRIYASEDD 215
DB 161 MESRIYASEDD 172

RESULT 8
US-10-029-386-33676
Sequence 33676, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33676
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004030.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.42
US-10-029-386-33676

Query Match 20.8%; Score 236; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 6,2e-14;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 ITGSYSVSSBPPSPFPIHLSNVAVTVEDPVDSAPPGQRKKEQW 173
DB 1 ITGSYSVSSBPPSPFPIHLSNVAVTVEDPVDSAPPGQRKKEQW 43

RESULT 9
US-09-050-516-43

Sequence 43, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PasteSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20010010904A1e
US-09-050-516-43

Query Match 16.7%; Score 189; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 8,7e-10;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRHLSSESSGKPLSTKQASKPPRCGPOANGVVR 36
DB 1 MSPRHLSSESSGKPLSTKQASKPPRCGPOANGVVR 36

RESULT 10
US-10-278-547-43
Sequence 43, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.

FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-278-547-43
Query Match 16.7%: Score 189; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. NO. 8.7e-10;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSPRLSSSGKPLSTKQKASKPRGCPQANRGVVR 36
Db 1 MSPRLSSSGKPLSTKQKASKPRGCPQANRGVVR 36
RESULT 11
US-10-646-873-43
Sequence 43, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.

KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-646-873-43
Query Match 16.7%: Score 189; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. NO. 8.7e-10;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSPRLSSSGKPLSTKQKASKPRGCPQANRGVVR 36
Db 1 MSPRLSSSGKPLSTKQKASKPRGCPQANRGVVR 36
RESULT 12
US-09-050-516-45
Sequence 45, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPD, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-45

Query Match 15.5%; Score 175; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 ALPEVFSPTPDNSDNRSSSQASGITGSYSVS 138
DB 1 ALPEVFSPTPDNSDNRSSSQASGITGSYSVS 35

RESULT 13
US-10-278-547-45
Sequence 45, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
CORPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-278-547-45

Query Match 15.5%; Score 175; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 ALPEVFSPTPDNSDNRSSSQASGITGSYSVS 138
DB 1 ALPEVFSPTPDNSDNRSSSQASGITGSYSVS 35

RESULT 14
US-10-646-873-45
Sequence 45, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
CORPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-646-873-45

Query Match 15.5%; Score 175; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 ALFPEVFSPTPDNSDONSRSSSQASGITGSYSVS 138
DB 1 ALFPEVFSPTPDNSDONSRSSSQASGITGSYSVS 35

RESULT 15
US-09-050-516-46
Sequence 46, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20010010904A1e
US-09-050-516-46

Query Match 15.1%; Score 171; DB 3; Length 33;
Best Local Similarity 97.0%; Pred. No. 3.3e-08;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 157 EDPVDSAPPGQRKKEQWYAGINPSDGINSEVLE 189
DB 1 EDSVDSAPPGQRKKEQWYAGINPSDGINSEVLE 33

Search completed: March 3, 2006, 14:18:11
Job time: 94.4412 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 14:10:51 ; Search time 10.2381 Seconds
(without alignments)
420.009 Million cell updates/sec

Title: US-10-646-873-47

Perfect score: 1132
Sequence: 1 MSPHRLSSSSKPKSTKQEA.....HKNAWERESRTYASEDD 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.New.*
1: /cgn2_6/pcdata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/pcdata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/pcdata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/pcdata/1/pubpaa/PCT_NEW_PUB.pep.*
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6: /cgn2_6/pcdata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/pcdata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/pcdata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97.5	8.6	386	US-11-087-099-12026	Sequence 12026, A
2	88.5	7.8	371	US-11-072-512-3421	Sequence 3421, Ap
3	87	7.7	388	US-10-858-730-83	Sequence 83, Appl
4	86	7.6	736	US-10-467-657-4760	Sequence 4760, Ap
5	82.5	7.3	1346	US-11-060-005-2	Sequence 2, Appl1
6	82	7.2	470	US-11-072-512-2022	Sequence 2022, Ap
7	80.5	7.1	390	US-11-098-686-10913	Sequence 10913, A
8	80	7.1	1596	US-11-060-005-4	Sequence 4, Appl1
9	79.5	7.0	287	US-11-072-512-2485	Sequence 2485, Ap
10	79.5	7.0	697	US-10-821-234-3058	Sequence 905, App
11	79	7.0	312	US-11-072-512-3568	Sequence 3568, Ap
12	79	7.0	1271	US-10-770-726-46	Sequence 46, Appl
13	78.5	6.9	706	US-11-087-099-4237	Sequence 4237, Ap
14	78	6.9	419	US-11-072-512-3514	Sequence 3514, Ap
15	78	6.9	571	US-11-072-512-2709	Sequence 2709, Ap
16	78	6.9	580	US-11-087-099-1375	Sequence 1375, Ap
17	77	6.8	748	US-11-150-756-2	Sequence 2, Appl1
18	77	6.8	1786	US-11-196-400-3	Sequence 3, Appl1
19	76.5	6.8	457	US-10-982-545-8	Sequence 8, Appl1
20	76.5	6.8	457	US-10-982-545-13	Sequence 13, Appl1
21	76.5	6.8	605	US-10-131-826A-160	Sequence 160, App
22	76.5	6.8	605	US-10-973-115B-160	Sequence 160, App
23	76.5	6.8	660	US-11-143-984A-114	Sequence 114, App
24	76.5	6.8	1268	US-10-995-561-918	Sequence 918, App
25	76.5	6.8	1268	US-10-995-561-919	Sequence 919, App

26	76.5	6.8	1268	US-10-995-561-920	Sequence 920, App
27	76.5	6.8	1347	US-11-087-099-5370	Sequence 5370, Ap
28	76	6.7	1142	US-11-044-051-73	Sequence 73, Appl
29	75.5	6.7	600	US-11-072-512-3397	Sequence 3397, Ap
30	75.5	6.7	662	US-11-072-175-184	Sequence 184, App
31	75.5	6.7	1823	US-10-995-561-988	Sequence 988, App
32	75	6.6	758	US-11-072-175-242	Sequence 242, App
33	75	6.6	787	US-11-072-512-3340	Sequence 3340, App
34	75	6.6	1410	US-10-821-234-1050	Sequence 1050, Ap
35	75	6.6	2238	US-10-330-773-42	Sequence 42, Appl
36	74.5	6.6	271	US-11-169-041-170	Sequence 170, App
37	74.5	6.6	336	US-11-087-099-1677	Sequence 1677, App
38	74.5	6.6	2392	US-10-330-773-907	Sequence 907, App
39	74.5	6.6	2505	US-11-126-313-33	Sequence 33, Appl
40	74	6.5	437	US-10-850-465-2	Sequence 2, Appl1
41	74	6.5	537	US-11-129-442-47	Sequence 47, Appl
42	74	6.5	1189	US-11-182-885-3	Sequence 3, Appl1
43	73.5	6.5	1189	US-10-887-770-11	Sequence 11, Appl
44	73.5	6.5	778	US-11-072-512-3477	Sequence 3477, Ap
45	73.5	6.5	2516	US-10-647-956A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-11-087-099-12026
; Sequence 12026, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12026
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-11-087-099-12026

Query Match 8.6%; Score 97.5; DB 7; Length 386;
Best Local Similarity 24.7%; Pred. No. 0.1; 62; Indels 45; Gaps 9;
Matches 45; Conservative 30; Mismatches

QY 41 RLRLFRAPDEPQOQVPHVWMEV-----AGAPALRLQKSS--SDL-----LERE 86
DB 150 RLTRYKQIRQDMESQIADVVRQLKSKSSGNTDSVGLQHAESGLSLRTLLALGKE 209
QY 87 -----RESVLRROEVAER-----RNALPEYFSPFPDSDNSNS 124
DB 210 ATRAAEVAEPAQOQITPRLTAMVDAERTYHQNVAIDILNKHDENLNPAPHEESDNN--- 266
QY 125 SQOAGITGTSYVSSEPFPIHLSNVAWTVEDP--VDSAPGCKKKEOWYAG--INPS 180
DB 267 DVVSPDPSSEPKSPKVSPTHVSN--ISEDPALETSEPTRNGGVHYGVYIHFP 324
QY 181 DG 182
DB 325 DG 326

RESULT 2
US-11-072-512-3421
; Sequence 3421, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI

```
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3421
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3421
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Query Match 7.8%; Score 88.5; DB 7; Length 371;
Best Local Similarity 22.1%; Pred. No. 0.69;
Matches 42; Conservative 33; Mismatches 86; Indels 29; Gaps 7;
```

```
QY 4 RHLSSESGKPLSTKQKASRPPGCPQANRGVVRWYFRLRLFRAPDEPQQAQVPHWG 63
DB 173 QMRKMSQIBCTLKKEKQODMRVRVEKLSKLNQMAEPLPPPPVSEVELQHLRK 232
QY 64 --WEVAGAPALRLQKSSQSDLE-----RRESVLRQCVAAERNALE-----PEV 109
DB 233 ELERVAGALQAVQKNNRISLNRQOEIRIKOEERLQOEHSKLOQLAKPOSV 292
QY 110 FSPPTDENS-----DQNSRSSQASGITGYSVSESPFPPIHLHSNVAMTVEDPV-DSA 163
DB 293 FEEPPNNEKSNALQLEQVKELEKKG-----EVKSESTP-----SKKGWEGSSLMWGE 343
QY 164 PEGQRKKEQW 173
DB 344 VEGQRQLPAM 353
```

```
RESULT 3
US-10-858-730-83
; Sequence 83, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
```

```
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Thermobifida fusca
US-10-858-730-83
```

```
Query Match 7.7%; Score 87; DB 6; Length 388;
Best Local Similarity 32.6%; Pred. No. 1;
Matches 28; Conservative 14; Mismatches 38; Indels 6; Gaps 3;
```

```
QY 6 LSESSGKPLSTKQKASRPPGCPQANRGVVRWYFRLRLFRAPDEPQQAQVPHWG-- 63
DB 15 ISSSGRRLATKAASSSTGRRTYAT-GDKCEELIRAGYRLFRPSSPRHTOTPIKISIT 73
QY 64 --WEVAGAPALRL--LQKSSQSDLEERE 86
DB 74 VQDLGSPTRPRPRPRRISLRLARK 99
```

```
RESULT 4
US-10-467-657-4780
; Sequence 4780, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Maria Grazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04
; SEQ ID NO 4780
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4780
```

```
Query Match 7.6%; Score 86; DB 6; Length 736;
Best Local Similarity 21.6%; Pred. No. 2.7;
Matches 44; Conservative 25; Mismatches 77; Indels 58; Gaps 8;
```

```
QY 3 PRHLSSESGKPLSTKQKASRPPG-----CPQANRGVVRWYFRLRLFRAPDEPQQA 56
DB 425 PRPADAAQTPTVQTAASAMPSEKTAGPVSHQENNDPPVE-----DAPDKTETA 475
QY 57 QVPHVWGVEVAGAPALRLQKSSQSDLEERESVLRQCVAAERRNALEPPEVSPPTDE 116
DB 476 -----AGTARTSAKSIQTASAEATPPBNQVSKKADNTEAST-----SEVSE 520
QY 117 NSDQNSRSSQASGITGYSVSESPFP-----PIHLHSNVAMTVEDPVDSAPPGQRK 169
DB 521 NPQIATPRDAVEVETEFHAPAPAPFPYGFPPNDCCP-----EDGVEIIPPD--- 566
QY 170 KEQWTAGINPSD---GINSEVLEA 190
DB 567 ----WAVLTPADTAGGGTDEEAEA 586
```

```
RESULT 5
US-11-060-005-2
; Sequence 2, Application US/11060005
; Publication No. US20050260693A1
; GENERAL INFORMATION:
; APPLICANT: Irwin H. Gelman
```

TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
FILE REFERENCE: A30558-A-FWC-A-A 070156.0597
CURRENT APPLICATION NUMBER: US/11/0660.005
CURRENT FILING DATE: 2005-02-17
PRIOR APPLICATION NUMBER: 09/902.432
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 08/978.277
PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: 08/665.401
PRIOR FILING DATE: 1996-06-18
PRIOR APPLICATION NUMBER: 08/635.121
PRIOR FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1346
TYPE: PRT
ORGANISM: Rattus norvegicus
US-11-060-005-2

Query Match 7.3%; Score 82.5; DB 7; Length 1346;
Best Local Similarity 19.4%; Pred. No. 12;
Matches 55; Conservative 36; Mismatches 109; Indels 83; Gaps 9;

QY 4 RHLSSESGKPLSTKOE-----ASKPPRCGPQANRGVMEYFR----- 41
DB 318 RGRSRIDAVPASTOEDQAGSSSPGSGEVSSTESFKRLVTPRKSKSLTEBK 377
QY 42 -----LR-----PLRRAPDEPQAOVPHWGMVAGAPALRLQKSO 78
DB 378 EAGRTLVGACPLRNSRVEKNIGFPLRNSSPDGGRKGQROQATVEDSGVEINDEB 437
QY 79 SS-----DLERERESVLRREQVEAERRNALFPEVFSPTDENSDQNSRSSQA 128
DB 438 PDVPAVPLSEYAVEREK-----MEAGNMELPSCMCVCVSELSKTLVHTVS 487
QY 129 SGITGSYSVSESPFPIHLHNVMTVEDPVDVA--PPGQRKEQ--WYAGINP----- 179
DB 488 AVIDGRAVATSVERSBPSWISASVTEPLEHTAGEAMPVEVETEKDIIAETVLTOTLP 547
QY 180 -----SDGINSV---LEAIRTRKHMAAEKESIVYSEE 213
DB 548 EGDHADDWVTSVDFTSEAVTATETSEALRTEEVTEASGAEE 590

RESULT 6

US-11-072-512-2022
Sequence 2022, Application US/11072512
Publication No. US2006029945A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: OTSUKI, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHITAMA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYU
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cdna
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072.512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350.978

PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2022
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-2022

Query Match 7.2%; Score 82; DB 7; Length 470;
Best Local Similarity 24.0%; Pred. No. 3.7;
Matches 52; Conservative 24; Mismatches 79; Indels 62; Gaps 8;

QY 18 QASKPPRCGPQANRGVME-----YFRLRPLRPAPDEPQAOVPHWGMVAGA 69
DB 123 QEARFRKAAQAARDLTFABAEIELQNLRLQKGEQFRL--EMERTGVG-----TGA 173
QY 70 PALRLQKSSDPLRERESVLRRE-----QVAAERRNALFPEVFS 111
DB 174 NSQVLEIEKLTMTERTORTVARLQNVLDLTGSDNKGFEVLEBIAELR----- 224
QY 112 PTPDENSDQNSRSSQASGI--TGSYSVSESPFPIHLHNVNVA-----WTVEDPV 160
DB 225 ----EVSYNDYITSMADPFKRGKYTFMPPPSSVSHSQATWDSGVGLKYSTV 280
QY 161 DSAPPGQRKEQWYAGINSDGINSEVLEAIRVTRHK 197
DB 281 RKPRPQODGKE---GSGPPASGVWVSPIRGLHK 314

RESULT 7

US-11-098-686-10913
Sequence 10913, Application US/11098686
Publication No. US2006024696A1

GENERAL INFORMATION:

APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098.686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416.395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10913
LENGTH: 390
TYPE: PRT
ORGANISM: Lawsonia intracellularis
US-11-098-686-10913

Query Match 7.1%; Score 80.5; DB 7; Length 390;
Best Local Similarity 21.5%; Pred. No. 4.1;
Matches 39; Conservative 19; Mismatches 58; Indels 65; Gaps 8;

QY 50 PDPEPQAOVP-----HW---GMEVAGAPALRLQKSSDPLRERESV 90
DB 87 POKRRLSTPLTTSVTLTSSNNDDEWDGDDMDAPHESSAVHEGMDQDFLEQO--- 143
QY 91 LRREQVEAERRNALFPEVFSPTDEN--SDQNSRSSQASGITGSYS---VSESPFSP 145
DB 144 -----SLTSSVANGTYSRNTISERBERQSSSPASSYQNGRLVDSSSCP 190
QY 146 IHLHNVMTVEDPVDV-----APPGQRKEQWYAGINSDGINSEVLE 189
DB 191 LSLHGE-----GPGDSFTAKAKLEVFQKRHEPPQOPTKKP-----IGRDEPNNAFKE 241
QY 190 A 190

Db 242 A 242

RESULT 8

US-11-060-005-4
; Sequence 4, Application US/11060005
; Publication No. US20050260693A1
; GENERAL INFORMATION:

APPLICANT: Irtwin H. Gelman
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
; FILE REFERENCE: A30558-A-FWC-A-A 070156.0597
; CURRENT APPLICATION NUMBER: US/11/060,005
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 09/902,432
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 08/978,277
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: 08/665,401
; PRIOR FILING DATE: 1996-06-18
; PRIOR APPLICATION NUMBER: 08/635,121
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1596
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-060-005-4

Query Match 7.1%; Score 80; DB 7; Length 1596;
Best Local Similarity 18.5%; Pred. No. 26;
Matches 46; Conservative 37; Mismatches 93; Indels 72; Gaps 10;

QY 5 HLSBSSGK-----PLSTKQK-----ASKPRGCPQANGVWEXEYFRLRPL 49
DB 699 HRAERASDKKAGTDAVPASTQEQDAQSSSPBAGSPSEGEVSTWESFK---RLVT 754
QY 50 PDEPOAOVPHYWGMEVAGAPALRLQKSSDLEERESVLRBOEVAERRNALPPEVF 95
DB 755 PRKRSKSKLE-----EKADSSVEQLSTEIEFSREBSVSIKKFTIPGRK 799
QY 96 EVAERRNALPPEVFSPTPDENSQDN-----SRSSQASGIT-----GSYS 136
DB 800 KRADKQEQATVEDGPEINEDDNPVAVPLSEYNAVERKMAQNTLPLQLGAVY 859
QY 137 VSESPFSPHLSNVAMTVEDPVDAPPGRKKQWYAG--INSDGINSVLEAIVT 194
DB 860 VSEELSKTLVH--TVSVAVIDGTRAVTSVEERSPSWISASVTEPLEHTAGEMPVEEV 916
QY 195 RHKNMAE 202
DB 917 TEKDIIE 924

RESULT 9

US-11-072-512-2485
; Sequence 2485, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YUKI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO

APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2485
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2485

Query Match 7.0%; Score 79.5; DB 7; Length 287;
Best Local Similarity 24.6%; Pred. No. 3.5;
Matches 33; Conservative 11; Mismatches 39; Indels 51; Gaps 4;

QY 23 PRGCPQANGVWEXEYFRLRPL-----RFRAP 50
DB 4 PSRCPPAHSG--WQYITLALGINORSHOPSCFSSVSSEVSSYGFSTSVKSHIP 60
QY 51 DEPOAOVPHYWGMEVAGAPALRLQKSSDLEERESVLRBOEVAERRNALPPEVF 110
DB 61 KVPKQPLVH-----HPRMRTTKSPSKMLR-----PAELLEDLPPTKSTSV 104
QY 111 SPTPDENSQNSRS 124
DB 105 SEMPTENLEGHSPS 118

RESULT 10

US-10-821-234-905
; Sequence 905, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:

APPLICANT: Strache-Crain, Birgit
; APPLICANT: Andaman, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 905
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-905

Query Match 7.0%; Score 79.5; DB 6; Length 697;
Best Local Similarity 23.3%; Pred. No. 10;
Matches 70; Conservative 30; Mismatches 103; Indels 97; Gaps 18;

QY 6 LSSSGKPLSTKQASKPRGCP--QANGVWME---YFRLR-----LRR 48
DB 3 LADRTGAPAPGVTHSSQPRMAPQAPHQATPMDAHPFLTSPVWGLSRWGRRLGL 62
QY 49 APDEPOAO-----VPHY-WG-----WEVAP-----ALTLQ 75
DB 63 GPLEFWLVEAVKGAALVEAGLEGARPLPLPHPPWGRPEEEDSGSGPEDRETTGLK 122
QY 76 KSQS-----DL-----ERRESVLRRE-QEVAERRNALPPEVFSPTPDENSQDN- 121

Db 123 TSSSLPEAWGLDDDDGMYGEREATSPVPGGSGQFADGQAPLSBLIRTL-QGSDKNP 181
 Qy 122 SSSSSOASGITGSYSVSESPFPIHLHNSVAMTWEDPDSAPPGQKKEQWYA----- 175
 Db 182 GEXKABEEGVABEEGVNKS-YPPSIRRECCPAVEEDDEAV-----KKEARTSTALS 235
 Qy 176 -GINSDDGIN-----SEVLEAIRVTRHKNM-----AERWESRI-YASEEDP 215
 Db 226 PQSKGSTWVSCPGEENQATBEDRTERSKGARTSVSPRSSGSDPRSMWEYSGEASEEREK 295

RESULT 11
 US-11-072-512-3588
 / Sequence 3588, Application US/11072512
 / Publication No. US20060029945A1
 / GENERAL INFORMATION:
 / APPLICANT: ISOGAI, TAKAO
 / APPLICANT: SUGIYAMA, TOMOYASU
 / APPLICANT: OTSUKI, TETSUJI
 / APPLICANT: WAKAMATSU, AI
 / APPLICANT: SATO, HIROYUKI
 / APPLICANT: ISHII, SHIZUKO
 / APPLICANT: YAMAMOTO, JUN-ICHI
 / APPLICANT: ISONO, YUUKO
 / APPLICANT: HIO, YURI
 / APPLICANT: OTSUKA, KAORU
 / APPLICANT: NAGAI, KEIICHI
 / APPLICANT: IRIE, RYOTARO
 / APPLICANT: TAMECHIKA, ICHIRO
 / APPLICANT: SEKI, NAOHITO
 / APPLICANT: YOSHIKAWA, TSUTOMU
 / APPLICANT: OTSUKA, MOTYUKI
 / APPLICANT: NAGAHARI, KENJI
 / APPLICANT: MASUHO, YASUHIKO
 / TITLE OF INVENTION: Novel full length cDNA
 / FILE REFERENCE: 084335-0191
 / CURRENT APPLICATION NUMBER: US/11/072,512
 / CURRENT FILING DATE: 2005-03-07
 / PRIOR APPLICATION NUMBER: US 60/350,978
 / PRIOR FILING DATE: 2002-01-25
 / PRIOR APPLICATION NUMBER: JP 2001-379298
 / PRIOR FILING DATE: 2001-11-05
 / NUMBER OF SEQ ID NOS: 4096
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 3588
 / LENGTH: 312
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-11-072-512-3588

Query Match 7.0%; Score 79; DB 7; Length 312;
 Best Local Similarity 27.4%; Pred. No. 4.3;
 Matches 51; Conservative 16; Mismatches 79; Indels 40; Gaps 9;
 Qy 12 KPLSTQKQASKP-PRGCPQA-----NRGVWMEYFRLRPLRFAPDEPQQAQVPHVWGWZ 65
 Db 110 KPRRSDPAPAPFRLKPKLLAARRGQSVKPSAASIRPPLPRADTPGAPAPTPP-A 168
 Qy 66 VAGAPALRLQKSSQSD--LLERERESVLRREQ-----EVAEERNALFP----- 107
 Db 169 PAAPALPTSSSGPSALTLLEELQEAIRRAQLLPNGIDIDLEDQVEPDPPLPILDF 228
 Qy 108 -----EVSPPTPDENSDDNSSSQAAGITGSYSVSESPFPIHLHNSVAM---TVEDP 159
 Db 229 PGSEFVSPSPDESGLSVSSSLPSPTN-----SSSP--SPRDPDTSLDLWLEALSGCP 281
 Qy 160 VDSAPP 165
 Db 282 LGSQPF 287
 RESULT 12

US-10-770-726-46
 / Sequence 46, Application US/10770726
 / Publication No. US20050266409A1
 / GENERAL INFORMATION:
 / APPLICANT: Wyeth
 / APPLICANT: Brown, Eugene
 / APPLICANT: Liu, Wei
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
 / FILE REFERENCE: AM101079 (031896-010000)
 / CURRENT APPLICATION NUMBER: US/10/770,726
 / CURRENT FILING DATE: 2004-02-04
 / NUMBER OF SEQ ID NOS: 48640
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 46
 / LENGTH: 1271
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-770-726-46

Query Match 7.0%; Score 79; DB 6; Length 1271;
 Best Local Similarity 28.8%; Pred. No. 24;
 Matches 42; Conservative 22; Mismatches 54; Indels 28; Gaps 9;
 Qy 15 STKQKASKP-RG-CQANRGV-VRMWEYFRLRPLRFAPDEPQQAQVPHVWGWZVAGA 69
 Db 221 SSVGDASRPYPYGRSSSSCGVDGYEDAEINLPRFLKNDLIDANGSRP-----W----- 271
 Qy 70 PALRLQKSSQSD--LLERERESVLRREQVVAEERNALFP-EVFSPP-----TPD 115
 Db 272 PPLEYQPYQSIYVGWMEBEGKGPLRSQSTSEQRLLWMPRRSYSPRPFEDCGGYTPD 331
 Qy 116 ENSDONSRSSSQAAGITGSYSVSESP 141
 Db 332 CSSENMTLSSEEDFSSGQSSRVSPSP 357

RESULT 13
 US-11-087-099-4237
 / Sequence 4237, Application US/11087099
 / Publication No. US20060041961A1
 / GENERAL INFORMATION:
 / APPLICANT: Abad, Mark S. et al.
 / TITLE OF INVENTION: Genes and Uses for Plant Improvement
 / FILE REFERENCE: 38-21(53450)B EP
 / CURRENT APPLICATION NUMBER: US/11/087,099
 / CURRENT FILING DATE: 2005-03-22
 / NUMBER OF SEQ ID NOS: 12464
 / SEQ ID NO 4237
 / LENGTH: 706
 / TYPE: PRT
 / ORGANISM: Fusarium oxysporum
 US-11-087-099-4237

Query Match 6.9%; Score 78.5; DB 7; Length 706;
 Best Local Similarity 22.6%; Pred. No. 13;
 Matches 43; Conservative 26; Mismatches 62; Indels 59; Gaps 10;
 Qy 12 KPLSTQKQASKP-PRGCPQA-----POANGVWMEYFRLRPLRFAPDEPQQAQVPHVW 62
 Db 497 RPHSRSQLRDEANTRPQGTPIPNPKKNK-PVRMPQ-----GINSRNP----- 540
 Qy 63 GWEVAGAPALRLQKSSQSD--LLERERESVLRREQVVAEERNALFP-EVFSPTPDENSQNS 122
 Db 541 -WEALCTHKALKKLGATYIPDEYES-----RTAEERAAAGGGSFA-----DSHDN 588
 Qy 123 RSSQASGITGSYSVSESPFPIHLHNSVAM-----TVEDPVDASAPPGOR 166
 Db 589 RGSSSSIDPKRRYLPADPW-----HINVRWDTSAIKKAAVPGTPSSP--STPEGQ 640
 Qy 169 KKEQWYAGIN 178
 Db 641 HPKEPFVALH 650

RESULT 14

US-11-072-512-3514
; Sequence 3514, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3514
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3514

Query Match 6.9%; Score 78; DB 7; Length 419;
Best Local Similarity 20.3%; Pred. No. 7.7;
Matches 43; Conservative 25; Mismatches 60; Indels 84; Gaps 9;
QY 5 HUSSSGKPLSTKQEA-----SKPPGCGPOANGVWMEYFRLRLPRAPDEPQQAQV 58
DB 230 HLYSATGTITSTPTGTWTIPVYSAPRG-----DPQOOSI 264
QY 59 PHVW-----GMEVAGAP-ALRLKSSQSDLLERERS-----VLRRQEVAEERRN 103
DB 265 THIAIPQEAIVNAHVHSGSTALAAVK-----LEDDKEMGCTTSVVKNSHEEVQTLAN 318
QY 104 ALFPEVFSPPTDENSDONSRRSSQASGITGSYSVESPFSPHLSNVAMTV----- 156
DB 319 SLFPAGF-----MNGNHIHVAVQAVAGTY-----QNTAQTVHIWDPQ 357
QY 157 ---EDPVDSAPPGQRKKEQWTAGINPSDGIN 184
DB 358 QPQOQTPOGQTPPPPOOQOQOLQVTCSSVSEDL 389

RESULT 15

US-11-072-512-2709
; Sequence 2709, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO

; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2709
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2709

Query Match 6.9%; Score 78; DB 7; Length 571;
Best Local Similarity 34.9%; Pred. No. 11;
Matches 29; Conservative 8; Mismatches 32; Indels 14; Gaps 4;
QY 92 RREQVAEERRNALFPEVFSPPTDENSDONSRRSSQASGITGSYSVESPFSPHLSN 151
DB 348 RAGTSVIXER---IPF--SPSPAPSLSEHNRHPSQTSHTSS--SVSSSPSQMDHLERM 400
QY 152 VAMTVEDPVDSAP-----PQ 167
DB 401 EEVVGQIPIMKSPIDKIQLTTRQ 423

Search completed: March 3, 2006, 14:19:06
Job time: 11.2381 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 14:18:31 ; Search time 77.679 Seconds
(without alignments)
1216.113 Million cell updates/sec

Title: US-10-646-873-47

Perfect score: 215
Sequence: 1 MSPRHLSBSGKPLSTKCEA.....HKNAAMRNESRIYASEDD 215

Scoring table: OTIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 20

Total number of hits satisfying chosen parameters: 30

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database :

1: Geneseq_21:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	215	100.0	215	2 AAW79681	AAW79681 Human CS1
2	215	100.0	215	4 AAE07324	AAE07324 Human CS
3	215	100.0	215	6 ADA26384	ADA26384 Synthetic
4	215	100.0	215	8 ADN17177	ADN17177 CS198 pro
5	215	100.0	679	4 AAW79676	AAW79676 Human CS1
6	215	100.0	679	4 AAE07319	AAE07319 Human CS
7	215	100.0	679	4 AAW78590	AAW78590 Human pro
8	215	100.0	679	6 ADA26379	ADA26379 Predicted
9	215	100.0	679	8 ADN17172	ADN17172 CS198 pro
10	215	100.0	692	8 ADX97562	ADX97562 Pancreat
11	215	100.0	692	8 AAW79574	AAW79574 Human pro
12	170	82.3	679	7 ADG14341	ADG14341 Human NC2
13	170	79.1	679	4 AAG73987	AAG73987 Human col
14	60	27.9	172	4 ABO60042	ABO60042 Human gen
15	43	20.0	43	8 AAW79677	AAW79677 Synthetic
16	36	16.7	36	2 AAE07320	AAE07320 Human CS
17	36	16.7	36	6 ADA26380	ADA26380 Synthetic
18	36	16.7	36	6 ADN17173	ADN17173 CS198 pep
19	35	16.3	35	2 AAW79679	AAW79679 Synthetic
20	35	16.3	35	4 AAE07322	AAE07322 Human CS
21	35	16.3	35	6 ADA26382	ADA26382 Synthetic
22	35	16.3	35	8 ADN17175	ADN17175 CS198 pep
23	31	14.4	31	2 AAW79678	AAW79678 Synthetic
24	31	14.4	31	4 AAE07321	AAE07321 Human CS

25	31	14.4	31	6 ADA26381	ADA26381 Synthetic
26	31	14.4	31	8 ADN17174	ADN17174 CS198 pep
27	30	14.0	33	2 AAW79680	AAW79680 Synthetic
28	30	14.0	33	4 AAE07323	AAE07323 Human CS
29	30	14.0	33	6 ADA26383	ADA26383 Synthetic
30	30	14.0	33	8 ADN17176	ADN17176 CS198 pep

ALIGNMENTS

RESULT 1

ID AAW79681 standard; protein; 215 AA.

AAW79681;
11-JAN-1999 (first entry)

Human CS198 protein C-terminal.

XX Gastrintestinal tract; GI tract; cancer; disease; detection; CS198;
XX human; Predisposition; treatment; Barrett's oesophagus; gastric ulcer;
XX gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
XX pancreatitis.

XX Homo sapiens.

XX MO9844159-A1.

XX 08-OCT-1998.

XX 30-MAR-1998; 98WO-US006251.

XX 31-MAR-1997; 97US-00828855.

XX (ABBO) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX Pi Granados EN, Hayden M, Hodges SC, Klase KM, Kratochvil JD;
XX Pi Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI; 1998-542714/46.

XX New gastrintestinal polynucleotides, CS198, and their detection - used
XX PT for developing products for the diagnosis and treatment of
XX PT gastrintestinal disorders, e.g. cancers, gastric ulcer or gastritis.

XX Claim 26; Page 103; 127pp; English.

XX This sequence represents the C-terminal of the human CS198 protein which
XX CC is used in a method to detect the presence of a target CS198

XX CC polynucleotide in a test sample. The CS198 gene is useful as a marker for
XX CC gastrintestinal (GI) tract disorders. The methods and products can be
XX CC used in detecting, diagnosing, staging, monitoring, prognosticating,
XX CC preventing or treating, or determining the predisposition to diseases and
XX CC conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
XX CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative
XX CC colitis, and pancreatitis

XX SQ Sequence 215 AA;

Query Match 100.0%; Score 215; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.3e-208;

Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSPRHLSSESGKPLSTKCEAKXP	PPRCPCPQANRGVWMEYRRLPLPRAPDEQAQVPH	60
DB	1	MSPRHLSSESGKPLSTKCEAKXP	PPRCPCPQANRGVWMEYRRLPLPRAPDEQAQVPH	60
QY	61	VMGWEVAGAPALRLQSSQSDLLERERESVLRREOEVAERRNAALPPEVSPPTDENSQD	120	
DB	61	VMGWEVAGAPALRLQSSQSDLLERERESVLRREOEVAERRNAALPPEVSPPTDENSQD	120	

```
Oy 121 NSRSSSQASGITGSYSVSESPFSPHLSNVAMTVEDPVDAPPGQKKEQWYAGINPS 180
Db 121 NSRSSSQASGITGSYSVSESPFSPHLSNVAMTVEDPVDAPPGQKKEQWYAGINPS 180
Oy 181 DGINSEVLEAIRVTRHKNAMAEWRMESRIYASEDD 215
Db 181 DGINSEVLEAIRVTRHKNAMAEWRMESRIYASEDD 215

RESULT 2
AAE07324
ID AAE07324 standard; protein; 215 AA.
XX
XX AAE07324;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human CS 198 protein C-terminal portion.
XX
XX CS 198, gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
XX gastritis; Crohn's disease; ulcerative colitis; pancreatitis.
XX Barrett's oesophagus; gene therapy; drug screening; human.
XX
XX Homo sapiens.
XX
XX US2001010904-A1.
XX
XX 02-AUG-2001.
XX
XX 30-MAR-1998; 98US-00050516.
XX
XX 31-MAR-1997; 97US-00828855.
XX
XX (BILL/) BILLINGEL P A.
XX (COHE/) COHEN M.
XX (COLP/) COLPITTS T L.
XX (FRIE/) FRIEDMAN P N.
XX (GORD/) GORDON J.
XX (GRAN/) GRANADOS E N.
XX (HAYD/) HAYDEN M.
XX (HODG/) HODGES S C.
XX (KLAS/) KLAAS M R.
XX (KRAT/) KRATOCHVIL J D.
XX (ROBE/) ROBERTS-RAPP L.
XX (RUSSE/) RUSSELL J C.
XX (STRO/) STROUPE S D.
XX
XX Billengel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
XX Granados EN, Hayden M, Hodges SC, Klaas MR, Kratochvil JD,
XX Roberts-Rapp L, Russell JC, Stroupe SD;
XX
XX WPI; 2001-496163/54.
XX
XX Detecting the presence of target CS 198 polynucleotide, useful for
XX detecting or diagnosing diseases of the gastrointestinal tract, comprises
XX contacting test sample with at least one CS 198-specific polynucleotide.
XX
XX Claim 17; Page 52-53; 68pp; English.
XX
XX The invention relates to a method of detecting the presence of a target
XX CS 198 polynucleotide comprising contacting the test sample with at least
XX one CS 198-specific polynucleotide. The method is useful for detecting
XX diseases of the gastrointestinal (GI) tract organs, particularly cancer.
XX The CS 198 polynucleotides, polypeptides and antibodies are useful for
XX detecting, diagnosing, staging, monitoring, prognosticating, preventing,
XX treating or determining predisposition to diseases and conditions of the
XX GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
XX ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
XX polypeptides are useful as standards or reagents in diagnostic
XX immunoassays, as components or as target sites for various therapies.
XX Antibodies directed against at least one epitope contained within these
XX polypeptides are useful as delivery agents for therapeutic agents, in
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CC diagnostic tests and for screening for conditions or diseases associated
CC with CS 198, particularly cancer. Monoclonal antibodies may also be used
CC for the generation of chimeric antibodies for therapeutic use. The CS 198
CC polynucleotide is also useful in gene therapy and drug screening. The
CC method of the invention provides an alternative, non-surgical diagnostic
CC method capable of detecting early stage GI tract disease such as cancer.
CC The present sequence is C-terminal portion of human CS 198 polypeptide
XX
XX Sequence 215 AA;
XX
XX Query Match 100.0%; Score 215; DB 4; Length 215;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-208;
XX Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 1 MSPRHLSESSGKPTSTKQASKPPRGCPQANRGVVRWYFRLRPRAPDEPQAOVPH 60
Db 1 MSPRHLSESSGKPTSTKQASKPPRGCPQANRGVVRWYFRLRPRAPDEPQAOVPH 60
Oy 61 VMGWEVAGAPALRLQKSSDLERERESVLRQEVAEERRNALPFEVFSPTPDENSQ 120
Db 61 VMGWEVAGAPALRLQKSSDLERERESVLRQEVAEERRNALPFEVFSPTPDENSQ 120
Oy 121 NSRSSSQASGITGSYSVSESPFSPHLSNVAMTVEDPVDAPPGQKKEQWYAGINPS 180
Db 121 NSRSSSQASGITGSYSVSESPFSPHLSNVAMTVEDPVDAPPGQKKEQWYAGINPS 180
Oy 181 DGINSEVLEAIRVTRHKNAMAEWRMESRIYASEDD 215
Db 181 DGINSEVLEAIRVTRHKNAMAEWRMESRIYASEDD 215

RESULT 3
ADA26384
ID ADA26384 standard; protein; 215 AA.
XX
XX ADA26384;
XX
XX 20-NOV-2003 (first entry)
XX
XX Synthetic peptide based on CS198 protein #5.
XX
XX CS198; cancer diagnosis; cancer staging; cancer monitoring;
XX cancer prognosticating; cancer prevention; cancer;
XX gastrointestinal tract disorder; gene therapy.
XX
XX Synthetic.
XX
XX US2003082619-A1.
XX
XX 01-MAY-2003.
XX
XX 23-OCT-2002; 2002US-00278547.
XX
XX 31-MAR-1997; 97US-00828855.
XX
XX 30-MAR-1998; 98US-00050516.
XX
XX (BILL/) BILLINGEL P A.
XX (COHE/) COHEN M.
XX (COLP/) COLPITTS T L.
XX (FRIE/) FRIEDMAN P N.
XX (GORD/) GORDON J.
XX (GRAN/) GRANADOS E N.
XX (HAYD/) HAYDEN M A.
XX (HODG/) HODGES S C.
XX (KLAS/) KLAAS M R.
XX (KRAT/) KRATOCHVIL J D.
XX (ROBE/) ROBERTS-RAPP L.
XX (RUSSE/) RUSSELL J C.
XX (STRO/) STROUPE S D.
XX
XX Billengel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
XX Granados EN, Hayden MA, Hodges SC, Klaas MR, Kratochvil JD,
XX Roberts-Rapp L, Russell JC, Stroupe SD;
```

XX WPI; 2003-596961/56.

DR Detecting the presence of a target CS198 polynucleotide in a test sample
XX PT compares the sample with a CS198 specific polynucleotide and
PT detecting the presence of the target CS198 polynucleotide in the test
sample.

PS Claim 52; Page 52; 67pp; English.

XX The invention describes a method of detecting the presence of a target
CC CS198 polynucleotide in a test sample. The method comprises contacting
CC the test sample with at least one CS198 specific polynucleotide or its
CC complement, and detecting the presence of the target CS198 polynucleotide
CC in the test sample, where the CS198-specific polynucleotide has at least
CC 50% identity to a polynucleotide having any of the 27 fully defined
CC sequences of 34-2894 bp (SI-27) given in the specification, or their
CC fragments or complements. The composition and methods are useful in
CC diagnosing, staging, monitoring, prognosticating, preventing or treating,
CC or determining the predisposition of an individual to, diseases and
CC conditions of the gastrointestinal tract, e.g. cancer and in gene
CC therapy. This is the amino acid sequence of a synthetic peptide based on
CC the predicted human CS198 protein sequence derived from the CS198
CC consensus sequence shown in seq id 27.

CC Sequence 215 AA;

XX Query Match 100.0%; Score 215; DB 6; Length 215;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-208; Indels 0; Gaps 0;
XX Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRHLSESSGKPLSTKQKASKPRGCPQANNGVWMEYFRLRPLFRAPDEPQQAQVPH 60
DB 1 MSPRHLSESSGKPLSTKQKASKPRGCPQANNGVWMEYFRLRPLFRAPDEPQQAQVPH 60

QY 61 VNGWEVAGAPALRLQKSSDILLERREBSVLRBOEVAERNNALFPEVFSPTPENSDQ 120
DB 61 VNGWEVAGAPALRLQKSSDILLERREBSVLRBOEVAERNNALFPEVFSPTPENSDQ 120

QY 121 NSRSSQASGIGTGSYSVSSPPFSPHLSNVAMTVEEDVDSAPGQRKKEQWYAGINPS 180
DB 121 NSRSSQASGIGTGSYSVSSPPFSPHLSNVAMTVEEDVDSAPGQRKKEQWYAGINPS 180

QY 181 DGINSEVLAIKRTYTRHKNAARWESRIYASEED 215
DB 181 DGINSEVLAIKRTYTRHKNAARWESRIYASEED 215

RESULT 4
ADN17177
ID ADN17177 standard; protein; 215 AA.

XX ADN17177;
XX 17-JUN-2004 (first entry)

XX CS198 protein #2.
XX Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.

XX Unidentified.
XX US2004043406-A1.

XX 04-MAR-2004.
XX 22-AUG-2003; 2003US-00646873.

XX 31-MAR-1997; 97US-00828855.
XX 30-MAR-1998; 98US-00050516.

XX (BILL/) BILLINGEL P A.
XX (COHE/) COHEN M.

PA (COLP/) COLPITS T L.
PA (FRIE/) FRIEDMAN P N.

PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.

PA (HAYD/) HAYDEN M A.
PA (HODG/) HODGES S C.

PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.

PA (RUS/) RUSSELL J C.
PA (STRO/) STROUPE S D.

XX Billingsel PA, Cohen M, Colpits TL, Friedman PN, Gordon J;
XX Granados EN, Hayden MA, Hodges SC, Klass MR, Kratochvil JD;
XX Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI; 2004-313754/29.

XX Diagnosing diseases such as cancer of the gastrointestinal tract, by
XX detecting aberrant expression or activity of the CS198 polypeptide, and
XX associated treatment methods.

XX Claim 17; SEQ ID NO 47; 67pp; English.

XX The invention relates to reagents and methods for detecting diseases of
XX the gastrointestinal (GI) tract. The method involves detecting the
XX presence of target CS198 polynucleotide in the test sample. The methods
XX and compositions of the present invention are useful for the diagnosis,
XX prevention and/or treatment of diseases or conditions associated with
XX aberrant expression or activity of the CS198 polypeptide, such as cancer
XX of the gastrointestinal tract. These are also useful in gene therapy. The
XX present sequence is a CS198 protein used to illustrate the method of the
XX invention.

QY 1 MSPRHLSESSGKPLSTKQKASKPRGCPQANNGVWMEYFRLRPLFRAPDEPQQAQVPH 60
DB 1 MSPRHLSESSGKPLSTKQKASKPRGCPQANNGVWMEYFRLRPLFRAPDEPQQAQVPH 60

QY 61 VNGWEVAGAPALRLQKSSDILLERREBSVLRBOEVAERNNALFPEVFSPTPENSDQ 120
DB 61 VNGWEVAGAPALRLQKSSDILLERREBSVLRBOEVAERNNALFPEVFSPTPENSDQ 120

QY 121 NSRSSQASGIGTGSYSVSSPPFSPHLSNVAMTVEEDVDSAPGQRKKEQWYAGINPS 180
DB 121 NSRSSQASGIGTGSYSVSSPPFSPHLSNVAMTVEEDVDSAPGQRKKEQWYAGINPS 180

QY 181 DGINSEVLAIKRTYTRHKNAARWESRIYASEED 215
DB 181 DGINSEVLAIKRTYTRHKNAARWESRIYASEED 215

RESULT 5
AAW79676
ID AAW79676 standard; protein; 679 AA.

XX AAW79676;
XX 11-JAN-1999 (first entry)

XX Human CS198 protein.

XX Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
XX human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
XX gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
XX pancreaticitis.

XX Homo sapiens.

XX MO9844159-A1.
XX 08-OCT-1998.
XX 30-MAR-1998; 98WO-US006251.
XX 31-MAR-1997; 97US-00828855.
XX (ABBO) ABBOTT LAB.
XX Billing-Medel PA, Cohen M, Colpitta TL, Friedman PN, Gordon J;
XX Granados EN, Hayden M, Hodges SC, Klas MR, Kratochvil JD;
XX Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 1998-542714/46.
XX New gastrointestinal polynucleotides, CS198, and their detection - used
XX for developing products for the diagnosis and treatment of
XX gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
XX Claim 26; Page 100-102; 127pp; English.
XX This sequence represents the human CS198 protein which is used in a
XX method to detect the presence of a target CS198 polynucleotide in a test
XX sample. The CS198 gene is useful as a marker for gastrointestinal (GI)
XX tract disorders. The methods and products can be used in detecting,
XX diagnosing, staging, monitoring, prognosticating, preventing or treating,
XX or determining the predisposition to diseases and conditions of the GI
XX tract, such as GI tract cancer, Barrett's oesophagus, gastric ulcer,
XX gastritis, leiomyoma, polyps, Crohn's disease, ulcerative colitis, and
XX pancreatitis
XX Sequence 679 AA;
SQ

Query Match 100.0%; Score 215; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.1e-208;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSPRHLSGSGKPLSTQKASKPPRGCPQANRGVVRMEYFLRLRFRAPDEPOAQVPH 60
Db 465 MSPRHLSGSGKPLSTQKASKPPRGCPQANRGVVRMEYFLRLRFRAPDEPOAQVPH 524
Oy 61 VMGWEVAGAPALRLQKSSDLERERSVLRROEVAERBNALFPVFSPPTDENSDQ 120
Db 525 VMGWEVAGAPALRLQKSSDLERERSVLRROEVAERBNALFPVFSPPTDENSDQ 584
Oy 121 NSRSSSQASGITGYSVSESPFPIHLSNVAMVTEVPVDSAPPGQRKKEQWYAGINPS 180
Db 585 NSRSSSQASGITGYSVSESPFPIHLSNVAMVTEVPVDSAPPGQRKKEQWYAGINPS 644
Oy 181 DGINSEVLEAIRVTRHKNAEMERMSRIYASEDD 215
Db 645 DGINSEVLEAIRVTRHKNAEMERMSRIYASEDD 679

RESULT 6
AAE07319
ID AAE07319 standard; protein; 679 AA.

XX AAE07319;
XX 06-NOV-2001 (first entry)
XX Human CS 198 protein.
XX CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
XX gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
XX Barrett's oesophagus; gene therapy; drug screening; human.
XX Homo sapiens.
XX Key Location/Qualifiers

FT Misc-difference 353 /note="Encoded by CGGN"
XX US2001010904-A1.
XX 02-AUG-2001.
XX 30-MAR-1998; 98US-00050516.
XX 31-MAR-1997; 97US-00828855.
XX (BILL/) BILLINGEL P A.
XX (COHE/) COHEN M.
XX (COLP/) COLPITTS T L.
XX (FRIE/) FRIEDMAN P N.
XX (GORD/) GORDON J.
XX (GRAN/) GRANADOS E N.
XX (HAYD/) HAYDEN M.
XX (HODG/) HODGES S C.
XX (KLAS/) KLAS M R.
XX (KRAT/) KRATOCHVIL J D.
XX (ROBE/) ROBERTS-RAPP L.
XX (RUSS/) RUSSELL J C.
XX (STRO/) STROUPE S D.
XX Billingel PA, Cohen M, Colpitta TL, Friedman PN, Gordon J;
XX Granados EN, Hayden M, Hodges SC, Klas MR, Kratochvil JD;
XX Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 2001-496163/54.
XX N-PSDB; AAD13637.
XX Detecting the presence of target CS 198 polynucleotide, useful for
XX detecting or diagnosing diseases of the gastrointestinal tract, comprises
XX contacting test sample with at least one CS 198-specific polynucleotide.
XX Claim 17; Page 49-51; 68pp; English.

XX The invention relates to a method of detecting the presence of a target
XX CS 198 polynucleotide comprising contacting the test sample with at least
XX one CS 198-specific polynucleotide. The method is useful for detecting
XX diseases of the gastrointestinal (GI) tract organs, particularly cancer.
XX The CS 198 polynucleotides, polypeptides and antibodies are useful for
XX detecting, diagnosing, staging, monitoring, prognosticating, preventing
XX or determining predisposition to diseases and conditions of the
XX GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,
XX ulcerative colitis, pancreatitis and Barrett's oesophagus. The CS 198
XX polypeptides are useful as standards or reagents in diagnostic
XX immunoassays, as components or as target sites for various therapies.
XX Antibodies directed against at least one epitope contained within these
XX polypeptides are useful as delivery agents for therapeutic agents, in
XX diagnostic tests and for screening for conditions or diseases associated
XX with CS 198, particularly cancer. Monoclonal antibodies may also be used
XX for the generation of chimeric antibodies for therapeutic use. The CS 198
XX polynucleotide is also useful in gene therapy and drug screening. The
XX method of the invention provides an alternative, non-surgical diagnostic
XX method capable of detecting early stage GI tract disease such as cancer.
XX The present sequence is human CS 198 polypeptide
XX Sequence 679 AA;
SQ

Query Match 100.0%; Score 215; DB 4; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.1e-208;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSPRHLSGSGKPLSTQKASKPPRGCPQANRGVVRMEYFLRLRFRAPDEPOAQVPH 60
Db 465 MSPRHLSGSGKPLSTQKASKPPRGCPQANRGVVRMEYFLRLRFRAPDEPOAQVPH 524
Oy 61 VMGWEVAGAPALRLQKSSDLERERSVLRROEVAERBNALFPVFSPPTDENSDQ 120
Db 525 VMGWEVAGAPALRLQKSSDLERERSVLRROEVAERBNALFPVFSPPTDENSDQ 584

XX Rosenthal A, Pilarsky C, Dahl E, Specht T, Brummendorf T;
 PI Lichtner R, Staub E, Roepcke S, Li X;
 XX MPI, 2004-768082/76.
 DR N-PsDB; ADX97491.

PT New nucleic acid differentially expressed in pancreatic tumor tissue, for
 PT use as diagnostic agents and in screening for therapeutic agents.
 XX
 PS Claim 2; SEQ ID NO 110; 28pp; German.

XX The invention relates to a novel human nucleic acid sequence of the
 CC pancreas and its encoded protein. The invention further comprises:
 CC proteins and peptides, preferably isolated, that contain a sequence
 CC encoded by the novel nucleic acid; and methods for diagnosis and
 CC treatment of pancreatic cancer, using a substance that inhibits or binds
 CC to the protein or its DNA, including: an antisense oligonucleotide, short
 CC interfering RNA or ribozyme directed against the pancreatic protein, an
 CC organic molecule, particularly having a molecular weight below 5000,
 CC especially 300, that binds to the pancreatic DNA, an aptamer or
 CC (monoclonal) antibody, preferably human or humanized, that binds to the
 CC pancreatic DNA, or an anti-idiotypic antibody raised against the
 CC monoclonal antibody, any of which may be derivatized with a reporter
 CC group, cytotoxic compound, immunostimulant and/or radioisotope. The novel
 CC human pancreatic proteins and their encoding DNA have cytostatic
 CC activity. The novel sequences are useful for inhibiting transcription
 CC and/or expression of genes and proteins associated with pancreatic
 CC cancer. This sequence represents one of the novel human pancreatic
 CC proteins of the invention. Note: This sequence is not shown in the
 CC specification, it has been electronically downloaded from a DVD-ROM
 CC provided with this specification by the European Patent Office.

XX Sequence: 692 AA;

Query Match 100.0%; Score 215; DB 8; Length 692;
 Best Local Similarity 100.0%; Pred. No. 9.3e-208;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRHLSSESGKPLSTKQESKPPRCGPQANRGVWMEYFRLLPLFRAPDEQQAQVPH 60
 DB 478 MSPRHLSSESGKPLSTKQESKPPRCGPQANRGVWMEYFRLLPLFRAPDEQQAQVPH 517
 QY 61 VMGMEVAGAPALRLQSSQSDLLERRESVLRREQVAEERRNALPPEVFSPTDENSDQ 120
 DB 538 VMGMEVAGAPALRLQSSQSDLLERRESVLRREQVAEERRNALPPEVFSPTDENSDQ 597
 QY 121 NSRSSSQASGITGSYSVSESPFPIHLNSNVAMTVEDPVDASAPGQRKKEQYAGI 180
 DB 598 NSRSSSQASGITGSYSVSESPFPIHLNSNVAMTVEDPVDASAPGQRKKEQYAGI 657
 QY 181 DGINSVLEAIRVTRHKNAAERWESRIYASEBD 215
 DB 658 DGINSVLEAIRVTRHKNAAERWESRIYASEBD 692

RESULT 11

AAAT9574
 ID AAM79574 standard; protein; 672 AA.

XX AAM79574;

XX 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 3220.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KM vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
 KM tissue growth factor; immunomodulatory; cancer; leukemia;
 KM nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

PN WO200157190-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US004098.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX 20-JUN-2000; 2000US-00598075.

XX 19-JUL-2000; 2000US-00620325.

XX 01-SEP-2000; 2000US-00654936.

XX 15-SEP-2000; 2000US-00663561.

XX 30-OCT-2000; 2000US-00693325.

XX 30-NOV-2000; 2000US-00728422.

XX (HYSB-) HYSEQ INC.

XX Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX MPI; 2001-476283/51.

XX N-PsDB; AAK52707.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.

XX Claim 20; Page 288; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78823-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccine or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication

XX Sequence: 672 AA;

Query Match 82.3%; Score 177; DB 4; Length 672;
 Best Local Similarity 100.0%; Pred. No. 2e-169;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRHLSSESGKPLSTKQESKPPRCGPQANRGVWMEYFRLLPLFRAPDEQQAQVPH 60
 DB 458 MSPRHLSSESGKPLSTKQESKPPRCGPQANRGVWMEYFRLLPLFRAPDEQQAQVPH 517
 QY 61 VMGMEVAGAPALRLQSSQSDLLERRESVLRREQVAEERRNALPPEVFSPTDENSDQ 120
 DB 518 VMGMEVAGAPALRLQSSQSDLLERRESVLRREQVAEERRNALPPEVFSPTDENSDQ 577
 QY 121 NSRSSSQASGITGSYSVSESPFPIHLNSNVAMTVEDPVDASAPGQRKKEQYAGI 177
 DB 578 NSRSSSQASGITGSYSVSESPFPIHLNSNVAMTVEDPVDASAPGQRKKEQYAGI 634

RESULT 12

ADG14341
 ID ADG14341 standard; protein; 679 AA.

XX ADG14341;

XX 26-FEB-2004 (first entry)

XX Human NC2.

XX Human; NC1; NC2; NC3; PHH; pancreas beta-cell; insulin; antidiabetic;

KM neuroprotective.
XX
OS Homo sapiens.
XX MO2003078631-A1.
XX
PD 25-SEP-2003.
XX
PE 06-MAR-2003; 2003MO-JP002620.
XX
PR 15-MAR-2002; 2002JP-00071592.
XX
PA (KANF) KANEKA CORP.
XX
PI Niwa H, Yamashita K;
XX
DR WPI; 2003-767524/72.
DR N-PSDB; ADG14344.
XX
PT Familial persistent hyperinsulinemic hypoglycemia of infancy (PHI)
PT patient-expressed genes for detecting and screening e.g. proliferative
PT insulin-producing cells in treatment of PHI.
XX
PS Claim 1; SEQ ID NO 2; 34pp; Japanese.
XX
CC The present invention relates to human NCI, NC2 and NC3 proteins and
CC coding sequences (ADG14340-ADG14345). The coding sequences are useful for
CC detecting and screening proliferative insulin-producing cells as well as
CC differentiation and proliferation of such cells and their precursors as
CC analogous cells in treatment of e.g. PHI and diseases due to
CC differentiation/proliferation abnormality, diseases of the nervous system
CC and pancreas. The coding sequences are also useful as spontaneous
CC proliferation models of pancreas beta-cells. The novel genes NCI, NC2 and
CC NC3 were isolated from the pancreas of PHI patients, which were used in
CC testing for the detection of proliferative insulin-producing cells or
CC pancreas beta-cells by Northern analysis.
XX
SQ Sequence 679 AA;

Query Match 79.1%; Score 170; DB 7; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.4e-162;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MSPRLSSSGKPELTKQKASKPRGCGQANNGVVRWFYRLRLPRFAPDPQOAVPH 60
DB 465 MSPRLSSSGKPELTKQKASKPRGCGQANNGVVRWFYRLRLPRFAPDPQOAVPH 524
CY 61 VWGWEVAGAPALRLQKSSDLRRERESVLRQEQVAERENALFPEVFSPTPDNSDQ 120
DB 525 VWGWEVAGAPALRLQKSSDLRRERESVLRQEQVAERENALFPEVFSPTPDNSDQ 584
CY 121 NSRSSSQASGITGYSVSESPFPIHLHSNVAMTVEDPVSAPGQRKK 170
DB 585 NSRSSSQASGITGYSVSESPFPIHLHSNVAMTVEDPVSAPGQRKK 634

RESULT 13
AAG73987
ID AAG73987 standard; protein; 172 AA.
XX
AC AAG73987;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:4751.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma.
XX
OS Homo sapiens.
XX
PN MO200122920-A2.
XX

PD 05-APR-2001.
XX
XX 28-SEP-2000; 2000MO-US026524.
PE
XX 29-SEP-1999; 99US-0157137P.
PR
XX 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA,
XX
DR WPI; 2001-235357/24.
DR N-PSDB; AAH33418.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 11; Page 6550-6551; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patient's own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B. at
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC
XX
SQ Sequence 172 AA;

Query Match 27.9%; Score 60; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 7.1e-52;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 99 EERNALFPEVFSPTPDNSQNSRSSQASGITGYSVSESPFPIHLHSNVAMTVED 158
DB 56 EERNALFPEVFSPTPDNSQNSRSSQASGITGYSVSESPFPIHLHSNVAMTVED 115

RESULT 14
ABO60042
ID ABO60042 standard; protein; 43 AA.
XX
AC ABO60042;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon protein #6276.
XX
KW Human; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
PN US2003194704-A1.
XX
PD 16-OCT-2003.
XX
PE 03-APR-2002; 2002US-00029386.
PR
XX 03-APR-2002; 2002US-00029386.
XX
PA (PENN/) PENN S G.

PA (RANK/) RANK D R.
 PA (HANK/) HANZEL D K.
 XX Penn SG, Rank DR, Hanzel DK;
 XX WPI, 2004-119264/12.
 DR
 XX New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 PS
 XX Claim 45; SEQ ID NO 33676; 80bp; English.
 XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above). The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=2030194704
 CC
 SQ Sequence 43 AA;
 Query Match 20.0%; Score 43; DB 8; Length 43;
 Best Local Similarity 100.0%; Pred. No. 3e-35;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 131 ITGSSVSESPPSPHHSNVAWTVEDPVDSAPPGORKKEQW 173
 DB 1 ITGSSVSESPPSPHHSNVAWTVEDPVDSAPPGORKKEQW 43
 RESULT 15
 AAW79677
 ID AAW79677 standard; protein; 36 AA.
 AC AAW79677;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Synthetic CS198 derived peptide #1.
 XX
 KW Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
 KW human; predileposition; treatment; Barrett's oesophagus; gastric ulcer;

KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
 KW pancreaticitis.
 XX
 OS Synthetic.
 XX
 PN WO9844159-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98WO-US006251.
 XX
 PR 31-MAR-1997; 97US-00828855.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PV, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Katochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 DR WPI, 1998-542714/46.
 XX
 PT New gastrointestinal polynucleotides, CS198, and their detection - used
 PT for developing products for the diagnosis and treatment of
 PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
 PS
 XX Claim 26; Page 102; 127pp; English.
 XX
 CC AAW79677-W79680 are synthetic CS198 derived peptide fragments which are
 CC used in a method to detect the presence of a target human CS198
 CC polynucleotide in a test sample. The CS198 gene is useful as a marker for
 CC gastrointestinal (GI) tract disorders. The methods and products can be
 CC used in detecting, diagnosing, staging, monitoring, prognosticating,
 CC preventing or treating, or determining the predisposition to diseases and
 CC conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
 CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative
 CC colitis, and pancreaticitis
 CC
 SQ Sequence 36 AA;
 Query Match 16.7%; Score 36; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3e-28;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSPRHLSSESGKPLSTKQASKPPGCCPQANGVVR 36
 DB 1 MSPRHLSSESGKPLSTKQASKPPGCCPQANGVVR 36
 RESULT 16
 AAE07320
 ID AAE07320 standard; peptide; 36 AA.
 XX
 AC AAE07320;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human CS 198 peptide #1.
 XX
 DE CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
 KW gastritis; Crohn's disease; ulcerative colitis; pancreaticitis;
 KW Barrett's oesophagus; gene therapy; drug screening; human.
 XX
 OS Homo sapiens.
 XX
 PN US2001010904-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 30-MAR-1998; 98US-00050516.
 XX
 PR 31-MAR-1997; 97US-00828855.
 XX
 PA (BILL/) BILLINGEL P A.


```

XX OS Unidentified.
XX PN US2004043406-A1.
XX PD 04-MAR-2004.
XX PF 22-AUG-2003; 2003US-00646873.
XX PR 31-MAR-1997; 97US-00828855.
XX PR 30-MAR-1998; 98US-00050516.
XX PA (BILL/) BILLINGEL P A.
XX PA (COHE/) COHEN M.
XX PA (COLP/) COLPITTS T L.
XX PA (FRIE/) FRIEDMAN P N.
XX PA (GORD/) GORDON J.
XX PA (GRAN/) GRANADOS E N.
XX PA (HAYD/) HAYDEN M A.
XX PA (HODG/) HODGES S C.
XX PA (KLAS/) KLAS M R.
XX PA (KRAT/) KRATOCHVIL J D.
XX PA (ROBE/) ROBERTS-RAPP L.
XX PA (RUS/) RUSSELL J C.
XX PA (STRO/) STROUPE S D.
XX PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
XX PI Granados EN, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD,
XX PI Roberts-Rapp L, Russell JC, Stroupe SD,
XX DR WPI; 2004-313754/29.
XX PT Diagnosing diseases such as cancer of the gastrointestinal tract, by
XX PT detecting aberrant expression or activity of the CS198 polypeptide, and
XX PT associated treatment methods.
XX PS Claim 17; SEQ ID NO 45; 67pp; English.
XX CC The invention relates to reagents and methods for detecting diseases of
XX CC the gastrointestinal (GI) tract. The method involves detecting the
XX CC presence of target CS198 polynucleotide in the test sample. The methods
XX CC and compositions of the present invention are useful for the diagnosis,
XX CC prevention and/or treatment of diseases or conditions associated with
XX CC aberrant expression or activity of the CS198 polypeptide, such as cancer
XX CC of the gastrointestinal tract. These are also useful in gene therapy. The
XX CC present sequence is a CS198 peptide used to illustrate the method of the
XX CC invention.
XX SQ Sequence 35 AA;

Query Match 16.3%; Score 35; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 3e-27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 ALPEVFSPTPDNSDQNSRSSQASGITGSYSVS 138
DB 1 ALPEVFSPTPDNSDQNSRSSQASGITGSYSVS 35

RESULT 23
AAW79678
ID AAW79678 standard; protein, 31 AA.
XX AC AAW79678;
XX DT 11-JAN-1999 (first entry)
XX DE Synthetic CS198 derived peptide #2.
XX KM Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
XX KM human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
XX KM gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
XX KM pancreatitis.

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XX OS Synthetic.
XX PN WO9844159-A1.
XX PD 08-OCT-1998.
XX PF 30-MAR-1998; 98WO-US006251.
XX PR 31-MAR-1997; 97US-00828855.
XX PA (ABBO ) ABBOTT LAB.
XX PI Billings-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
XX PI Granados EN, Hayden M, Hodges SC, Kلاس MR, Kratochvil JD,
XX PI Roberts-Rapp L, Russell JC, Stroupe SD,
XX DR WPI; 1998-542714/46.
XX PT New gastrointestinal polynucleotides, CS198, and their detection - used
XX PT for developing products for the diagnosis and treatment of
XX PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
XX PS Claim 26; Page 102; 127pp; English.
XX CC AAW79677-W79680 are synthetic CS198 derived peptide fragments which are
XX CC used in a method to detect the presence of a target human CS198
XX CC polynucleotide in a test sample. The CS198 gene is useful as a marker for
XX CC gastrointestinal (GI) tract disorders. The methods and products can be
XX CC used in detecting, diagnosing, staging, monitoring, prognosticating,
XX CC preventing or treating, or determining the predisposition to diseases and
XX CC conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
XX CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative
XX CC colitis, and pancreatitis
XX SQ Sequence 31 AA;

Query Match 14.4%; Score 31; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 RLOXSQSDLLERERSVLRBOEVAERRN 103
DB 1 RLOXSQSDLLERERSVLRBOEVAERRN 31

RESULT 24
AAE07321
ID AAE07321 standard; peptide; 31 AA.
XX AC AAE07321;
XX DT 06-NOV-2001 (first entry)
XX DE Human CS 198 peptide #2.
XX KM CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
XX KM gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
XX KM Barrett's oesophagus; gene therapy; drug screening; human.
XX OS Homo sapiens.
XX PN US2001010904-A1.
XX PD 02-AUG-2001.
XX PF 30-MAR-1998; 98US-00050516.
XX PR 31-MAR-1997; 97US-00828855.
XX PA (BILL/) BILLINGEL P A.
XX PA (COHE/) COHEN M.
XX PA (COLP/) COLPITTS T L.

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OS Unidentified.
 XX US2004043406-A1.
 XX
 XX PD 04-MAR-2004.
 XX
 XX PF 22-AUG-2003; 2003US-00646873.
 XX
 XX PR 31-MAR-1997; 97US-00828855.
 XX PR 30-MAR-1998; 98US-00050516.
 XX
 XX PA (BILL/) BILLINGEL P A.
 XX PA (COHE/) COHEN M.
 XX PA (COLP/) COLPITTS T L.
 XX PA (FRIE/) FRIEDMAN P N.
 XX PA (GORD/) GORDON J.
 XX PA (GRAN/) GRANADOS E N.
 XX PA (HAYD/) HAYDEN M A.
 XX PA (HODG/) HODGES S C.
 XX PA (KLAS/) KLAS M R.
 XX PA (KRAT/) KRATOCHVIL J D.
 XX PA (ROBE/) ROBERTS-RAPP L.
 XX PA (RUSSE/) RUSSELL J C.
 XX PA (STROU/) STROUPE S D.
 XX
 XX PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 XX PI Granados EM, Hayden MA, Hodges SC, Kلاس MR, Kratochvil JD;
 XX PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 XX DR WPI; 2004-313754/29.
 XX
 XX PT Diagnosing diseases such as cancer of the gastrointestinal tract, by
 XX PT detecting aberrant expression or activity of the CS198 polypeptide, and
 XX PT associated treatment methods.
 XX
 XX PS Claim 17; SEQ ID NO 44; 67pp; English.
 XX
 XX CC The invention relates to reagents and methods for detecting diseases of
 XX CC the gastrointestinal (GI) tract. The method involves detecting the
 XX CC presence of target CS198 polynucleotide in the test sample. The methods
 XX CC and compositions of the present invention are useful for the diagnosis,
 XX CC prevention and/or treatment of diseases or conditions associated with
 XX CC aberrant expression or activity of the CS198 polypeptide, such as cancer
 XX CC of the gastrointestinal tract. These are also useful in gene therapy. The
 XX CC present sequence is a CS198 peptide used to illustrate the method of the
 XX CC invention.
 XX
 XX SQ Sequence 31 AA;
 XX
 XX Query Match 14.4%; Score 31; DB 8; Length 31;
 XX Best Local Similarity 100.0%; Pred. No. 2.9e-23;
 XX Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 73 RLQKSGSSDLLRRRESVLRREQVAAERRN 103
 XX |||||
 XX 1 RLQKSGSSDLLRRRESVLRREQVAAERRN 31
 XX
 XX RESULT 27
 XX AAW79680
 XX ID AAW79680 standard; protein; 33 AA.
 XX
 XX AC AAW79680;
 XX
 XX DT 11-JAN-1999 (first entry)
 XX
 XX DE Synthetic CS198 derived peptide #4.
 XX
 XX KM Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
 XX KM human; predilection; treatment; Barrett's oesophagus; gastric ulcer;
 XX KM gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
 XX KM pancreatitis.
 XX

OS Synthetic.
 XX W09844159-A1.
 XX
 XX PD 08-OCT-1998.
 XX
 XX PF 30-MAR-1998; 98MO-US006251.
 XX
 XX PR 31-MAR-1997; 97US-00828855.
 XX
 XX PA (ABBOT) ABBOTT LAB.
 XX
 XX PI Billings-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 XX PI Granados EM, Hayden M, Hodges SC, Kلاس MR, Kratochvil JD;
 XX PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 XX DR WPI; 1998-542714/46.
 XX
 XX PT New gastrointestinal polynucleotides, CS198, and their detection - used
 XX PT for developing products for the diagnosis and treatment of
 XX PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
 XX
 XX PS Claim 26; Page 103; 127pp; English.
 XX
 XX CC AAW79677-W79680 are synthetic CS198 derived peptide fragments which are
 XX CC used in a method to detect the presence of a target human CS198
 XX CC polynucleotide in a test sample. The CS198 gene is useful as a marker for
 XX CC gastrointestinal (GI) tract disorders. The methods and products can be
 XX CC used in detecting, diagnosing, staging, monitoring, prognosticating,
 XX CC preventing or treating, or determining the predisposition to diseases and
 XX CC conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
 XX CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative
 XX CC colitis, and pancreatitis
 XX
 XX SQ Sequence 33 AA;
 XX
 XX Query Match 14.0%; Score 30; DB 2; Length 33;
 XX Best Local Similarity 100.0%; Pred. No. 3.1e-22;
 XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 160 VDSAPPQRRKKEQWYAGINPSDGINSEVLE 189
 XX |||||
 XX 4 VDSAPPQRRKKEQWYAGINPSDGINSEVLE 33
 XX
 XX RESULT 28
 XX AAE07323
 XX ID AAE07323 standard; peptide; 33 AA.
 XX
 XX AC AAE07323;
 XX
 XX DT 06-NOV-2001 (first entry)
 XX
 XX DE Human CS 198 peptide #4.
 XX
 XX KM CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;
 XX KM gastritis; Crohn's disease; ulcerative colitis; pancreatitis;
 XX KM Barrett's oesophagus; gene therapy; drug screening; human.
 XX
 XX OS Homo sapiens.
 XX
 XX XX US2001010904-A1.
 XX
 XX PD 02-AUG-2001.
 XX
 XX PF 30-MAR-1998; 98US-00050516.
 XX
 XX PR 31-MAR-1997; 97US-00828855.
 XX
 XX PA (BILL/) BILLINGEL P A.
 XX PA (COHE/) COHEN M.
 XX PA (COLP/) COLPITTS T L.
 XX PA (FRIE/) FRIEDMAN P N.
 XX

PA	(GORD//)	GORDON J.
PA	(GRAN//)	GRANDADOS E N.
PA	(HAYD//)	HAYDEN M.
PA	(KODG//)	KODGES S C.
PA	(KLAS//)	KLASS M R.
PA	(KRAT//)	KRATOCHVIL J D.
PA	(ROBE//)	ROBERTS-RAPP L.
PA	(RUSS//)	RUSSELL J C.
PA	(STRO//)	STROUPE S D.
XX		
PI	Billingel PA,	Cohen M, Colpitls TL, Friedman PN, Gordon J;
PI	Granados EN,	Hayden M, Hodges SC, Klaas MR, Kratochvil JD;
PI	Roberts-Rapp L,	Russell JC, Stroupe SD;
XX		
DR	WPI; 2001-496163/54.	
XX		
PT	Detecting the presence of target CS 198 polynucleotide, useful for	
PT	detecting or diagnosing diseases of the gastrointestinal tract, comprises	
PT	contracting test sample with at least one CS 198-specific polynucleotide.	
XX		
PS	Claim 17; Page 52; 66pp; English.	
XX		
CC	The invention relates to a method of detecting the presence of a target	
CC	CS 198 polynucleotide comprising contacting the test sample with at least	
CC	one CS 198-specific polynucleotide. The method is useful for detecting	
CC	diseases of the gastrointestinal (GI) tract organs, particularly cancer.	
CC	The CS 198 polynucleotides, polypeptides and antibodies are useful for	
CC	detecting, diagnosing, staging, monitoring, prognosticating, preventing,	
CC	treating or determining predisposition to diseases and conditions of the	
CC	GI tract such as cancer, gastric ulcer, gastritis, Crohn's disease,	
CC	ulcerative colitis, pancreatitis and Barrett's esophagus. The CS 198	
CC	polypeptides are useful as standards or reagents in diagnostic	
CC	immunoassays, as components or as target sites for various therapies.	
CC	Antibodies directed against at least one epitope contained within these	
CC	polypeptides are useful as delivery agents for therapeutic agents, in	
CC	diagnostic tests and for screening for conditions or diseases associated	
CC	with CS 198, particularly cancer. Monoclonal antibodies may also be used	
CC	for the generation of chimeric antibodies for therapeutic use. The CS 198	
CC	polynucleotide is also useful in gene therapy and drug screening. The	
CC	method of the invention provides an alternative, non-surgical diagnostic	
CC	method capable of detecting early stage GI tract disease such as cancer.	
CC	The present sequence is a peptide derived from human CS 198 polypeptide	
CC	consensus sequence	
CC		
XX		
SQ	Sequence 33 AA:	
XX		
Query Match	14.0%; Score 30; DB 4; Length 33;	
Best Local Similarity	100.0%; Pred. NO. 3.le-22;	
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
OY	160 VDSAPPGQRKEQWYAGINPDSGINSEVLE 189	
DB		
4 VDSAPFGQRKEQWYAGINPDSGINSEVLE 33		
RESULT 29		
ID ADA26383		
ID ADA26383 standard; protein; 33 AA.		
XX ADA26383;		
XX AC		
XX DT 20-NOV-2003 (first entry)		
XX DE		
XX Synthetic peptide based on CS198 protein #4.		
XX CS198; cancer diagnosis; cancer staging; cancer monitoring;		
KM cancer prognosticating; cancer prevention; cancer;		
KM gastrointestinal tract disorder; gene therapy.		
XX OS		
XX Synthetic;		
XX FN US2003082619-A1.		
XX		

```

PD 01-MAY-2003.
XX
XX 23-OCT-2002; 2002US-00278547.
XX
XX 31-MAR-1997; 97US-00828855.
PR 30-MAR-1998; 98US-00050516.
XX
PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HAYD/) HAYDEN M A.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L.
PA (RUSS/) RUSSELL J C.
PA (STRO/) STROUPE S D.
XX
XX Billingel PA, Cohen M, Colpitts TU, Friedman PN, Gordon J;
PI Granados EN, Hayden MA, Hodges SC, Klaas MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
XX WPI; 2003-596961/56.
XX
XX Detecting the presence of a target CS198 polynucleotide in a test sample
XX comprises contacting the sample with a CS198 specific polynucleotide and
XX detecting the presence of the target CS198 polynucleotide in the test
XX sample.
XX
XX Claim 17; Page 52; 67pp; English.
XX
XX The invention describes a method of detecting the presence of a target
XX CS198 polynucleotide in a test sample. The method comprises contacting
XX the test sample with at least one CS198 specific polynucleotide or its
XX complement, and detecting the presence of the target CS198 polynucleotide
XX in the test sample, where the CS198-specific polynucleotide has at least
XX 50% identity to a polynucleotide having any of the 27 fully defined
XX sequences of 34-2894 bp (SI-27) given in the specification, or their
XX fragments or complements. The composition and methods are useful in
XX diagnosing, staging, monitoring, prognosticating, preventing or treating,
XX or determining the predisposition of an individual to, diseases and
XX conditions of the gastrointestinal tract, e.g. cancer and in gene
XX therapy. This is the amino acid sequence of a synthetic peptide based on
XX the predicted human CS198 protein sequence derived from the CS198
XX consensus sequence shown in seq id 27.
XX
XX Sequence 33 AA;
XX
XX Query Match 14.0%; Score 30; DB 6; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-22;
XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 160 VDSAPPGQRKKKEQWYAGINPSDGINSEYLE 189
XX |||||
XX 4 VDSAPPGQRKKKEQWYAGINPSDGINSEYLE 33
XX
XX RESULT 30
XX ADN17176
XX ID ADN17176 standard; peptide; 33 AA.
XX
XX ADN17176;
XX
XX 17-JUN-2004 (first entry)
XX
XX CS198 peptide #4.
XX
XX Gastrointestinal tract; GI tract; CS198; cancer; gene therapy.
XX
XX Unidentified.
XX

```


XX US200403406-A1.
 PN
 XX
 XX 04-MAR-2004.
 PD
 XX
 XX 22-AUG-2003; 2003US-00646873.
 PF
 XX
 XX 31-MAR-1997; 97US-00828855.
 PR
 XX 30-MAR-1998; 98US-00050516.
 PR
 XX
 PA (BILL/) BILLINGEL P A.
 PA (COHE/) COHEN M. T.
 PA (COLE/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HAYD/) HAYDEN M A.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAS M R.
 PA (KRAY/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUS/) RUSSELL J C.
 PA (STRO/) STROUPE S D.
 XX
 XX Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden MA, Hodges SC, KLAS MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI, 2004-313754/29.
 XX
 XX
 PT Diagnosing diseases such as cancer of the gastrointestinal tract, by
 PT detecting aberrant expression or activity of the CS198 polypeptide, and
 PT associated treatment methods.
 XX
 PS Claim 17, SEQ ID NO 46; 67pp; English.
 XX
 XX The invention relates to reagents and methods for detecting diseases of
 CC the gastrointestinal (GI) tract. The method involves detecting the
 CC presence of target CS198 polynucleotide in the test sample. The methods
 CC and compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of diseases or conditions associated with
 CC aberrant expression or activity of the CS198 polypeptide, such as cancer
 CC of the gastrointestinal tract. These are also useful in gene therapy. The
 CC present sequence is a CS198 peptide used to illustrate the method of the
 CC invention.
 CC
 SQ Sequence 33 AA;
 Query Match 14.0%; Score 30; DB 8; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.1e-22;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 160 VDSAPFGQRRKKEQWYAGINPSDGINSEYLE 189
 DB 4 VDSAPFGQRRKKEQWYAGINPSDGINSEYLE 33

Search completed: March 3, 2006, 14:24:32
 Job time : 77.679 secs

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OM protein - protein search, using sw model

Run on: March 3, 2006, 14:24:52 ; Search time 12.5056 Seconds
(without alignments)
1654.188 Million cell updates/sec

Title: US-10-646-873-47

Perfect score: 215
Sequence: 1 MSPRLSSSSGKPLSTKQEA.....HKMAERWESRIYASEED 215

Scoring table: OLIGO
Gapop-60.0, Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word-size: 20

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 500 summaries

Database: PIR 80:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	215	100.0	679	2 T00636	hypothetical prote

ALIGNMENTS

RESULT 1
T00636
hypothetical protein F21856.2 - human
C/Species: Homo sapiens (man)
C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C/Accession: T00636
R/Lamerdin, J.E.; McCreedy, P.M.; Skowronski, E.; Adamson, A.W.; Burkhardt-Schultz, K.; Grgescu, A.; Avila, J.; Liu, S.; Bruce, R.; Quan, G.; Montgomery, M.; Ow, D.; Nolan, M.; submitted to the EMBL Data Library, January 1998
A/Description: Sequence analysis of a 3.5 Kb contig in 19p13.3 between CDC34 and D19S342
A/Reference number: Z14195
A/Accession: T00636
A/Status: preliminary;
A/Molecule type: DNA
A/Residues: 1679 <LAM>
A/Trans-References: UNIPROT:Q81VT2; UNIPARC:UPI00000745CD; EMBL:AC004030; NID:g2804590;
C/Genetics:
A/Map position: 19p13.3
A/Intons: 594/1; 637/3; 650/3
A/Note: F21856_2

Query Match 100.0%; Score 215; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 7.5e-215;

Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSPRLSSSSGKPLSTKQEA	SKPPRGCPQANRGVYRWYFRLRPAPADPEQOAYPH	60
DB	465	MSPRLSSSSGKPLSTKQEA	SKPPRGCPQANRGVYRWYFRLRPAPADPEQOAYPH	524
QY	61	VGMWEVAGAPALRLQKSSD	LLERERESVLRREQVAERNNALFPEVFSPTPENSQ	120
DB	525	VGMWEVAGAPALRLQKSSD	LLERERESVLRREQVAERNNALFPEVFSPTPENSQ	584
QY	121	NSRSSQASGITGYSVSESP	FFSPILHNSVAMTVEPDVDSAPPQCKKQWYGINPS	180
DB	585	NSRSSQASGITGYSVSESP	FFSPILHNSVAMTVEPDVDSAPPQCKKQWYGINPS	644
QY	181	DGINSEVLEAIRVTRHKMA	ERWESRIYASEED	215
DB	645	DGINSEVLEAIRVTRHKMA	ERWESRIYASEED	679

Search completed: March 3, 2006, 14:30:52
Job time: 12.5056 secs

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OM protein - protein search, using sw model

Run on: March 3, 2006, 14:19:21 ; Search time 76.4765 Seconds

(without alignments)
1983.466 Million cell updates/sec

Title: US-10-646-873-47

Perfect score: 215

Sequence: 1 MSPRLSSSGKPLSTKQEA.....HNNAWERMESRIYASEED 215

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size: 20

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database: UniProt 05.80.*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215	100.0	679	1 CS021_HUMAN	O81YR2 homo sapien
2	48	22.3	685	1 CS021_PONPY	Q5R3H3 pongo pygma

ALIGNMENTS

RESULT 1
ID CS021_HUMAN STANDARD; PRT; 679 AA.
AC O81YR2;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Protein C19orf21.
GN Name=C19orf21;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
RC TISSUE=Brain, and Colon;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL: BC042125; AAH42125.1; -; mRNA.
CC EMBL: BC052236; AAH52236.1; -; mRNA.
CC PIR: T00636; T00636.
CC DR Ensembl: ENSG00000099812; Homo sapiens.
CC DR HGN: HGNC:27000; C19orf21.
CC KM Coiled coil.
CC FT COILED 545
CC FT COILED 569
CC FT COILED 589
CC FT COILED 599
CC FT COILED 609
CC FT COILED 619
CC FT COILED 629
CC FT COILED 639
CC FT COILED 649
CC FT COILED 659
CC FT COILED 669
CC FT COILED 679
CC FT COILED 689
CC FT COILED 699
CC FT COILED 709
CC FT COILED 719
CC FT COILED 729
CC FT COILED 739
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CC FT COILED 769
CC FT COILED 779
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CC FT COILED 979
CC FT COILED 989
CC FT COILED 999
CC FT COILED 1000

Query Match 100.0%; Score 215; DB 1; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.5e-212;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQEA...PPGPPQANGVWMEYFRLPRFRAPDPQQAQVPH 60
DB 465 MSPRLSSSGKPLSTKQEA...PPGPPQANGVWMEYFRLPRFRAPDPQQAQVPH 524
QY 61 VWGWEVAGAPALRLQKSSD...LRRERESVLRREOVAEERNAALFPEVSPPTPENSQ 120
DB 525 VWGWEVAGAPALRLQKSSD...LRRERESVLRREOVAEERNAALFPEVSPPTPENSQ 584
QY 121 NSRSSQASGITGSYSVSP...PFFSPHLSNVAWTEVDPSAPGQRKEQMYAGINS 180
DB 585 NSRSSQASGITGSYSVSP...PFFSPHLSNVAWTEVDPSAPGQRKEQMYAGINS 644
QY 181 DGINSEVLEAIRVTRKNA...MAERWESRIYASEED 215
DB 645 DGINSEVLEAIRVTRKNA...MAERWESRIYASEED 679

RESULT 2
ID CS021_PONPY STANDARD; PRT; 685 AA.
AC Q5R3H3;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Protein C19orf21 homolog.
GN Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
RC TISSUE=Kidney;
RX Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not
removed.

CC -----
DR EMBL; CR858675; CAH90887.1; -; mRNA.

KW Coiled coil.

FT COILED 551 575 Potential.
SQ SEQUENCE 685 AA; 75892 MW; A3A99F4343396E81 CRC64;

Query Match 22.3%; Score 48; DB 1; Length 685;
Best Local Similarity 100.0%; Pred. No. 5.5e-40;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 47 FRAPDEPQQAQVPHVWGWGVAGAPALRLQKSSQSDLERERESVLRRE 94
|||||

Db 517 FRAPDEPQQAQVPHVWGWGVAGAPALRLQKSSQSDLERERESVLRRE 564
|||||

Search completed: March 3, 2006, 14:29:55
Job time : 76.4765 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 3, 2006, 14:30:17 ; Search time 15.8725 Seconds
(without alignment)
1119.880 Million cell updates/sec

Title: US-10-646-873-47

Perfect score: 215
Sequence: 1 MSPRLSSSGKRLSTKQEA.....HKNAERWESRIYASEDD 215

Scoring: Gapop 60.0, Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size: 20

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database:

Issued Patents AA: *
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2: /cgn2_6/prodata/1/1aa/6.COMB.pep: *
3: /cgn2_6/prodata/1/1aa/H.COMB.pep: *
4: /cgn2_6/prodata/1/1aa/PCTUS.COMB.pep: *
5: /cgn2_6/prodata/1/1aa/RR.COMB.pep: *
6: /cgn2_6/prodata/1/1aa/beckfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215	100.0	215	2	US-09-050-516-47
2	215	100.0	215	2	US-10-278-547-47
3	215	100.0	679	2	US-09-050-516-42
4	215	100.0	679	2	US-10-278-547-42
5	36	16.7	36	2	US-09-050-516-43
6	36	16.7	36	2	US-10-278-547-43
7	35	16.3	35	2	US-09-050-516-45
8	35	16.3	35	2	US-10-278-547-45
9	31	14.4	31	2	US-09-050-516-44
10	31	14.4	31	2	US-10-278-547-44
11	30	14.0	33	2	US-09-050-516-46
12	30	14.0	33	2	US-10-278-547-46

ALIGNMENTS

RESULT 1
US-09-050-516-47
; Sequence 47, Application US/09050516
; Patent No. 6627414
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLETTIS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN

APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-47
Query Match 100.0%; Score 215; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.2e-202; Indels 0; Gaps 0;
Matches 215; Conservative 0; Mismatches 0;
QY 1 MSPRLSSSGKRLSTKQEA KPRGCPQANRGVMEYFRLLPLFRAPDEPQAOVPH 60
DB 1 MSPRLSSSGKRLSTKQEA KPRGCPQANRGVMEYFRLLPLFRAPDEPQAOVPH 60
QY 61 VMGMEVAGAPALRLQKSSQSDLLERRESVLRREQVAERERNAALPEVFSPTPDNSDQ 120
DB 61 VMGMEVAGAPALRLQKSSQSDLLERRESVLRREQVAERERNAALPEVFSPTPDNSDQ 120
QY 121 NSRSSQASGITTSYVSSESPFSPHLHSNVAVTWEDPVDASAPQORKKEQNYAGINPS 180
DB 121 NSRSSQASGITTSYVSSESPFSPHLHSNVAVTWEDPVDASAPQORKKEQNYAGINPS 180
QY 181 DGINSEVLEAIRVTRHKNAERWESRIYASEDD 215
DB 181 DGINSEVLEAIRVTRHKNAERWESRIYASEDD 215

RESULT 2
US-10-278-547-47
; Sequence 47, Application US/10278547
; Patent No. 6660834

GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-OCT-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-278-547-47
Query Match 100.0%; Score 215; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1,2e-202;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-42
Query Match 100.0%; Score 215; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 3,4e-202;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 585 NSRSSQASGITGYSVSESPPFSPIHLHSNVAWTVEDPVD SAPGQRKEQWYAGINPS 644
Qy 181 DGINSEVLBAIRVTRHKNAEMRWESRIYASEED 215
Db 645 DGINSEVLBAIRVTRHKNAEMRWESRIYASEED 679

RESULT 4

US-10-278-547-42

Sequence 42, Application US/10278547

Patent No. 6660834

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITTS, TRACEY L.

FRIEDMAN, PAULA N.

GORDON, JULIAN

GRANADOS, EDWARD N.

HAYDEN, MARK

HODGES, STEVEN C.

KCLASS, MICHAEL R.

KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSER: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547

FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065-US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 679 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6660834e

SEQUENCE DESCRIPTION: SEQ ID NO: 42:

US-10-278-547-42

Query Match 100.0%; Score 215; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 3,4e-202;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPHLSESSGKPLSTQKASKPRGCGPOANRGVVRWEYFLRLRLRRAPPEPOAOYVPH 60
Db 465 MSPHLSESSGKPLSTQKASKPRGCGPOANRGVVRWEYFLRLRLRRAPPEPOAOYVPH 524

Qy 61 VWGWEVAGAPALRLQKSSDLERERESVLRROEVAEBRRNALFPVEFSTPDENSQ 120
Db 525 VWGWEVAGAPALRLQKSSDLERERESVLRROEVAEBRRNALFPVEFSTPDENSQ 584
Qy 121 NSRSSQASGITGYSVSESPPFSPIHLHSNVAWTVEDPVD SAPGQRKEQWYAGINPS 180
Db 585 NSRSSQASGITGYSVSESPPFSPIHLHSNVAWTVEDPVD SAPGQRKEQWYAGINPS 644

RESULT 5

US-09-050-516-43

Sequence 43, Application US/09050516

Patent No. 6627414

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITTS, TRACEY L.

FRIEDMAN, PAULA N.

GORDON, JULIAN

GRANADOS, EDWARD N.

HAYDEN, MARK

HODGES, STEVEN C.

KCLASS, MICHAEL R.

KRATOCHVIL, JON D.

ROBERTS-RAPP, LISA

RUSSELL, JOHN C.

STROUPE, STEPHEN D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSER: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065-US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6627414e

US-09-050-516-43

Query Match 16.7%; Score 36; DB 2; Length 36;

Best Local Similarity 100.0%; Pred. No. 6.1e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQASKPRGCGPOANRNV 36
Db 1 MSPRLSSSGKPLSTKQASKPRGCGPOANRNV 36

RESULT 6

US-10-278-547-43

; Sequence 43, Application US/10278547

; Patent No. 6660834

; GENERAL INFORMATION:

; APPLICANT: BILLING-MEDEL, PATRICIA

; COHEN, MAURICE

; COLPITTS, TRACEY L.

; FRIEDMAN, PAULA N.

; GORDON, JULIAN

; GRANADOS, EDWARD N.

; HAYDEN, MARK

; HODGES, STEVEN C.

; KLAS, MICHAEL R.

; KRATOCHVIL, JON D.

; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

; FOR DETECTING DISEASES OF THE GASTROINTESTINAL

; TRACT

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Road

; CITY: Abbott Park

; STATE: IL

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/278,547

; FILING DATE: 23-Oct-2002

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/09/050,516

; FILING DATE: <Unknown>

; APPLICATION NUMBER: 08/828,855

; FILING DATE: 31-MAR-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Becker, Cheryl L.

; REGISTRATION NUMBER: 35,441

; REFERENCE/DOCKET NUMBER: 6065.US.P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 847/935-1729

; TELEFAX: 847/938-2623

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6660834e

; SEQUENCE DESCRIPTION: SEQ ID NO: 43:

; US-10-278-547-43

Query Match 16.7%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.1e-28;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQASKPRGCGPOANRNV 36
Db 1 MSPRLSSSGKPLSTKQASKPRGCGPOANRNV 36

RESULT 7

US-09-050-516-45

; Sequence 45, Application US/09050516

; Patent No. 6627414

; GENERAL INFORMATION:

; APPLICANT: BILLING-MEDEL, PATRICIA

; COHEN, MAURICE

; COLPITTS, TRACEY L.

; FRIEDMAN, PAULA N.

; GORDON, JULIAN

; GRANADOS, EDWARD N.

; HAYDEN, MARK

; HODGES, STEVEN C.

; KLAS, MICHAEL R.

; KRATOCHVIL, JON D.

; ROBERTS-RAPP, LISA

; APPLICANT: RUSSELL, JOHN C.

; APPLICANT: STROUPE, STEPHEN D.

; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

; FOR DETECTING DISEASES OF THE GASTROINTESTINAL

; TRACT

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Road

; CITY: Abbott Park

; STATE: IL

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/050,516

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/828,855

; FILING DATE: 31-MAR-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Becker, Cheryl L.

; REGISTRATION NUMBER: 35,441

; REFERENCE/DOCKET NUMBER: 6065.US.P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 847/935-1729

; TELEFAX: 847/938-2623

; TELEX:

; INFORMATION FOR SEQ ID NO: 45:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 35 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6627414e

; US-09-050-516-45

Query Match 16.3%; Score 35; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 5.7e-27;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 ALPEVPSPTDENSDQNSRSSQASGITGSYSVS 138
Db 1 ALPEVPSPTDENSDQNSRSSQASGITGSYSVS 35

RESULT 8

US-10-278-547-45

; Sequence 45, Application US/10278547

; Patent No. 6660834

GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065-US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-278-547-45

Query Match 16.3%; Score 35; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 5.7e-27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 ALPEVPSPTPDSNDNSRSSGASGITSYSYS 138
DB 1 ALPEVPSPTPDSNDNSRSSGASGITSYSYS 35

RESULT 9
US-09-050-516-44
Sequence 44, Application US/09050516
Patent No. 6627414
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065-US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-44

APPLICANT: GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STEIN, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065-US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-44

Query Match 14.4%; Score 31; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.2e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 RLOKSOSDILLERESVLRBOEVAEBERN 103
DB 1 RLOKSOSDILLERESVLRBOEVAEBERN 31

RESULT 10
US-10-278-547-44
Sequence 44, Application US/10278547
Patent No. 6660834
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065-US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-44

```
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-OCT-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6660834e
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-278-547-44

Query Match          14.4%; Score 31; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.2e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6627414e
US-09-050-516-46

Query Match          14.0%; Score 30; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.3e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 73 RLQKQSSDLRERESVLRQEVAAERRN 103
DB 1 RLQKQSSDLRERESVLRQEVAAERRN 31

RESULT 11
US-09-050-516-46
; Sequence 46, Application US/09050516
; Patent No. 6627414
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HAYDEN, MARK
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
; TITLE OF INVENTION: TRACT
; NUMBER OF SEQUENCES: 49
```

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QY 160 VDSAPPGQRKKEQWYAGINPSDGINSYLE 189
DB 4 VDSAPPGQRKKEQWYAGINPSDGINSYLE 33

RESULT 12
US-10-278-547-46
; Sequence 46, Application US/10278547
; Patent No. 6660834
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HAYDEN, MARK
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: KRATOCHVIL, JON D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
; TITLE OF INVENTION: TRACT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESS: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
```

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/      COMPUTER: IBM Compatible
/      OPERATING SYSTEM: DOS Windows Version 2.0
/      SOFTWARE: FASTSEQ for Windows Version 2.0
/      CURRENT APPLICATION DATA:
/      APPLICATION NUMBER: US/10/278,547
/      FILING DATE: 23-Oct-2002
/      CLASSIFICATION: <Unknown>
/      PRIOR APPLICATION DATA:
/      APPLICATION NUMBER: US/09/050,516
/      FILING DATE: <Unknown>
/      APPLICATION NUMBER: 08/828,855
/      FILING DATE: 31-MAR-1997
/      ATTORNEY/AGENT INFORMATION:
/      NAME: Becker, Cheryl L.
/      REGISTRATION NUMBER: 35,441
/      REFERENCE/DOCKET NUMBER: 6065,US.P1
/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE: 847/935-1729
/      TELEFAX: 847/938-2623
/      TELEX: <Unknown>
/      INFORMATION FOR SEQ ID NO: 46:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 33 amino acids
/      TYPE: amino acid
/      STRANDEDNESS: single
/      TOPOLOGY: linear
/      MOLECULE TYPE: No. 6660834e
/      SEQUENCE DESCRIPTION: SEQ ID NO: 46:
/      US-10-278-547-46

Query Match      14.0%; Score 30; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.3e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      160 VDSAPGCRKKEQWYAGINPSDGINSEVLE 189
DB      4 VDSAPGCRKKEQWYAGINPSDGINSEVLE 33

Search completed: March 3, 2006, 14:32:05
Job time : 16.8725 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 14:45:41 ; Search time 58.9206 Seconds
(without alignments)
1524.651 Million cell updates/sec

Title: US-10-646-873-47

Perfect score: 215
Sequence: 1 MSPRLSSSGSKPLSTKQEA.....HKNAWERESRIYASEEDD 215

Scoring Table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size: 20

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database : Published Applications AA.Main:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215	100.0	215	3	US-09-050-516-47
2	215	100.0	215	4	US-10-278-547-47
3	215	100.0	215	4	US-10-646-873-47
4	215	100.0	215	3	US-09-050-516-42
5	215	100.0	679	4	US-10-278-547-42
6	215	100.0	679	4	US-10-646-873-42
7	60	27.9	172	4	US-10-106-698-4761
8	43	20.0	43	4	US-10-029-386-33676
9	36	16.7	36	3	US-09-050-516-43
10	36	16.7	36	4	US-10-278-547-43
11	36	16.7	36	4	US-10-646-873-43
12	35	16.3	35	3	US-09-050-516-45
13	35	16.3	35	4	US-10-278-547-45
14	35	16.3	35	4	US-10-646-873-45
15	31	14.4	31	3	US-09-050-516-44
16	31	14.4	31	4	US-10-278-547-44
17	31	14.4	31	4	US-10-646-873-44
18	30	14.0	33	3	US-09-050-516-46
19	30	14.0	33	4	US-10-278-547-46
20	30	14.0	33	4	US-10-646-873-46

ALIGNMENTS

RESULT 1
US-09-050-516-47

Sequence 47, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILTING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050.516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-47
Query Match 100.0%; Score 215; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.1e-198;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGSKPLSTKQEA.....HKNAWERESRIYASEEDD 60
DB 1 MSPRLSSSGSKPLSTKQEA.....HKNAWERESRIYASEEDD 60
QY 61 VMGWEVAGAPALRLQKSSDILLERESVLRERQVAAERNNALPPEVFSPTDENSDQ 120
DB 61 VMGWEVAGAPALRLQKSSDILLERESVLRERQVAAERNNALPPEVFSPTDENSDQ 120
QY 121 NSRSSSQASGITGSYSVSSEPPSPITHLSNVAWTVEDPYDASAPQQRKKEQYAGINRS 180
DB 121 NSRSSSQASGITGSYSVSSEPPSPITHLSNVAWTVEDPYDASAPQQRKKEQYAGINRS 180
QY 181 DGINSEVLAIKIVTRHKNAWERESRIYASEEDD 215

DB 181 DGINSEVLEAIRVTRHKNAMAMERWESRITYASEDD 215

RESULT 2
US-10-278-547-47

; Sequence 47, Application US/10278547
; Publication No. US20030082619A1

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITTS, TRACEY L.

FRIEDMAN, PAULA N.

GORDON, JULIAN

GRANDOS, EDWARD N.

HAYDEN, MARK

HODGES, STEVEN C.

KLASS, MICHAEL R.

KRATOCHVIL, JON D.

TRACT

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESS: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547

FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065.US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. US20030082619A1e

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-10-278-547-47

Query Match 100.0%; Score 215; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.1e-198;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQASKPPRGCPQANRGVVRWEYFRLRLFRAPDEPQQAQVPH 60
DB 1 MSPRLSSSGKPLSTKQASKPPRGCPQANRGVVRWEYFRLRLFRAPDEPQQAQVPH 60
QY 61 VVGWVAGAPALRLKQSSDLERERESVLRQEVAEERNALFPVEVFSPTPENDQ 120
DB 61 VVGWVAGAPALRLKQSSDLERERESVLRQEVAEERNALFPVEVFSPTPENDQ 120

QY 121 NSRSSQASGTTGSYSVESPPFPIHSHNVATVEDPYDSAPPGQRKKEQWYAGINPS 180
DB 121 NSRSSQASGTTGSYSVESPPFPIHSHNVATVEDPYDSAPPGQRKKEQWYAGINPS 180

QY 181 DGINSEVLEAIRVTRHKNAMAMERWESRITYASEDD 215

DB 181 DGINSEVLEAIRVTRHKNAMAMERWESRITYASEDD 215

RESULT 3
US-10-646-873-47

; Sequence 47, Application US/10646873
; Publication No. US20040043406A1

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITTS, TRACEY L.

FRIEDMAN, PAULA N.

GORDON, JULIAN

GRANDOS, EDWARD N.

HAYDEN, MARK

HODGES, STEVEN C.

KLASS, MICHAEL R.

KRATOCHVIL, JON D.

TRACT

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESS: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/646,873

FILING DATE: 22-Aug-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: 30-MAR-1998

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065.US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. US20040043406A1e

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-10-646-873-47

Query Match 100.0%; Score 215; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.1e-198;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQASKPPRGCPQANRGVVRWEYFRLRLFRAPDEPQQAQVPH 60

Db 1 MSPRLSSSGKPLSTKQASKPPGCPQANRGVWMEYFRLRPLRFPAPDPPOQAVPH 60
Qy 61 VGMWEVACAPALRLQKSSDILLERERESVLRREQVAEERNALFPEVFSPTPENSQ 120
Db 61 VGMWEVACAPALRLQKSSDILLERERESVLRREQVAEERNALFPEVFSPTPENSQ 120
Qy 121 NSRSSQASGTTGTSVSESPFFSPHLSNVAMTVEDVPVDSAPPGQRKKEQWYAGINPS 180
Db 121 NSRSSQASGTTGTSVSESPFFSPHLSNVAMTVEDVPVDSAPPGQRKKEQWYAGINPS 180
Qy 181 DGINSEVLEAIRVTRHKNAEMERESRIYASEDD 215
Db 181 DGINSEVLEAIRVTRHKNAEMERESRIYASEDD 215

RESULT 4

US-09-050-516-42
Sequence 42, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065, US, P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-42

Query Match 100.0%; Score 215; DB 3; Length 679;
Best Local Similarity 100.0%; Pred. No. 1,7e-197;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQASKPPGCPQANRGVWMEYFRLRPLRFPAPDPPOQAVPH 60
Db 465 MSPRLSSSGKPLSTKQASKPPGCPQANRGVWMEYFRLRPLRFPAPDPPOQAVPH 524
Qy 61 VGMWEVACAPALRLQKSSDILLERERESVLRREQVAEERNALFPEVFSPTPENSQ 120
Db 525 VGMWEVACAPALRLQKSSDILLERERESVLRREQVAEERNALFPEVFSPTPENSQ 584
Qy 121 NSRSSQASGTTGTSVSESPFFSPHLSNVAMTVEDVPVDSAPPGQRKKEQWYAGINPS 180
Db 585 NSRSSQASGTTGTSVSESPFFSPHLSNVAMTVEDVPVDSAPPGQRKKEQWYAGINPS 644
Qy 181 DGINSEVLEAIRVTRHKNAEMERESRIYASEDD 215
Db 645 DGINSEVLEAIRVTRHKNAEMERESRIYASEDD 679

RESULT 5

US-10-278-547-42
Sequence 42, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065, US, P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-278-547-42

Query Match
Best Local Similarity 100.0%; Score 215; DB 4; Length 679;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQKASKEPRGCPQANRGVVRWEYFRLRLFRAPDEPQQAQVPH 60
DB 465 MSPRLSSSGKPLSTKQKASKEPRGCPQANRGVVRWEYFRLRLFRAPDEPQQAQVPH 524

QY 61 VMGWEVAGAPALRLQKQSSDILLERERESVLRREQVAAERRNALFPEVFSPTDENSDQ 120
DB 525 VMGWEVAGAPALRLQKQSSDILLERERESVLRREQVAAERRNALFPEVFSPTDENSDQ 584

QY 121 NSRSSQASGITGYSYSVSESPFPIHLSNVAMTVEDPVDASAPPGQKKEQWYAGINPS 180
DB 585 NSRSSQASGITGYSYSVSESPFPIHLSNVAMTVEDPVDASAPPGQKKEQWYAGINPS 644

QY 181 DGINSEVLEAIRVTRHKNAAMERWESRIYASEED 215
DB 645 DGINSEVLEAIRVTRHKNAAMERWESRIYASEED 679

RESULT 6
US-10-646-873-42
Sequence 42, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/10/646,873
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-646-873-42

Query Match
Best Local Similarity 100.0%; Score 215; DB 4; Length 679;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRLSSSGKPLSTKQKASKEPRGCPQANRGVVRWEYFRLRLFRAPDEPQQAQVPH 60
DB 465 MSPRLSSSGKPLSTKQKASKEPRGCPQANRGVVRWEYFRLRLFRAPDEPQQAQVPH 524

QY 61 VMGWEVAGAPALRLQKQSSDILLERERESVLRREQVAAERRNALFPEVFSPTDENSDQ 120
DB 525 VMGWEVAGAPALRLQKQSSDILLERERESVLRREQVAAERRNALFPEVFSPTDENSDQ 584

QY 121 NSRSSQASGITGYSYSVSESPFPIHLSNVAMTVEDPVDASAPPGQKKEQWYAGINPS 180
DB 585 NSRSSQASGITGYSYSVSESPFPIHLSNVAMTVEDPVDASAPPGQKKEQWYAGINPS 644

QY 181 DGINSEVLEAIRVTRHKNAAMERWESRIYASEED 215
DB 645 DGINSEVLEAIRVTRHKNAAMERWESRIYASEED 679

RESULT 7
US-10-106-698-4761
Sequence 4761, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 4761
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (55)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (116)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-4761

Query Match
Best Local Similarity 100.0%; Score 60; DB 4; Length 172;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 EERNALFPEVFSPTDENSDQNSRSSQASGITGYSYSVSESPFPIHLSNVAMTVED 158
DB 56 EERNALFPEVFSPTDENSDQNSRSSQASGITGYSYSVSESPFPIHLSNVAMTVED 115

RESULT 8
US-10-029-386-33676
Sequence 33676, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEWICA-X-2 US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Locating Engine vers. 1.1
SEQ ID NO 33676
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004030.1
US-10-029-386-33676
Query Match 20.0%; Score 43; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 2,3e-33;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 131 TCGSYSVSSPPSPPHLSNVAWTVEDVDSDAPPCQKKEQW 173
DB 1 TCGSYSVSSPPSPPHLSNVAWTVEDVDSDAPPCQKKEQW 43
RESULT 9
US-09-050-516-43
Sequence 43, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPF, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUBE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065, US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010904A1e
US-09-050-516-43
Query Match 16.7%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPRLSSSGKPLSTKQKASKPPRCQPNRGVVR 36
DB 1 MSPRLSSSGKPLSTKQKASKPPRCQPNRGVVR 36
RESULT 10
US-10-278-547-43
Sequence 43, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065, US.P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-278-547-43

Query Match 16.7% Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQKASKPPRCGCPQANRGVVR 36
Db 1 MSPRLSSSGKPLSTKQKASKPPRCGCPQANRGVVR 36

RESULT 11
US-10-646-873-43
Sequence 43, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-AUG-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-646-873-43

Query Match 16.7% Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPRLSSSGKPLSTKQKASKPPRCGCPQANRGVVR 36
Db 1 MSPRLSSSGKPLSTKQKASKPPRCGCPQANRGVVR 36

RESULT 12
US-09-050-516-45
Sequence 45, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20010010904A1e
US-09-050-516-45

Query Match 16.3%; Score 35; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 9e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 ALPPEVPSPTPDNSDQNSRSSQASGITGSYSVS 138
DB 1 ALPPEVPSPTPDNSDQNSRSSQASGITGSYSVS 35

RESULT 13
US-10-278-547-45

; Sequence 45, Application US/10278547
; Publication No. US20030082619A1
; GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITTS, TRACEY L.

FRIEDMAN, PAULA N.

GORDON, JULIAN

GRANDOS, EDWARD N.

HAYDEN, MARK

HODGES, STEVEN C.

KLASS, MICHAEL R.

KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: PastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,547

FILING DATE: 23-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065, US, P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. US20030082619A1

SEQUENCE DESCRIPTION: SEQ ID NO: 45:

QY 104 ALPPEVPSPTPDNSDQNSRSSQASGITGSYSVS 138

Query Match 16.3%; Score 35; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 9e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 ALPPEVPSPTPDNSDQNSRSSQASGITGSYSVS 35

RESULT 14
US-10-646-873-45

; Sequence 45, Application US/10646873
; Publication No. US20040043406A1
; GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

COHEN, MAURICE

COLPITTS, TRACEY L.

FRIEDMAN, PAULA N.

GORDON, JULIAN

GRANDOS, EDWARD N.

HAYDEN, MARK

HODGES, STEVEN C.

KLASS, MICHAEL R.

KRATOCHVIL, JON D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: PastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/646,873

FILING DATE: 22-Aug-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE: 30-MAR-1998

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065, US, P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. US20040043406A1

SEQUENCE DESCRIPTION: SEQ ID NO: 45:

QY 104 ALPPEVPSPTPDNSDQNSRSSQASGITGSYSVS 138

Query Match 16.3%; Score 35; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 9e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 ALPPEVPSPTPDNSDQNSRSSQASGITGSYSVS 35

RESULT 15
US-09-050-516-44

; Sequence 44, Application US/09050516
; Patent No. US20010010904A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HAYDEN, MARK
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLAS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
; TITLE OF INVENTION: TRACT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/050,516
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,855
; FILING DATE: 31-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6065.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20010010904A1e
; US-09-050-516-44

Query Match 14.4%; Score 31; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.6e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 RLOKSOSDILREBSVLRREQEVAERRN 103
DB 1 RLOKSOSDILREBSVLRREQEVAERRN 31

RESULT 16
US-10-278-547-44
; Sequence 44, Application US/10278547
; Publication No. US20030082619A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.

; FRIEDMAN, PAULA N.
; GORDON, JULIAN
; GRANADOS, EDWARD N.
; HAYDEN, MARK
; HODGES, STEVEN C.
; KLAS, MICHAEL R.
; KRATOCHVIL, JON D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE GASTROINTESTINAL
; TRACT
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,547
; FILING DATE: 23-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/050,516
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/828,855
; FILING DATE: 31-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6065.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20030082619A1e
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
; US-10-278-547-44

Query Match 14.4%; Score 31; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.6e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 RLOKSOSDILREBSVLRREQEVAERRN 103
DB 1 RLOKSOSDILREBSVLRREQEVAERRN 31

RESULT 17
US-10-646-873-44
; Sequence 44, Application US/10646873
; Publication No. US20040043406A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HAYDEN, MARK
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLAS, MICHAEL R.

KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065, US, P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-646-873-44
Query Match 14.4%; Score 31; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 5,6e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 73 RLOKSSDILLERESVLRQEVAEERN 103
1 RLOKSSDILLERESVLRQEVAEERN 31
RESULT 18
US-09-050-516-46
Sequence 46, Application US/09050516
Patent No. US20010010904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065, US, P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20010010904A1e
US-09-050-516-46
Query Match 14.0%; Score 30; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 5,4e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 4 VDSAPGRKKEOWYAGINPSDGINSEVLE 33
RESULT 19
US-10-278-547-46
Sequence 46, Application US/10278547
Publication No. US20030082619A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HAYDEN, MARK
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,547
FILING DATE: 23-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030082619A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-278-547-46

Query Match 14.0%; Score 30; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 VDSAPGQRKKKEQWYAGINPSDGINSEVLE 189
DB 4 VDSAPGQRKKKEQWYAGINPSDGINSEVLE 33

RESULT 20
US-10-646-873-46
Sequence 46, Application US/10646873
Publication No. US20040043406A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/646,873
FILING DATE: 22-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20040043406A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-646-873-46

Query Match 14.0%; Score 30; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 VDSAPGQRKKKEQWYAGINPSDGINSEVLE 189
DB 4 VDSAPGQRKKKEQWYAGINPSDGINSEVLE 33

Search completed: March 3, 2006, 14:50:28
Job time : 58.9206 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 3, 2006, 14:46:31, Search time 6.0123 Seconds
(without alignments)
715.215 Million cell updates/sec

Title: US-10-646-873-47

Perfect score: 215
Sequence: 1 MSPRHLSSESGKPLSTKQEA.....HKMAAEKRWESRIYASEED 215

Scoring method: OMCO
Gapop 60.0, Gapext 60.0

Searched: 135346 seqs, 20000420 residues

Word size: 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database:

- Published Applications_AA_New.*
- 1: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep.*
 - 2: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep.*
 - 3: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep.*
 - 5: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pep.*
 - 6: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pep.*
 - 7: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB.pep.*
 - 8: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: March 3, 2006, 14:50:59
Job time: 6.0123 secs

THIS PAGE BACK (15010)